

- (iii) NUMBER OF SEQUENCES: 534
(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US/08/936,165A
(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 396 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCCTGA TAATTATTTN GCGATATAAG TCGTCAACGT ACCAATATTA TCAATAGTCA
60
CTTTANATNC ATCACCTGGT TGGAAAAATT TAGGTGGTTG AATACCTGNA CCANCGTCTG
120
AGTGGTGTAC CAGTTGCAAT AATATCTCCC GGATGNAGTG CAACACATCA TGACATCACT
180
ACTATTACAA CAACATATAT CAGAATCAAG TCGCCAGNGT NACCATCTTG TCTAATTTCA
240
TNGTGACCTC NTGTAACAAT ATTCACATTT CCAGGTAATG GCAGTNCGTC TTGAGNAANG
300
ATTTAAGGAC CCATNGGNTN ANCCNNCAGT TAACTNNGT GGTA AAAATG CTTGATCTTG
360
NTCACTGCGG GCTNTGAGAT CAAGTGATAT CGTAAA
396

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 696 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCCCTCTATT GCTTNNTTGA TACGTTTCTG TTCTTTAAAT CCAAGATATA CCGCAAACAA
60
CATAACAAGA ATGAAACCTA TTATTTGAAT AGGTATTAAT CCATACCATA ATTCATTGAC
120
ACTTTTGGCT TTAAACACTG CAGCTACACG AGCCATTGGA CCTCCCCAAG GTNCCATGTT
180
CATAATCGCC GCGCTTAATG CTAATAGTAA AATCAATAAA TATTTATTCA TATTTAACGC
240
TTTATATAAA GGTAATAATG CAGGAATAGA AAGCAAAAAT GTTACCGCAC CGGCCCCATC
300
TAATTGGGCT ATTGTGCCAA TTAAAGCTGT CATTGCACAG ACAATGACGA CATTGCCTCG
360
TGTCATTAAT ATTAAGCGTT TGACAAGCGG CTTGAATAAA CCACTATCGT TCATGATGCC
420
AAAGAAAATA ATGGCANAGA TAAACATAAT AACAACTNG ATGACNTGAT CTAACCTTTT
480
AGCAAAAAAT CCAACCAAAT CTGNCACACT ATATCCTAAA ATCATTGCCC CTAAGCAAGG
540
TATGATTGTC ATACCTACAN CTGGATTTAT CTTNNIGGGC AATGAGTAAN CCTACAAC TG

600
AAATAATAAT NATGNGCCCC ATCACTGTCA ACCACATATT ATCACTATTC ATTTATTTTC
660
TCCCTCCACT TNCAATACAA TTTACATTCA CCCCCC
696

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCCTTGNC AA TTCATNGGGT TTTCTGTTTA ATATTTTTCG GGTTCTAANC CCACCATATC
60
AAGTGATTCA TCTACTCTTT TATCAATATC TTTTCTTCC CACTTTTTC A TTTGTGCCAC
120
TTTGTGCAAA AATTTCTTTT GGGCCTCAA TGGGGNATAA TTCCAATCTN CCTCCAANAC
180
GTANCCAATA TCCCAACGCA TTTGTAATA CTGGATAATC ACTTATTGGT TTATCTTTAA
240
AATAAATATA ACCTTCACTT AAGTGAATGA GTCGATTAAT CATTTTAAAT GTCGTAGTTT
300
TTCCACAACC TGAAGGTCCA ATTAGCACAA AAAATTCACC CTCATTAATA TTGAAACTAA
360
TGTTATCGAC AGCAACATGT TTGCCATAAC GCTTAGTTAC ATTTTAAAC TTAATCACTT
420
TGCCACCTCT TTTTCTCTCA TAGCATAAAA CCGAGATTAT ATGTATGTAT TCCCTATTTA
480
ACCACGTTTA TTACAATTTT CAAATTTAAA TGATTTATCC TTGAACTTTT TTAACAAAAT
540
AATGAATAAT AGGTAATCTC CAGTTAAGAA ATAGTGTTAT TTTACCTT
588

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGGCAGNCT TTANAATTAT TTNAATGATG ATTAGCAATG CATATACGAT TAATTCGATT
60
ATGGNTTATA TCTNNATTGA TTAANTCACT TATATTTTAC AAGTGTGTTG CTTTGGAGCG
120
TCAACGATGC TATCACATAT TACGGCATAT GAAATTTTAT CTGAAATTCG NAAAAAATTA
180
GCTCAAAAAT TAATGCGCCT CCCTTTAGGN GTAGTGGAAT CTAAGAAAAT AGGTGAATTA
240
AAAAATATAT TTGNCGATAA GGTTGAAACA ATAGAATTAC CTTTAGCACA TATGATTTCCT
300

GAAGTTATNG GAAACTTACT TGTGGCAGCT GCTATCTTCT TATACATAAT GNTCATNGAT
360
TGGCGTATTG GATAGGTGNC TTANTAGATA ACGATACCAA TNTCAATTTN CGCTTCTAAA
420
AAAGTNATGT CTTGGATTTT AATGAGANAA TTTGCTGGAC AAANTGAAAT CCAATTTNTN
480
TTTTTNATTT GNCGNAATGG
500

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 808 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACCCTGTTGT CCCCNGGGGT CAATAGACCC CGACATACTT TNNGGCTTCT GAAAATAAAA
60
TTTCAGGNNC GACTTTTAAA GATGGACGTC GATGTCGACT AATGTGATGA CNGCCTTTCA
120
TCTTTTTTAAA AANTCATTAA TTTCCCTTCT TGTTTAAANAC GTACATANAA GAAATACGCA
180
TACGGTACTA ATAAAATAGT TGTATATGTT GCGTGTGTTA ATAATAATAC ACCGATTAAT
240
TCAGGAATGA TGTTTAAGAA GTAATTTGGG TGTTTTGGTA ATTTTATATA ATCCAGATTT
300
AATAATAGGA TGTTTAGGTA AAATGAATAA TTTTAATGTC CAAATACCAC CTAAAGTTTT
360
AATAACCATA AATAACATGA TATAAGCAAA GATTAATATA ACTAAGCCAA TACCATTTGC
420
AAAGCTAAAT GTATCTTTAT TAATAAATGC CTCTACACCA GCCAATACAT AAATTAAAAC
480
GTGTGTTATT GCTAAAACT TCGAATTTTT AACGCCATAT TCAACTGCAC CGTCTGCTTT
540
TAATTGTTTT GAGTGANTAA TACATATCTT TAAGCTGACA AGTCTGATAC AGAGAAAGAT
600
AAGTAATATA GATAGANTCA TGATGTCCTC CGTCATTATG TCATATGTAT AAGCGTTGAT
660
TTTGACAACA TAAAGTATTT TATAGATAAA ACTTGTCACA TACTATTAAC TATTTATTAA
720
TTTTAGTACA TAAATATGTT TCTAAGTATG TGTTTATGTT CAGTATTTTG GATAATTTAA
780
TAATTTTAAG GATATTAAGC GCTTACAG
808

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 806 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGGAATTCTT ATTCATTTAT AAAATAATAT TCGTATGATT TGATGTTTTA ATTAGTCCAC
 60
 CATTTTCGATT TGTGCTATGA TAATAGTGTT AAGTAAACGA AATAAGGGGT TATTAAGTTG
 120
 AATAACTACA AAATTGGCCA ACATATCAAG GTGCGTGTA CTGGTATTCA NCCATACGGT
 180
 GCGTTTGTTG AGACCCCTAA TCATACTGAA GGACTGATTC ATATATCAGA AATTATGGAT
 240
 GACTACGTTT ATAATTTGAA GAAATTTCTA TCAGAAGGAC AAATTGTTAA AGCTAAAATT
 300
 NTGTCTATAG ATGATGAAGG AAAGCTTAAT CTATCATTA NGGATAATGA TTA CTTCAAA
 360
 AATTATGAGC GTAAGAAGGA AAAACAATCA GTATTAGATG AAATCAGAGG NACAGAAAAA
 420
 TATGGGTNNC AAACACTTAA AAGAACGCTT ACCAATCTTG GATAAAACAG GCAAAGCGAG
 480
 CAACTCGAAA CNGACTAAAG GAACAAGATA AATCCGNACC CGAAAATCAA ACAAAGGGTC
 540
 TTGAAATGAA AGTTTCTTAG ACTATAAAAG AGATTAGGTA TCTATTAAAT TTTATTAGAT
 600
 ACTAATCTCT TTTTGTCTAC GATAACGTAA TATGATTGAT TCTATTTACA CGTACAAATG
 660
 GTTTAAGGTG ACATATCCAT TATCTTTGTT AGATAGAATC GTTGATTTGC AATATTGTAT
 720
 GTGGATTTGT TTTTTTTATT TATTTTAGAA ATGAGAACTA CAACTTAAAG TATTAAACGA
 780
 ATTGCAACTA TATAAACAGA TAATTG
 806

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1033 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTACGGCATA CCATGCGAAA TAATTGTTGA TTCTAATGCT ACAATCGGTT GATTGTTCTC
 60
 CCGTGCTTGC TGAAC TTCTC GAGAATACTC AATATACTTG TGTA AATTTG CCATTTTTAT
 120
 AATCCTCCAT ATCGTGATAA AGTTGCTGTT GATCTAGGTT GTGCCTAACT GTATATTTCTG
 180
 TTTCTATCGT TTTCTNTGCG TTAACCATAC CAGCAATTAA TATATCTACA GTAGACATCC
 240
 CATTTANCCA GCTATATACT ACTGCAGCAC AGAATGAATC GCCTGCACCT GTAACATCTT
 300
 TCACACTATG TGGATGGCAT AACTGACTTG ATGATTCTTC CTCACCACTN CGGATAATTA
 360
 ATTCTTNCAC GCCATNTGTC ACAATAACAT TTNTACACCT AAATCATTC AGCGGTTTTA
 420
 GCAGCTATTT NTANATCAAC AAGTAGATTC TTATTTNTAA NTTAAGTAT GGTCTGGCN
 480
 CANCTTNANT CGGGGATAAT CCAATCAATA GCATGTAATG AATCAGGCAT ATTTTTCATT
 540
 TTTGGGGAAG AAACCGTGGT GATAACTAAT TTGATTTGAT GTTTCGTGGT ATAGGCACAT

600
 AAGAAGTTTA ATGCCTCTTT GCCTAAATTC AAATCGACAA TAATGCACTT AGCCTTTTTTC
 660
 AATAAGTGTG AACGCTTAAT TAAAAATTCA GCGTAATGT AGTCANACAC TTCCATATCT
 720
 GCTAAGCCAT ATGTCATGTC GCCTTCTTTA CTAATTAAAG CTGTATATGA ACCTGTACTC
 780
 GCATTTTCAA ATTGTTGAAC ATGANCCCAA ATTCATAAAT GGTGTGGNCA ATCGTTGAAT
 840
 CATTTCCCAN TCACTATCTT GTCCACTAGC AGATAANAAA GCGACCGTTT CGCCAAGCCT
 900
 ACCTAAGTTC TCAGCAATAT TTCTTGCTAC GCCACCAATA GAGCGTGTTG ACGTTACAGG
 960
 ATTTGATGTT TCTGCAACTA AATCTTTATG CACATAAAAC TTACGATCTA CATTGCTGCTC
 1020
 GCCAATACAA ACG
 1033

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTTACACAAC AAGTTGTCAN AAATTATTTT TATGATAATG ATCGNNCATT TACTAGAAAA
 60
 GTAAAAGAAT TATTTGTAGC TCATCGAGTT GAAAAACAAT ATAATAAGAA CGAAATTTTA
 120
 CGCTTTTATT TAAATAATAT TTACTTTGGG GATAATCAAT ATACGCTTGA GGGCGCAGCA
 180
 AACCATTATG TGGNACACCC GTGAATAAAA ATAGNACAAC AATGTCTCAC ATCACAGNTT
 240
 NACAAAGCGC TATTTTAGCT AGTAAAGTCA ATGCACCTAG CGTATATAAT NTCAATAATA
 300
 TGTCAGAGAA TTTCACGCAA CGTGTTAAGC ACGANCTTAG AAAAAATGAA GCAACAACAT
 360
 NATATCAATG ACACACAATA TCAACAGGCT ATGTCACAAC TAAATCGCTA AATACTNGCA
 420
 TTCATGTGTA AGATGCTTGG AACTATAATG TAGAAGGTTT AATTGAAATG TCATAATGAT
 480
 AAAGTTGAAT TGTTTCTGCT TAATAAATTT TACAGATTTG CTTGTAATCA CACTNTCATT
 540
 TTAAAAGATG ATAGTGTGAT TTTTGTGTTAG CATCGAAAAA TATTTAAAGT TAAACATTTG
 600
 CTATAGGAAG TGGCTTATTG AATAATAAAA GAGTATTGTA TAAACTTGA GAAAGTAACG
 660
 GGGTGATCCA GTGCCGAAGA TTACTAAAAT AGAAGTTCAA AAGAAAAACA AAGAACGTCT
 720
 TAATCTTTTT TTAGACGAAC AATTGTGANAN GGNNANTGGG TATAGATATC GATACATTAG
 780
 TCAAATTTAA TTTAAAAAAA GGGCAACAAC TTGAAGCTGC TGACATGGNA GAGGTTCAAN
 840
 AGTATGATCA TTATCGCATA GGTTTAAACA AAGCAATCCA NTATTTATCA TATAAAAAGA
 900
 GAACTGAAAA AGAAGTTATT CAATATTTAC AANAAGAAGA GATATCAGAG CAAGCGATTT

960
CTGANGTGAT TGAATATTGT TATCGCGAAA AGTTANTCGA CCATCAAGAT TATGCGGAAA
1020
GTTTACNAAA TACAANGATT CGCACGACAG ATAATGGACC TANANTTNAT CANCAAAAAC
1080
TNTTTCAACC TCGGGTATNG NACCACCTAT CATTGANATG TTTACAGANC TTTCTTAGNG
1140
AACAAACAGNN CTTGGTTGAT ATTCATCCAA AN
1172

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAAGGCTTGT CGTCCCATTT AAGCATCACT CCGTTTGT TCGCTTAAAA TCCCTTGCAT
60
CGATGCTAAC AATTGATCAA CATCTTTAAA TTCTTTATAG ACTGATGCAA ATCTAACATA
120
TGAAACTTGA TCAACATGCA TTAACAAGTT CATAACGTGT TCACCTATAT CTCGTGAAGA
180
CACTTCCGTA TGACCNTCAT CTCGTNATTG GCATNCAACC TTGNTTGNTA TGTCTTCAAG
240
TTGTTGGATA TCTAACTGGT CGGTTCTCAC AAGAACGCAC AAGTCCAATA AGTATTTTNT
300
CTCTTGAAAA CTGNTCTCTT GCGCCATCTT TTNNCACAAC TATAAGCTGA CTTAACTTCG
360
ATATGTTCAA ATTGTAGGGG GAAACCGTGG TTCCCACAA
399

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 632 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATTTATATAT AGTAACAAAA CTAAATTATA AATGACAATA TCATATTTTCG CAATCACTGT
60
TAGTAATTTA AATATTTTTTC AAAAACGACA TAATCATCAG TTTGTTTCGAT TTCAACGAAA
120
TTACTATTTA AACATAATGG TTTAAAATCA TTATTCTCTC CAAACAGAAT CATCGTAATC
180
ACATTAAGGT TGTTCATAGTT TTTTCTTAAG TAAGTTGGCA ATTGTCGCAG CGCACTTGAA
240
CCAATACCAT TAAAGCGATA TGATTTATCC ACTTCAATAG CAGCAATGTT CATGCGTTCA
300
CCAATCTGCT CCAATGCGAT AAAGCCACCT NTTGGCANCA GCATCATAAA NTTAATGATA
360

TNTACATNGG CCACTTCTTG AACGACTTTC TTCCTCCAAG CTTTAAATGA CGAACATTGT
420
TTNGATCTTA AGTCCAAGTA TTTGGCCGGT CCTTTGCATT GGTCCCTCTTC TTAGTCGNNT
480
GATTGAATGA TCCAGACGTC CGTTGGTCCA GATTGGNCAA TTTCCGANTC TACTACTGNN
540
TTTGNTGATA AATCAGGAAT CACCCTGACA TTTTGGGAAT GAATCAATNT TTCCNGGCCA
600
ATTCCAAACC TGGTTTTTTC CAATAATCGN TT
632

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GATATACAGC ACTCAGAATT TTAATGACAA TTAATGCAGC AGTTAACACG ACAACGCCAT
60
TAAATGCTTC TTTATGCTTC ATCACTGATT CTCATGCTTT CTTCAATGCA CTTAACTAAA
120
AACTTCAAAC TATCAAGCCA TTGATTTTGT TTCGTTAAAG TAATTGTCAT TGCATTATTT
180
TGAACACCAA CCTTCATTGT TCTACCTAAA GGTTGTGTTG CTTTGAACAG CACTTCGCCA
240
TCAATATTTT CAGTGGCTTT TACAGATAAA TGAATATCAA TTATTTTCCC TTTATCTTTA
300
ATCAACGTGA TACCTGAATG TAATGCGTGT ACTTTTATTT CCACTATATC AAGCAAACGT
360
GCTACTTCAA CAGGNTAATC CAATTAAACG ATCAATTANT TCATCTTTAN TGTCGATAAT
420
TGGGNCAAAT TGTTCAG
438

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TACCAAAGTT CTTCTTTAGA GGCTGGGGAA TATNTCCNAA CTACATCACG ACGCACTCGA
60
AACGGTTCCT CGTTGGAAAA TCGATGTCAT TTCGTGTATA TTGCACATCT ACAAGTTTTT
120
TAAGTAATTC ACTTCTATCC ATTTCCATAC CAACTCGAAC ACTTACTACT AAATCTTTAT
180
ATTCTTCAGG ATTACCTAAA CCATATATAC AACTTACACT AGCAATAATA ATTACATCAT
240
CGCGTTCAAA TAATGCACTT GTAGCAGAAT GTCGNAGNTG ATCAATTTCA TCATTGATTG

300
AGGCATCTTT TTCAATAAAA GTGTCAGTAG ACGGTACGTA TGCCTCAGGT TGATAATAAT
360
CATAGTAACT TACAAAGTAT TCCACCCTGT TTTCAGGAAA AAATTCTTTA AACTCACTAT
420
ATAATTGCCC TGCTNATGTT GTGGTAGGTG CGATAATTAA CGTTGGTTTC CCAACTTCTT
480
TAATAACATT ACTCATCCGN CAATGTTTTT CCTCGNGGCA GG
522

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATCGCCACCT GTACCATGCA ACAATATTAG CGTTGGTGCA CCTTTNTTGT CCTTCACGAA
60
AAATATGTTC CATCACAAAT CCTCCTCATT CCAATTAATC ATGTTAACGC TTAGTATTAA
120
ATGGTCTTAT TTCTGATTCT ATATACTCTC TTTTATTTTC TAAAAATGGT GGCAATGATA
180
AACCTNCACC TAATGTTTCA TACGGNTCAT CTTCCATAAA TCCTGGTCCA TCTGNTGAAA
240
TTTCTATTAA AATATGCCCC ACACGTGNAT ATAATGCTTC AAAATAGAAA CGATTAAACGA
300
TGCCTGAGTT GGTTAATACC TACCTCTTTA TATTNCGGGT GCCCACGCTT CTTATTTGCA
360
TCAGGATCTT TCCACAACGA AATGACACAT GATGTACCTC ACCATAACTT GAGGGNGGTT
420
GNTGGCCTNN ATCATCTTTT ATTAAGATTA CTGGNCACAT TGGCGNCTTC GCAACTTCAA
480
GGTAATGCGA CATATCTTCA AGCGCAATAG GTGGCATAACC
520

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAATTCCATC AGTGCGACAA CTGAAGTATT TANACCAATA ATGTCATCGA CACTAGTTAC
60
TATTATCGTC TTCTTACCAC TTGTGTTTGT ATCAGGTTCA GTAGGCGAAA TGTTTAGACC
120
TTTTGCATTG GCTATTGCAT TTAGTTTATT AGCATCGTTA TTAGTGTCAA TTAACTCGT
180
NCCAGCTTTG GCAGCAACAC TATTTAAAAA AGGCGTTAAA CGTCGTAATA AACAAATCA
240

AGAAGGATTA GGTGTTGTTA GTACAACTTA TAAAAANGTA TNGCATTGGG TCACTAAATC
300
ATAAGTGGGA TNGGTAATTA TATTAAGTAC ATTAATTTGG GGNTGNAACT ATTGTTTTTG
360
GGGGGACCNA GACTAGNCAC TTAGCTTTTT TCCAGAA
397

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AACCATCTTA CCGATATCAG TACAGTACGG CGTAGGAACG GGCATCCAGC GGATTAGAGG
60
TGGTGAAACC AACCTGGTTG TTGATAACGA TACGTACCGT ACCGCCAACT TCATAACCAC
120
GCGCTTTCGA CATGTTTCAGG GTTTCCTGAA CCACGCCCTG CCCGGTCACT NTGGGGTCCAC
180
CGNGGATGGT GATTGGNAGN ACTTTGTTGN TGCTCGGNTC ATCAAGTCTG TCCAGACGGG
240
CACGAACAGA ACCGATANCT ACCNNGGCTTA CAATCTCAAN GTGAGACGGG TTAAACGCCA
300
GNGCCAGGTG NACCAGGGCG CCATCGGTCT NTAAGTCAGA CGAGAAGCCC ATGTGGTATT
360
TCACGTCACC CNTGCCGAGG TGTTCNTAT GTTTACCCGG GGGAAGTCCG TCGNAACAAN
420
TCTTTGGGGG TTTTTTACCC CAGC
444

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAATTCCTTG GAGGGCAATT TTGGGCTTGC AATAACAAT CATCAAAATA TTGTTGGTAC
60
TATAGGTTTG ATTAGACTAG ATAATAATAT GTCTGCACTT AAAAAATGT TTGTTGATAA
120
AGTTATAGG AATTTAAAAA TAGGTAAAAA ACTTTTAGAT AAAGTTATAA TGACATGTAA
180
AGAACAAAT ATCGATGGNA TNTATTTAGG AACAATNGAT AAATNTATNA GTGCACAGTA
240
TTNTTATNCT AATAANGGCT TCCGCGNAAA TTAAGCGAGG AGATTTACCA AGNAGCTTTC
300
CTAAATCAGA TGTAGATAAT AGGTTCCATT ACAGCAAANT CNAAAGATTA ANTCGANGCA
360
CTGAATAANT GNNATGACAN CCCTCAG

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTCCTAG AAGGAGAATT TGTTAGTGGT GTTGCAGAAA AGCAATGGTT GGAAGAAAAA
60
GGTTATGAAG TAGACTTTGA ATTAATGGCT GAAATAAATC CAACAAGATT ATCATTAAGT
120
GATTGGCTTA AAGTCCAAAA CTATAATAAG TAATGAATGG GGTGCAATCA TGATTCAATC
180
AATGTGGTTT AATTTGCATG TGCAAGATTT AGAAAAGAGC GCACAGTTTT ATAAAGCGTT
240
AGGATTTAAA ATAAATAGAA ACCCACAAAT GTTAGATAAA ATGGTCGGTA TTCAAATAGG
300
TCAAACAACC GCAATTTTAA TAGAAAACAA GCATTTTCAA AATGTAAGTC AGCAAAGCCT
360
TAATACTGAA CCAAATGAAG TGATGATTTT TCTAGGTGTG ACACAATGAG AGTTGAC
417

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAATTCCTAT ATACTACTTT GAAAAGGTGT GAGCTTAATG ACAACTTTTA GTGAAAAAGA
60
AAAAATTCAA TTACTAGCAG ATATTGTTGA ACTACAACT GAAAATAATA ATGAAATAGA
120
CGTTTGTAAT TATTTAAAAG ATTTATTCGA CAAGTACGAT ATTAAATCTG AAATTTTGAA
180
AGTTAATGAA CACCGCGCCA ATATCGTTGC AGAAATCGGT AACGGNTCAC CTATACTCGC
240
ATTGAGTGGT CATATGGATG TTGTTGGATG CAGGAAATCA AGATAATTGG ACTTATCCCC
300
CTTTNCAACT CACAGAAAAA GCTGGCAAAT TATACGGTCC G
341

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTCCTCA GGTATAACAC TTCNCATATC TTTACGAGNA ACTTTTCAAA CTAGATACCC
60
CTGCACCAAC CAACGTCCAT AATGGTTGAT AGTAATGATG GTCTGCTGGG TCTATAATTG
120
CTATTTTCTC TTTTAAGTTN TGATTTTTTC TTAATAGTCT TGATGCTACG GTAACACCTG
180
CTGTACCGCC ACCAATAATA ACAATNTGAT AATGCTTATT CATTTNTTCC ACATCCTTAA
240
ATTATTTTAA TGATTCTGGA AAATCTTGAT AGCCTTCTCT AATATTCACC ACATTTTCAA
300
AACCTNTGCT TTCCAATATA CCCACTGCAA TTGAACTTCT AACACCTGAC T
351

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GAATTCCTGT TTAAGAAACA AGATTAAAG AGCAATACGT GAAAATTTCA AAGTACATAA
60
GTCGNATATA TTGGNCAAAG ATATTATTGN TATAGNAAGA CAGGCAGCTA AAGATATGAC
120
GACTTTACAA ATACAGNATA GTCTTGAGCA CGTNCTTAAA ATTGGCAAAG TTTTAAATAA
180
AAAGATTAAAG TAAGGATAGG GTAGGGAATG AAAACATTAA CCCCTCAACG CATCCCGAAG
240
TCTTACCTCA GACAAACGTT AGACTGACCC TAGGGTTAAG ACTTGGCCCN AGGGNTATNN
300
TAACTTACTT TAAAATGTTT TCAC
324

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAATTCCTAT TATCGAATTG CATGCTACCC CTCCTAAAAN CCAAATGCTC TTAATTTATC
60
TACAGATAAT TGGTCTTTAT CTTTATTTAA AATATTTTCA ACATATTTAA ACAAACGTC
120
TGTTTCTAAA TGTACTTTAT CTCCTAATTT TGTGGATGAT AAAATCGTTG AACGCCTCGT
180

TTCTGGAATA AGATGAATGT CAAAACCTGTT ATCATGCTTA TCAAATACCG CTAGACTTAC
 240
 ACCATCCACA GTAATAGACC TTGCTTAACT AACTGATTAT TAATATGTTG GCTACATTGA
 300
 ATCGNAATAA TTGTGGCATT GGTGTTTCAT TTATTTGTGA ANTGTCCTAG TCACTACATG
 360
 ACCGAGGAAA AATGTCCACC AAACCTACCG NTACACTCAT GGAAGNTCTA AATTACTTCT
 420
 GATTGGCGCT TACANCTGCT AATAGGTTTA TTTCAAGGCT TTATTACTTG ACAGGAAAGA
 480
 TGCT
 484

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GAATTCCTTA CTGTATGATA AAGGTATTAC CAAACAATAC TTAAGGGGGA TTATATACTG
 60
 TGGNTCAATC ATTATATGAG TTTTGTAGAG AAAATATAAA TTATCTAAAA GAAAATGGTN
 120
 TGTATAATGA AATAGATACA ATTGAAGGTG CAAACGGACC AGAAATCAAA ATCAATGGGA
 180
 AATCATACAT TAACTTATCT TCANATAATT ATTTAGGACT AGCAACAAAT GAAGATNTGA
 240
 GATCAGCTGC AAAAGCAGCT ATTGATACAC ATGGTGTAGG TGCAGGCGCT GNTCGCACAA
 300
 NCAATGGTAC ATTAGATTTA CACGACGAAT TAGAAGAAAC ACTAGCAAAA TTTANNGGAA
 360
 CAGAAGCTGC AATAGCTTAT CAAGNCAGGA TTTANTTGGN NATATGGCTG CTATNTCAGC
 420
 TTGTCAANGA ATNAAAATGA TGCTATTTTN TCAGATGAGC TTAATCATGC ATCAATTATT
 480
 G
 481

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GAATTCCTGT TTAGGTGGTA ACGTTACAGA AACACATACC TTAAATTGC CAGAAGATGC
 60
 TGGAGAGCGC CAGATGTTCA TTATTGATAA AAAAAGACAG ACGCCGAAAA AGTACCCAAG
 120
 AAAACCAGGG ACGCCTAATA AGACTCCTTT ACTTGAAAAA TAATGCATAA TCCTTTACAA

180
CTAACATAAA AGGAGCGAAT GGATAATGAA AAAACCTTTT TCAAAATTAT TTGGTTTGAA
240
AAACAAAGAT GACATCATTG GACATATTGA AGAAGGATCG CAATAGTAAT GTTGAATCCA
300
TTCAAATTGA ACGTATCGTT CCCAACCCGT TATCAACCCA AGACAGGTGT TTGAACCCAA
360
ATAAAATTAA AGAACTTGGT GAATCAAATA CAATGAACAT GGGTTTACTA CAAACCTATT
420
GTTGGTAAGA CCGATGAGAA GATATGTTTG AAATTATTG
459

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAATTCNNNA AAGATACNAT NCNATTTAAA TGGATATCAT TCCAAGAAGC TGTAGATAAG
60
AATCGGGAAC NAATGTCTCT GTTTAATGAA ATTCTTAAGA GTCATCAAAA GACTCCANTT
120
TTTGATACAT CTAGCTTGCG ACATACTTCG AAAAAATTAT CAACAATTTT AAAAGGGGAT
180
TTGTAAAATG AATATTGAAA AAATCGAACA AATAATCAAA TTAGTGAAGG AAAATGATGT
240
TAAGAAATTT AAATATAAAA ATTTTGANGA TGAAATAGAA ATTGACTTCA CTGACTCGAA
300
TCATTTGGCT GCACACAGGT AATCAATCAA NTCAANGTAT GAACAATAAT GATTTGACAG
360
CTTCAANAGC GAATGATAAC TCCGATGTNT CGACAAATTG ATTATCATGA CATTAAANTCA
420
CCANTGGNAG GTACATTCTT
440

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCCCCGGGCT GCCACGGTAA CTGATGCCTC CGCGGTACTG GCGACAGATT ACAAATCTC
60
GTTGATAAT AATCAGTGGC AGGTCACCCG CCTTGCCAGC AATACCACTT TTACGGTGAC
120
GCCGGATGCC AACGGTAAAG TGGCATTGTA TGGTCTGGAG TTGACGTTTA CAGGAACGCC
180
TGCCGTAAAC GACAGCTTCA CGCTGAAACC AGTAAGTGAC GCCATCGTCA ACATGGATGT
240

ATTAATCACC GACGAAGCGA AAATAGCGAT GGCGAGCGAA GAAGATGCGG GTGATAGCGA
300
TAACCGCAAC GGTCAGGCCC TGCTGGATCT TGCAAAGCAA CAGTAAAACG GNNGGCGG
358

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GAATTCCTAC CAGACGTCGC AATGGTCTAT AATTTGCTC TAGATAATCT TGAATAATA
60
TCTTTTATTG TTAAATATAC TTCTGGTTGT CCAAACATTG CTGTTGAAAT AGCAAAGTAA
120
CTTTCTAAGC GCCCCATTCT CGTTATTTTA TTAATAGCGA TACCTACATA TTTGATAATA
180
AATGGTAATA CCTTAATATA ATTAAAAATG CCTATTAATA CAGAAATGAA CACTAATGGC
240
AGTAACACAT TTAAAAAGAA CGTAAAGCCA TTTNTATTTT GTATATCTCC AAAAACAAAG
300
TTTATACCTG CTTTACTAAC ATTTATTAAC CCTTCCAAAA AATGAGCCTA ATGCAGGTAA
360
GATTGGTTAA ACCAATCGTG GTGTTCATCC ATTAAATTAC AACAATCCAA CAACTTTGGA
420
TTAAATTATC AATTATTAAC NGCCNTTTTT GGAAGTCTAT GTTTTACGG ATCCCAAAAA
480

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GAATTCCTCT TTCACTTCTA TGATTTTTTT TAACTTCGAA ACGTCAAGTT GTGCATCAGG
60
TTCTGCTGTT ACTTCCATTA CATAACCTTG AATCGTTCTT GGTCCAAAAG GTACAATTAC
120
ACGCACACCA GGTGGATGA CAGATTCGAG TTGTTCCGGA ATTATATAAT CAAATTTATA
180
GTCAACGCTC TTCGACGCGA CATCGACTAT GACTTTCGCT ATCATTATTG CCACCTAGTT
240
TCTAGTTCAT CTAAAATTG TGCAGCTAAT ACTACTTTTT TTCCTTTCTT GATATTTACC
300
TTTTCATTTT TTCTAAAATG CATTGTCAAT TCATTATCAT CAGAACTAAA TCCGATAGAC
360
ATATCCCCAA CATTATTTGA AATAATCACA TCTGCATTTN TCTTGCGTAA TTTTGTGTGT
420
GCATAATTTT CAATATCTTC AGCCTCTGCT GAAAGGCTAT TAATACTGNG ATGTTTATGT

480

CACCTAAATA TTAAGAATGT CTTGAGACGT TTAAAAGATA CTGACAATCA CCACCTGGTT

540

TTTCA

545

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 429 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GAATTCCTNA CCATCCATAG CTGTGNACAC AACATGATCT TTATCAATCA TCATAATGTT

60

GCAAAGGGAT TTCTTTNATC AAACCTCAGGT GCATATGCTC GNACTTCTTC CATAGTTANG

120

GGCAATTTTCG TTGGGGTTAA AGGGTGTGTT GGATGCCCCT CTGGNNCCAA GCTCTCAGAA

180

TAAGTTAACT CATCTGTCTT ATCACTATCT TTTACATGTT GTANCCATGA AAAAAAGTTA

240

ATATCTTGTG GTAATCTNGA AAATTTAAAA CTGTGACTTA TTAATGTGTG TCTGTGAGAC

300

ATGTGNTTAT ATGTCACATC TAACTATCT CGACTGTGTA TTANCTCCTT CGNNGTAGTC

360

GCTCTGANNA NTAGGGATAT CAANGGTCAT GACTCAACAC ATCTAACAAC NCCTTCTTAA

420

NGGTTATTA

429

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 434 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAATTCCTAA TGCANAAAAAN TTCCCCGAGT CACAGTACAA TTTGCCGTGC TTCGGNGGAT

60

TACTTTGTTT ATTTTTATTG TGTANCATTA ATAATGAGTT GTCTTAACGA TTGTCGCTTT

120

ATAACTACAC GTGCTGTGAC ATCTTTTAAAG AAAAACACAG AAGGCTTGTG CATGTGATTG

180

TAATTGGATG NCATAGAGTA ATGATATGCA CCAGNTGATA ATATAGCAAG ATAGTCTCCA

240

CGTGTGACTG ATGAAGGTAA TTAGCGTCT TTTAATAATG ATATCACCAG ACTCACATAA

300

TTTTCCAGCT ATAGNTACAC TGACATCTGC TTCTACATCT CTTATTTAAC AAAGCAATGC

360

TTGATACTGT GCGGTCATAA AGGTGAAGGT TCTTGATATT GAATCACTCA TNCCGCATCG

420

AGTTGAACAT ATTT
434

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GAATTCCTAC AAGGATTCAA AATAAAATAC AAGTGTTTTG CGAATATTTG TTCGTATAAA
60
ATCTTGAAAT CAAAACGCAA AAACGAACAA ACGTGCTTAT ATTTTATCG ATAATACAAT
120
TANTTTGTTG TTCTAAGCCA ATTTAATAAT CTTATGAGCA CATNATTTTG ACTTCTGTTC
180
TTTAATAAAT TTCTAGATTT AGACATTTTA AATTGCTCAG TTTTAAATTC AAAGTTATTA
240
TCATAGCCTA TATGGACTAC ACCATCATAC TCTAATAGAA TAATTGCTGA TGACACATTA
300
AACAAATTTAT TAACAAATTG CACTGCATCT TTTAATTGCT GCTCAATAGG TTTATTAATA
360
TCAACAAAGT TTTCATTGGT GATTAATCAT ACCCTTTAGA ACATCGGNTT AAATCCNCTT
420
CTTNCAATCG ATGATATTAA GCACCATTAG TAATACCATC ATTTTACAA AAGGGTCANG
480
AATTTTCTTN ATTACAGCTT GGTCAATTAT GTGTCANCTT GAACCATARR DCTNS
535

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GAATTCGTC ATTTCCAGGA GGATANGAAA TAAGAATTGA GTTATTAATC AGTGGTTTTA
60
TTTTTATATT GGCTTCCCTT AGCGATTGTG GTTGATGGTT ATTTAGCTAG AAAATGGAAT
120
TTAGTTACAA ATATGGGGAA ATTTGTGGGN TCCATTAGCG GATAAATTAT TAGNTGCAAG
180
TGCTTTAATT GTNCTTGTGC AACTAGGACT AACAAATCT GTAGTAGCAA TCATTATTAT
240
TGNCAGAGAA TNTGCCGTAA CTGGTTTACG TTTACTACAA ATTGAACAAG GATNTGGTAA
300
GTGCAGCTGG NCAATTAGGT AAAATTAACA CAGCAGTTAC TATGGGTAGC AAATTACTTG
360
GGTGGGTATT AGGGTG
376

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GAATTCTCAG TTCATGTTGT GGNGACACTT TAAACGGNCT GTGCCAGTAG CGACCCAGTC
60
ATTTCAAGAA TGACCATTTC ACATTTATAT TATAACACTT GTCGNGCGTA ACTGTATAGN
120
TTTTCAGNNG TGTTTAAAGT TAAGTTATCT ACTTCGCGCT TTCCTTGGCT TAATTGTGAA
180
ATTACATATT GCGCTACGCC AGNTTGTTG GGAATTTGGT AACCTGTTAT ATCACTTNTG
240
GTCAANNCAA TTATTTTTTAA TTTATAATCA CTCATATTAT CTACGTCCAC TCNTTTTATC
300
TAAACAATAA AAATGTGTTT NTCTCCCNCT AAATAATAAC AATGGCAGGC TTAATAAAAA
360
CAATATTAAA TACAATTTGC TCTTGTCAAA ATTGAAAACC CCCACATAAT ATTATTTTAT
420
TTAAGNGTAA GAGGGGGGCA ATCAGGGCTC CAGCATAATG TTAATCTTTG TCGGGTGGGG
480
TTCCNGTCTT GGGTNGCCCN AGATGCCAC TCTCTAGG
518

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GAATTCCACT AGAAGTTNCA ACATTACGCA TTTTACATTT CGTAAGTGGA GACGGTGGCA
60
AGCTAAAGAT TCATTATGAA TTATATCAAG ATAATGAAAA AATGGGTTCT TATCAATATG
120
AAATTAACTA TNAGGAGATA GGCGAATGAA TATTATTGAT CAAGTGAAAC AAACATNAGT
180
AGAAGAAATT GNAGCAAGTA TTAACANAGC AGGATTAGNA GNTGAGATTC CTGATTTTAA
240
AANTGAAGTT CCNNNGNNT NCAAAAAATG GAGATTATGC TACTAATATT GCGATGGTAC
300
TGACTAAGAT TGGAAAGNNG TNCTCCNCNC TGNNNATTGC TCANGCGGAA NGNTTGNNNA
360
CCTTAGCTCC NGGACACCNG CACATGNAAC ACAACTNGAC ATTGCCTGGC CCCACGGCTT
420
CAA
423

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 943 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AATGACAAAA TATTAATCAA TTGGCGTATT ATACAAGAGT AATAGACATA TAAAAGTCGA
60
ATGTA ACTAC GTGAGTACTG ATTTTATTCT TTGTAAATTA CAAGCATTTT ATATCATAAA
120
GTTTGAAAAG AGGTATATTG AAGTGGAGAA AAACGAATAT ACAGCTAAAT ATAATGAATA
180
TAGTCAATTA TTAGACGCTA CTTACTCGCA AGCTGTAGCA TACCTTTTAA ATAAATATGG
240
CGCTGTAACC GATGATTATT ATAAGGAAAA ATCATAACAG CGATTTTTAA ATGGAGAAAT
300
CAAAGTATT TCAAAGGAA AATACACTAG AGCTAGCGAA GGATTATATT GTCATCACAT
360
AAGCGAAGAC AAATTCCAAA ACTTATCTTG ACCTAAGATT CATTTCCGAA TTTAAGTACT
420
CATACAACGT CAAAAGAAAG AAAACTTAGT GTACTGTGAT CTTATCGAGC ATTTANTTTT
480
ACATGCAATT ATTACAAAAG AATCCAATGG CAATTGGGGT GTGGGCTGGA TTATGTCAAA
540
TGATCAAACC AACAGTCATT GATTGGGACA TTAGCGAATA TACTCCAAAA CCAGCATGGA
600
TGCAAGCCAC CAAAGCACGT GCCTATGTGC CTAGAATATT AGTAGAGAAA CTACTCATTA
660
NNATTGACGA TATGTTAGAA GGAATAGAAA TATATGATNT CCNTGAGTCT AGATAAATGA
720
TTAANGGAGA TATATTTCTG GNTCGNTGAG ATTGTGNTAT AGATAGNNTA ACCCNNTAAT
780
TAAATATTAT TCTATNAAAT AGACCACGCA TNCCTATCTA TAAACGGACA ACGTTTATAA
840
ATGAGTTTGC ATGGTCTTGA ATTGTATTAA ATNTCTTNTT GGGTTTTAAT AGNTCACTTA
900
GNGGGTATGT CAACATTCTT TNGACAGCTT CACGTGTATT TTT
943

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CAGATATACC TGCACTAATC AAAGTTTCAC CAAAATTTAA AGCTGTGTGA TATATCACAA
60
ATCCACAAAA TCCTAAAATA AAAATAACAG GGATATCTCT TAGTTCAGGG GTAGGCAATT
120
TCTTTATAAT TACGAACGGC AAGAGAATTA TTGTTGCTAA AATTAAACGA AATGCCGACA

180
 ATGATTCTGC ACTAAAATCA TTTAACGCAA TCTTTATCAT TGGAAATGCA GATCCCCACA
 240
 ATATGATAGT AAATAAATAT GATAGAAAAG TAGTGTCTCG AAGTTTATTC ATTAATATCA
 300
 TCACTCCTTT AATTATGTGT TTCTATATTA AAAAATATGA TTTAAATGA GTACAACCAA
 360
 TTGGGAATGG ATTTACCTAT CCAATTTTAA AAGGGAGGGA GAAGATGGCT AAATATTAAG
 420
 ATATTGCTAG TGACATAAGA GATAAAATAA TCACAGGGGG ATTGGGTTTT ATGGAATGAA
 480
 GATACCTCCA CAGAGGCAGG TGGCGATACA AATACAACGT NAATAGAGTG ACGATTATTA
 540
 AAAGTATTGG AGTTATTAGA GGCTGAAGGA TTTACTATAC TAAAGTGGGG AGTGGGNACA
 600
 TATGTTAATG ACTATTTGAA TGAAGCACAT ATTACAAATA AGTGGTCTGA AATGATGTTA
 660
 TGGTCCTCTC AACAAAGAAG TCAGTATACG GTGCAATTAA TTAATAAAAT TGAGACAGAT
 720
 GATTCGTATA TACATATAAG TAAAGGTGAA TTGGGTATAT CGTTAATGCC ACATATTCAA
 780
 TTGAAAAAAG CCATGTCTAA TACAGCCAGT CATATTGAAG ACTTATCTTG TGGGTATATA
 840
 TAATGGCTAT GGTATATCA AGGTTAAGAG ATATTATCCG GNTGAACGAA TTGTCAAAGC
 900
 AAGGTATTAA ATTGTAGGTA GAGGAAAATT GTAATGGATC AACTCCAGGC GCTTTTACAA
 960
 TGCCANACCA ACTTNTTATC TTATTGGGGT TTNTAGGGTC AAAGATGCCA TAATAATTTT
 1020
 GGATACAACC ATCATATTTT CCACTCTACA AANTGTTTGN GGAACAAATG GAATTTTAGA
 1080
 CATATTGATG TCCCCNTATT ATCAAATTTA ATGAAATTA
 1119

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AAGAAATGTT CTAGAGATTT AGGTATCGAA GAACCCAGGA TTAAGACGAT TAAAAGAGCN
 60
 ACTATGATAT TAGGATTATC AACATATTTA CTGCTGTGTG CAAGAAGTAC GTGCTTGGAC
 120
 AATTTAAACC AGGTATGACT GCACCTCAAT GTGCTGGTAT CATTCACTACT GATTTTGANC
 180
 GTGGATTTAT CCGTGCCGGA AGTAACAAGT TATTGATGAC TATGTACAAT ATGGCGGCGA
 240
 AAGTGGCGCT AAAGAAGCGG GCAGACACCG ATTAGAAGGT AAAGAATATA TTATGCAAGA
 300
 TGGCGATATC GTTCATTTCA GATTTAATGT ATAAACGATA GAGTGAAGTT AATTAAATAG
 360
 TATATATGTA GAAGAGGCGG AATCAATTGT TCGCCTCTTT TAATTATGCG TATAATTTAT
 420
 TAAAAGAATG GAATGATTTT ACTCGCGTAA ATAATATCTT GAGTGCTGAA AAATTGTTTG

480
CCTTCGCCAG TATAAGCAGG CTCTAAAACA AGATTAGCCT TTGCACAATA AAGCCATTCA
540
GGATGAATGC CACTATTAAG TATCTCTTGG AATTCGATAT CAAGCTTATC GATACCGTCG
600

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GAATTCGNAA ATGTTGGCTT TGGCGCAATG AAGAAGCAAC CACCNTCTAA AAGCTAAGTT
60
AANCTTATTT GAACACATGA TNNCGANTGC ACGTACATCA NCAGAACAAG GAATGCTTGT
120
NTCTGCGGNA ACAATGCTCA NNCANAGTAC GCTACCCACA TTTACGAAAA ATACATCAGC
180
AAGTCGTTCA TGATATGAAA TGTAGCAGAC ACGAGATTCA CCCTNTGTNT CCAGCTGACT
240
TCGCAAGTCA NNNAATGTG TTAACCTCTAG CGGAAATGAA AAGGACAATT CATGATATAT
300
TGGATTTTCAAG AGATGAAGAT ATTTGGGNTT GTTATTTGGG TACTTTGGCT GTGTCTCCAN
360
GCTTAANGGA TGATGANGGT CANNNGTTAC TATCACGTNT ANGAAATGCT TACAATNNTT
420
ACGANTAGAA ATGACCCGGA TGGCGNGGNC NGNTAAATTG TCAATGNNTT NAAAGGTAA
479

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 733 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GCGAGCTTAG TTCATTTTAA AGTAAAGAGT TTTTGTATG TAAAGTATAT TAGTAAAACA
60
CAGATTACTT GTCTCTGTGA AATTAATACG TTTATACTAA AAGATATAGT CTTTCTAGAA
120
AATCTGTAA TTAATTGTGA ATTTTGTAGAA AATTTAATTGA ACAGCAAAAT ATGGATTGTT
180
ATAATTTAAG TTAAACAAAT TCTTATACAA TATTATTAGG AGGCAATCAC CATGTCACAA
240
GCAGTTAAAG TTGAACGACG AGAAACATTA AAACAAAAAC CAAATACATC TCAACTAGGT
300
TGTGGGTAAA TATTTTACTG ATTATATGTT GAGTTATGAT TATGATGCAG ATAAAGGATG
360
GCATGATTTG AAGATAGTAC CTTATGGGCC TATTGAAATT TCACCTGCTG CACAAGGTGT
420

TCAATTATGG TCAATCGGTA TTCGAAGGAT TAAAAGCATA TAAAAGAGAT GGGGAAGGTT
 480
 GCACTTTNCC CCNNCCCGAA GAAAATTTTA AGCGTCTTAA TAACTCGTTA GCACGATTAG
 540
 AAATGCCTCA AGTAGACGAT GCAGAATTGT TAGAGGGGCT AAAACANTTA GTTGATATAG
 600
 AAAGAGATNG GNTTCCTGAA GGGGAAGGTC AATCATTATA TNTTCGNCCA TTTGGTCTNG
 660
 CAACAGAAGG GGGACTNNGC GTTGGCGCAT CACATCAGTA TNAAATTTAT TAAATTATNT
 720
 TATCTTCCTT CAG
 733

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1263 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ACTTGTGCAC TGCCAATAAT AATTAATCCT TTCATATTTG ACCCCTCTTT TTTTATTAA
 60
 ACTTGTGTGTT CACGTAATAA TTTCATAATA GCTTTTCCAA CACCACTATT TTCATTCGTA
 120
 TCTGTGACAT ATTTGCTAT TTTTTTAACT TCTTCTGCAC CATTTTCCAT CGCAACTGGA
 180
 TAGCCAACTT TCTCTAACAT TGATAAGTCA TTTAAATTGT CACCTATTGG CATGACATCT
 240
 TTCATTTCAA TCCCTAATCT TTCGGCAATT GTTTCTAGCG CAATACCTTT NGGTGCATCT
 300
 GAATGCGTTA TTTCTATATT TCCTCTCGAA GATGATGATA TAGCTAAATT CGGAGATTCA
 360
 GCTAAATTT TACTAGCTTN GGCAATTTTT TCTTAAATTT CCATCAAATG CTAATATTTT
 420
 CATAATTAAT TCAACAGGTA TGTTTTCAAT AGGATCATAA TTATCAACAA CTTTCAACGG
 480
 TNCCAATATC TATGCGTCTT TGNATACCAT CTTNAATACG CTCAACGTNT GGATGTTGAC
 540
 CTGCACGCTC AGCAATATCT ATGTAAATGT CTAAATCTCT TGGGGGATCT TCCAGTATAA
 600
 ATCGCACGAC TCGGNTATNC TGGATAATAA GTACCTGNAT CTTTTAAAAC ATNTGTAATG
 660
 NGGTGTACTA ACGATTTATT ANGGNGTGAA GTGCTCATT AATTGAAAGT TTCATCACGT
 720
 TCTTCAGNAC CATTCAGACA AATATATGGT ACTGNTAAAT CTGTGTCAGC AANTGGTGCT
 780
 TGTGCTTCAA AAAATGCTCG ACCTGGCACG AGCGATAACA ACCGTTATCC CTTGTTCTTG
 840
 AGCGTATTNA NTCGCATCAA TATTAGGTTG AGAAATTTCA TNTGCTGCAT TAAGGTAGCG
 900
 NGCCATCCAT ATCAGNGGNT ATTAGGTTTN TCANTATGTT NCCNCGCCCN CGNCTTTCGT
 960
 AAATTTAAAA TCTTGTTCTT AAATAAGAAT ATATACTCAG CGCACATACT TTTCTATTAA
 1020
 CATTATATTT GTCATTAATT TATCATATAA TGTAATTCTA ACAAATTTTA ATTAGTATGT
 1080

ACTATCGTCT TAATTGGTGG ATTTCTTATT GGCTCTTAAG TTTTAAAAA ATGTTGGTTA
 1140
 ATAATGGTGC TACATGCTTC TTTTAAGGTA CAACCTTTAT CAACAAATTG GACGGATGAT
 1200
 TAAAAATTAG GTTNGGTTGG AAATAAATTC AATTAACTT GCTACTACAA ACCACRRDC
 1260
 TNS
 1263

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATTATGCCTA TTTGACACAT TATTGAAATT TTTAATATAC CCCTTATACG TTACGGCTTT
 60
 GTACTGTGTT TAGGTATATA AAGCTTTGAC ATATCGATAT TCTCCAACCTC TAACAGCTTA
 120
 ATTTTATTAT TAATCGTTCC ACCGAATCCT GTTAAGCTAC CCGTTTTACC GACAACACGA
 180
 TGACATGGCA CGATAATTGA TAATGGATTA CTTCCGACTG CACCTCCAAC CGCTTGGGCT
 240
 GACATTTGTG GCTTATCAAG CACCTTACCT ACTTTTGTGG CAATAGCACC ATACGTTGTT
 300
 AGAGTCCCAT AAGGAACCTG TCTTAATTCA TTCCAAACAC ACTGTTGAAA ATGACTACCT
 360
 GTTGGCTTTA AAGGTATTGT GATTTTCAGGA TTGTCAACCT TTAAAATACG CGTCTTAACC
 420
 ACTGTGTCGN CTCTCTAAAT ATCGCTAAAG ACGTATTTTC TTCCCTAGTA CCAACACCTT
 480
 GTTGATTTTC AAACAAACAG CGGTCAGATT ACCCATCACT CAAAAGTCCA ATCGTCTACA
 540
 GCGATCATAG TACTCTATCT CCATAAATCC CCCTTTTCTT ATCATACGCC TATG
 594

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

AATGGGAAGT TCAATACCCA TAATGNCAAG CACCCTTGCA TTTAATTGCA TTTTCCNACC
 60
 GTTATTACNG GCCCATCTC CAACAATATG TAAAGTTAAT ATCTGCATAA TCTTTTTTTA
 120
 AAGACTTCTT TTGCTGTAA GAAATCAGCA AGANCTTGAG TAGGATGATC TTCATCAGTT
 180
 AAACCATTCC AACTGGTAC GCCTGAATAT TCAGCTAAAG TTTCTACTGT TCTTTGTGTN

240
 AAACCCGCGG TATTCAATGC CATCATACAT TCCACCAAGC ACACGTGCAG TATCTTTAGT
 300
 TGTTTCTTTT TTACCCATTT GTGATCCAGT TGGGCCTAAA TAAGTTACAT TTGCACCTTG
 360
 ATCATGCGCT GCAACTTCAA ATGCACATCG CGTTCTTGTA GAATCTTTTT CAAATAACAG
 420
 TGCAATATTT TTATTTTTTA ACATAGGCTT TTCAGTGCCA ATATATTTAG CACGTTTTAA
 480
 ATCCTCGGAG AGNGTTAATA ATNNGNAATT C
 511

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTGCCTTTTC TCTATCTGAT AAACCACGCT TTATTAAAAT TAAATCTCCT AACCATACCC
 60
 CGTCTAAATT ATCTGGAAGT ACATCAGCCT CTCTTACTTC AATATAATCA TGTTGTATTA
 120
 AAGTTTCTTC ATATAATCCC ATCTGATACA TCCTTTACTT ACGTTTACTT CTTATATAAT
 180
 CTGCATAATC TAAAACTCTT TGGCATT CATCTGTCAA TTCTCCTTCA AGGTGAGCTG
 240
 CACGATGTTG TACTTCGNTT TCTGGTTGTC TATTTNNTAA TAGTAAATAT TCTGGGGTAA
 300
 CTTTCAATGC ATTGGCAATT TCAGCTATAT CCTCCATAGG TATTTNTCTG CTACCGNNTN
 360
 CGTATCGGGA TAAGGTAGAT TTATTGACAC CTATCTTAGG TGGAAAATCA GGTAAATTCA
 420
 CATTATTTNC TTTTCGGAGG TTGGGTGATT AATTTANCTA TTTCCGCTGA AGTNCTCATA
 480
 TTCAAATTTA CTCCCGTTTA TTTATACAGT ATAATAACAC TTCCCATATT AGGAAACACT
 540
 AGCATT
 546

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TTATATTATG TTCTGTTGGA CCCAGTAAAA TGTTGCAATG TATGATAAAA AGCCCTTGTT
 60
 TCAATTAATC GAAAATCGAC ACCAATCGTT TCATCATCAT ACGCTAATTC TAATGAAACT
 120

TGTGTGTTCC CCACTGCAAC TTCTTTTACT TTATTGGGAA TATTTAATAA TTGCTGCTGC
 180
 ACTGCTTGTG GGTATCGGT ACTTATTATG AAATCTAAAT CTTTGCTCAT TTCTTTAAAA
 240
 CGACGGAAGC TTCCTGCAGA TGAATATTGA TCGATATAAT TTAATGTATC TATATAATCA
 300
 ATGATTTCTT GATTAAGTCT TCTCATTGGA TCAATTGGAT ATCTATCTTT CTTAGCACAG
 360
 NGGGGTTTCA CAGCTTCTAA TATGGTGTGG TCCGNTTCTT TTAGCAAATC CGCTTAATTC
 420
 ACTTAACTTN TCCCAATNTC ACAANCAACT TGGAAGTGAC GCTTNTATCA ACAAATATTC
 480
 CAACTCTTTA TATAGCTTAG CAATTTCTTG GTTCCAAGTC TGGAANTTTC AAAAGTGGAT
 540
 TAAGACCTCC CGGACTTCTT CCCGGTAATG GT
 572

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1115 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGATGCACTC TGTTAGCATT ATCTTTAAAC ATTAAATATG GATAACCTGA TTGTAATTGT
 60
 GTNTGCGCAA TTAAATTCAA CATTTACGC GCATTCTTTT TCTTTTCTC AACATTTGGG
 120
 TTTGCAACCA TGTCATCATA ATATTTTCT AAATCGATAT CGTCTAATGT CACACCATAT
 180
 TCTTCTTTAA CTGTATGAGG TGCAAACATA TAAAAGTCCT TACCTTCTTT AGCTAAATCG
 240
 AAGAATTTAG ATGGAACAAT TAAACCAGTT GATATTGTAG ATAAACGTAA ATCTTCATCC
 300
 GCATTTACTT NNTTAGTATC TAAAAATTCT TCTACATCAT AATGGAAGAT ATTTAAGGTA
 360
 CACAGCACCA GCACCAGGGC GGTGGACAA GTTGGATCTG CATAGCTAAA GCCACCTTCA
 420
 AGTGACTTAG CAATAGGTAA AACGCCTTNC GCTACGCCTT TAATTCCTTT AATTGCTTCA
 480
 CCACGTGCAC GCAATTTAGA TAAGTTAATT GCAACGCCGC CCCCAATTTT ACTTAATTGG
 540
 TNGNGCAAGG NGGANTCAAT AAAGTTAANT TGAATTTAAG NTGNCAACCC ACTTCTTNNA
 600
 TNNGAAACAT GACTAGCT CACCACGACG CGCACGGNCT GCGTTTAAAA ATGTTGGTGT
 660
 CGCTGGNTGA TATCTTTGTT CAACCATAGC AGAAATAAAT TGTTTAGCTT GTGCTTTATT
 720
 ACCATNTGCT AGGTATAAAG CAACAATGGC AACGTGTTGA TTATAGCTT CTAAGTATTG
 780
 ACTTTTATCA TTTGTTNCA AAGCGTAATC TTTGAAAAAT TTACTAGCTG ACATATAACT
 840
 TGCAAAATTA AACGAGATTG ATNTGGATA ATCAGTGATT TCAATTAGAT CCNCTTCACT
 900
 ATAAATATCA AACACATTGA AATAAAAATC GGTGTCTTCT AAATAACGTA AAACGCTCGA
 960

TTTCAATATT CGAAGAAGAT NGCGTGGGCT TTTTACTTCT TTCTTAAATT AAGCTTACNT
1020
AAAGGTTCCCT TGGGGCTTTT TTCTTAAACT TAAAGGAATC CCATCTTCCT CTTCCCGGTT
1080
NGGGGACCCC AAATATTTTA CTCAAATATT GATGG
1115

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TTCCATGGAG GCATGCGCAC AATCTGCATT GTAATTCATA CAAAATGTT CACCGACTCC
60
CAACCGAATC CACCGAAAAT GCCAACATCT AGAATCGGTT GCACATCATG TTCAACACAT
120
TCTTCGTGCA ATAAATTAGA GAGTTCATTA TTGATGCCAT AACCGATGCT AATTGTATCN
180
CCATAAGTTA AAAACTGAGC AGCACGTCGG AGAATCAATT TCCGACTANT AAAAGGTAAT
240
GCGGGTTCAG GTATTCCATC AATTCGTTCT TCTCAAGACA AGGCTGGTAA ATAATGACTC
300
TGAATTACTT GGCGGTGATT CTTTTCATCT TCTGTGACGA ATACATAATC GACAAGATTT
360
CCTGGGATAA CAACTTCATT CGGTTTTAGG TGATAGTCGT CAACTAAAGC TTTAACTTGN
420
ACAATAACTT TCCCATGATT GGCTTTCGCG TTTAATGCGA CATGATAACA CTCGCTCAAG
480
TACGCTTCTT GAGNTAAATA AATGTTACCT TGTTGATCTG CGTATGTTCC TCTCAGTAGT
540
GCCACATCAA CGCTAGGGAA TGTGTAATGT AAGTATGTTT CATCGTTGAT GGTTACTAAT
600
GAAACTAAAT CATCAGTTGT TCGTGTATTT ACTTTACCGC CACCGTATCT AGGATCAACA
660
GCTGTGTTTA ATCCGATTTT AGTAATAACT CCAGGTAATA ATTGATTACT CTGACGATAA
720
TGAGTTGCAA TGATACCTTG TGGTAAAAAA TAAGCTTCAA TGTCATTATT TTTCATTGCT
780
TGTGCCGTTT TGGAAGAAGC CGTTAAAATG CTCATAATGA CACGTTTAAT CATGCGACGT
840
TCTATAAAAT CATCTAAATC CGGTGCGGCA CCTAAACTAT GGATATCATT CGCTAATATA
900
AACGTTAAAT CTTTGGGCGT ATGATATGTG TCATGTTGCG CTAACACAGC ACGTAGAACT
960
TCGGCGGGTA AGTTGGCTAC AGCTAATGCT GGTAAACCAA TCACATCACC ATCTTTAATG
1020
ATATGTTGTA AGTCGTGCCA TGTGATTTGT TTCAAGCAAG TCACCTCCAT CACATTTGAT
1080
AAAATATAGC GTTTTTACAC TTTGTGTAAA CCCTTACAAG AAG
1123

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 960 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```
CTCCATTTGC ATTTGGGTCT TTAAAACTAA ACACATACTT ATAGTTGCCA TTATGTTCTT
60
CAATAGAATA ATCATTATAC ACTTTATTAT TACTACCAA TTTATTTGCT TCATTATTAG
120
CCGCATTTAA AGCTGTTTGG AAATTTGGCA ATTGCTGTAA AGCTTGAGTT TTATTTCCAT
180
TAAACGGATA AATTTGACGT GCAACCGGCG CGGCATTTTG TCCATAATAT GGTGCAACGT
240
AACTTGATTN TTGATTATTA CTTGATTGGG TTATTATTTG TTTGGGTNTT GGGTCATTGT
300
TTGTTGCATT TGGAATTAGA TTGTTGCTGG TTATCGTTTG CACTATTATC TTTATTATCT
360
TTGNTTACGT CTTNACTATC ATCTTNATTG TCTTTCTTAT CTTNAGATGA ATCANTTGNT
420
TTNTTATCTT GTTGNTCAGT TCTCGCTTTA TCATCTTTTT CTNNATTACT GTCTTTTTGG
480
TGGNGCACTA TCTTGACCAC ATGCAGCTNA AAATAATGAT AATGCTAGTG GACCCTGTAN
540
CTAATCTTTT CATACATATC TCCTCCTATA ATTCGATATT CATTGAATAA GCTTGAAATA
600
CATATCTNCC ATGTGTATCA TTTCATGGCT TGTTACCANA GACGTCAACA TTAATATGAT
660
TTGANTTATC ACAATACCCA TAACTACAAT CTAAGGTTCT TTTTATTATA CCCTAATTTT
720
TGTTCATTAT TATTTAATTT TTGTGAATTT TATGTTTTCT ATAAATTTAA TTATTTTACT
780
TTAACAATTC ATTACGCATT TAGCATTTCA AGGCATACAC AATAGGAATT CCGATGATTT
840
CATTTTATCT TGCTGCAAAA AACAATCATT ATTACTTCTT TTTTCCATAA TTAAATCTTG
900
TATCCCGTTA CATCACCTGG TNTGGAAATG ATGTTCAACC CAACCACTTT TAAATCCAAG
960
```

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```
TTGGCCCTTT GGAGANTCCG GATTATTGAT AAAGATATTC CTAGCGTTCG CTAAGCATAG
60
TTATGTGATG GANAATAGTC TTGTTGAAGA GTTGTTC AAT ATTGCCTCGN CTGTCGCTCC
120
AAGTAATGAT AAGCAGGGTG TTTTANCGAT TATCGAACAA GAAGTATTGN NCAAGTAGGT
180
AGCACATCAT CAATGAAGCG GCTATCATGA TACCTAAATA CATGTTNNAT GNAANCTTTG
```

240
 NATACCGAAT CATCNAACAT TAATATATCT CCAAACAGGT TAGCCAATAA TCCCATAGTA
 300
 AAATAAGCCC ACTACAATCA GTTGAATAGA TGATAAAATA AAGCAGATTT TAATCAANCC
 360
 GATTTTGATA CAGATAAACA ANATANNAAN CAAAGGCACA TGGTGC GCCT GTGCTTTTAA
 420
 ATATATATTA ATTTAAACGT GTTTCACATG TACCCAAGTT GTTAATNGAC AAGATAATTG
 480
 CTGCGTTTAA ANCCACCTT CCAACAAGGT TTTGTACCTG CTTCATCAGA GAAGAAACCA
 540
 ATATGTGGTG TTAATAAAT TCCTTTCATG TTCCGATTAA CTCTAATAAT GTTTTATCGT
 600
 CAATGTCTTT ATTAGTCCAG TCATTTGTGA AGTATGCAGC TTCATTTTCA TAAGTATCAA
 660
 TCGCAGCACC TAACAAAGTA CCATCGTTCA CTGCAGCGAN TAAATCAGGT GTATTGATGA
 720
 CTGCACCACG TGCTGCGTTA ACTAAGATTG CACCTTTTTT CACATGATCA AACATTGCTT
 780
 TATCGAATAA ATGATAGCTT TCTTTGTTTG CTGGAACATG TAAAGAAATA ATATCGGCAT
 840
 CTTTAATAGC TTCTTTAACA CTATCTTTAT AAGTTAAAAA GTCTAAATCT TTATTAGGAT
 900
 AAGCGTCATA AGCTGTAATT GTAGCACCAA ATCCTGCATA TATTTTAGCT GTAGCAGCAC
 960
 CGATACGACC CGTACCGATA ATTGCAACAG TCATATTTTT AACTGGTTTA GACATGATTT
 1020
 CTGCTTGCCA AGTAAAATCA TGTGTTTGTA CACGGCGTTC AATATCTGGG AAGCGACGCA
 1080
 CTAATTGTAG GGCGATAGAA ACAGAATACT CTGCAGTGTT TCAGGGGAAG
 1130

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GCAGTATCAA TAGTAGTTGG TTCATCATTG CCAAACACCT TTTTCAAATT ATCATTTTCA
 60
 AGTTGAAGCG CTACATTTTC TTCTACTAAT TCAACTGCAA GTGCCTTTAA TTCTGAAGTT
 120
 TCCTTTGAAA GTTGATTGAC ATTCATTTCT AAACGCATTA TTTTTCAAA TATTTTCATTG
 180
 CGATCCAAAT GTAATAATGC CTCCTTAATG CATAGTTTCT ATTTCTTCTA ATTTATATTC
 240
 AAGTGGCTGT TCATGTCCCT CAAGCTTCAC CTGCATAGAA ATGTCTAATA TATTTAAAGC
 300
 AACTACTTTC CCGGTTACCA TCAGGCGTTT CAATTGCTTC ACCAATATCA GGTAATTGTG
 360
 CACGTACTTC CTCATAATAG TCATTTTCAT ATTTTAAACA ACACATCAAG ACGACCACAT
 420
 GCAACCAGAA ATTTTAGTTG GATTTAATGA TAAATTTGGG TCCCTTAGCC ATCTTTAATC
 480
 GATACTGGGT TCAAAATCCC CCTAGAAAAT GTAGGAACAA CATAACGACC TACCCACAAG

540
GGTCCCGATA CCGCCAAGCA ATTGGGCTTC AAT
573

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 870 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CCTTAAGAAG CACCTTTACC AATTCCGCCA AAATCTGTAA ANTCAAATGT AGTAGGTAAT
60
GTTTTTTTAG GTTGAACCAT TTCTTCTAAT TTAAGTAGTC TTGCATCTGN CACTTCNACA
120
ATACCCACAT TTGGGTCNAT AGTTGCGANC GGATAGTTTN CTCCCAAGGC ACCCGCCTTT
180
GTAATTGCAT TAAATAATGT TGATTTACCA ACGTTTGGTA AGCCAACGAT ACCTGCTGTT
240
AAAGCCATGA ATCATTCTCC TATCTTNGTG TATCATCCTG AGATACGATG ATTTTTTTTA
300
GTTTTTTATC AAACGTTTGA CGTGGAATCA TAATGCTTCG TTGACAATTT TCACACTTAA
360
TTCTAATGTC AGCACCCATT CTAATAATTT TAAAACGATT GGTTCCACAC GCATGTTGTT
420
TTTTCATTTT TACTATATCA TTTATTCCAT ATTGNGACGC CATTAAATAT GACCTCCATG
480
TATTATAAAC TACTAAACAC CGNTTTCCT ATGATTAAAA GGTGTCATTA TTGGNTGTGG
540
TGTCTTGATA CCTTCTTGTA AAAACATTTT GTGGACTTCT TTACGAATAA TACGCGCACC
600
AGAGAAACCN TCACCTGGTA TTGTTTCTGC TGAAACCCNT AATATTACTC TAGTATCTTC
660
AAAGGCATCA ATACCAATCA CAACAGGATC ACTTACAAAT AAATNNATAT TTAATACGCA
720
GAGGATGGTA AATAATGTGT TTAATTTCTT CTCAACATTA TCAATATTTT CATCTACAGA
780
TACTGGAATT TTAACAATTG CTGTTCCAC TCGGNAATTG AGTAANTCGG TATTCACCCC
840
NTNCTACTAT TTGGGAAGAT TGRRDCTNS
870

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TAAGATATTA AGTTATAAAA ATGATTTGAA AAATAAAGTA GAAACTTAA ACAATTTAAG
60

TCCAAC TAAT ACNATGTTGC GTGGATATGC AATTGTTAAT AAAAAAGACG AAGTCATTAC
 120
 GAGTACTAAA GATTTAACAG AAAATGATCA ATTGACGTTA ACAATGAAAG ATGGCTTAGT
 180
 AGATGCAAAA GTTACGAAAG TAAGGTGTAA TAATGACTAA AGAAACGCAA AGTTTTGAAG
 240
 AAATGATGCA AGAATTAGAG CAAATTGTTC AAAAATTAGA TAATGAAACA GGTATCTTTA
 300
 GAGGAATCAT TAGATTTATA TCAACGTGGG TTTTGAAACT ATCAGCAGCT TGGTGACACA
 360
 ACTTTTAAAA AATGCCGANA AAAAGNGNAA TGA CTTAATA AAAGAAGAAG CTGAGATTGT
 420
 TAAAAATGAC GATCTTCCGA NTGANTTAAT TATAGANGGA NGTCAATATG ATNTCCGGTG
 480
 GCGATAATTA NCCCAGNAAT GGTTCTCNGT NGGAAGGAG
 519

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 734 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CCAATCGCNT GTNTGACTGT NTTGTCACTG ANAGCGTTAT CTTNTTTACC AGANTTGACA
 60
 ACTNACATTN TCGTANTCAT AGGTTGACTA CGCNTAACTT GATAGTCACC TGTATCTTTT
 120
 AATTGTTTTA AAGAGTCTTT GNCTAAGCTA TCCGTACCTC TATCATCTGT GAGCCANAGT
 180
 CGTTTCACCT TTTTTCATTG ATAGGAATGC TGTTTCACCA GCAGGCATTA CTTTGTCTTG
 240
 TACTTTGTTA AGTTAAGACT TTTCGCCCCA GTATTGATCA TTTTGTAA AGTCTGCAGA
 300
 CTCATCTTTT TTGTGTTTAC CTAATTTAAA TGGACCAGTA CCATCGAACT TTTTAACGCC
 360
 ATCTTTTGTT GTACCGTTTT TAAAGTCTTT TGGAGACACA AATACATATG GACGAGGCAT
 420
 CGCTAATTCA GCCAATGCAG GTTGATATGC TTCTTTCAAA TTCAATTCAA CCGTGTACTT
 480
 ATCTTTAACT TTAACATTGT CAATTAATGT TGAAATCTTT AACCAAGAAT GCAATTTTTT
 540
 ATTTTGTGTA NCCGCATCAA TATTTTCTT AACTGCGTCA GCATCAAATG TTGNTCCATC
 600
 ATGGAATCTC ACATCATCTC TTAAATGGAA TTGTATTAAG TCTTCCCATC TTCAAGACAC
 660
 ATCCCATTTT TTAGCTAGGT AAAGGCTTAA TACCATCTTT CGGTGTTACG GTACAAAGCG
 720
 GCTCGTARRD CTNS
 734

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1219 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GNGNTNCTTA TNCGATTCAC AGTGAAGTAG GTGATAAGAT GATTGGTCCC AAGCTGAAAT
60
CCCCAAAATT GTGCCAATTG ACTATATTTT NCAACAGGC GATATTGTTG AAATACGTAC
120
TAGTAAACAT TCATATGGAC CAAGTCGTGA TTGGTTGAAN ATTGTTAAAT CGTCTAGTGC
180
CAAAGGTAAA ATTAAAAGTT TCTTCNCAAN ACAAGATCGT TCATCTAATA TTGAAAAAGC
240
CCGAATGATG GTTGAAGTTG AAATAAAAGA CCAAGGATTT AGAGTCGAAG ATATTTTGAC
300
AGAGAAAAAT ATTCAGGTTG TTAATGANAA ATATAACTTT NCAATGAAG ATGATTTATT
360
CGCAGCTGTA GGATTTGGCG GCGTGACATC CTTACAGATT GTTAATAAAT TAACTGAAAG
420
ACAACGTATT TTAGATAAAC AACGTGCTTT AAATGAAGCA CAAGAAGTTA CGAAATCATT
480
GCCTATTAAA GACAACATCA TTAGTGATAG TGGTGTCTAT GTAGAAGGTT TAGAAAATGT
540
ACTTATCAAG TTGNCAAAAT GTTGTAATCC TATACCAGGT GATGATATTG TAGGTTATAT
600
CACCAAAGGT CACGGCACGA AAGTACATCG CACTGATTGC CCAAATATTA AGAACGAAAC
660
TGAACGACTA ATTAATGTTG AATGGGTAAA ATCNAAAGAC GCAACTCAAA AATATCAGGT
720
TGATTTAGAG GTAACGCGT ATGACCGAAA TGGCTTGTTG AATGAAGTAC TACAAGCTGT
780
TAGCTCGACA GNCGGCAATT TAATTAAAGT TTCAGGACGT TCAGATATTG ATNNAATNC
840
AATAATAAAT ATTAGTGTC TGGTGAAAAA CGTGAATGAT GTTTATCGTG TGGTAGAAAA
900
GACCAAACAA CTTGGTGATG TTTATACAGG TAACAAGAGT TTGGGAACAA GAGGGTCCAA
960
AAATATTGAA AGTAGGTGGT ACAAAGAGG TTAAAGAAGC ATCGGGTGGG CGAATTGATA
1020
CATTAATAA TCAAATCAAA AAAAGGATAT TGGTTTATTA GTCGGGGATC CGGNCAAGAA
1080
CTCTACAAGA GCAAAGATGC AGATGTAATT GCAAAGAAAA TTGCTAATGC AAGATTATTT
1140
GAAGATGACA ATAATAAATT AAACTTTAAT ATCCAACAAA TGAATGGTGA AATACTATCA
1200
GTTTCACAAT TTAGTCTCG
1219

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 498 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ACTAAAATGA TTAAATTACT TATCTCTTTT CATCTGATTG ATTATCGAAA TTTCTTCCTT
 60
 CTAACCTGC TAACTCTTCT TTAGAAGCTG NAGGTGCTTT CATTTCAAAT ATCTCATTCA
 120
 CTACTGTGTA ATCGGAATAT CCTAATCTGG CAATAGGTTT AATCGACTTA ATGTCCAATT
 180
 TACCATTATC AAGAATAACC NTATCGGCAA TATGAACTTG GGCAACTCTT CCTATAACAA
 240
 TATCTACGGT AGATACTGGG TCTCCTGGCG GAATACGAAT CGGGTGAACG GTACTCACAT
 300
 NCAAAATGTA CTGGCGATCT TNGACTCGAT AACCNNGGGG CTTCTATACA ATGNTNCTTN
 360
 CGGGCACAAC CGGNATATTN AAAATNCAAC CCCCCNCAGG TGGGTAGGTG CCTTCCGACG
 420
 GATAAATTAA CAGGCTTCTC TTAAATCAT ACGGTGGCCA TGTNCCAATA CAAACCCACC
 480
 CCGGTTTCTT CCTGGAAT
 498

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 922 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CTGTCAATGA ATATGATGAT ACTGATAAAA TTTTCTCTAA CCCATCAAAC AAGAAAACAG
 60
 AAGATTATAT TTCAGGAAGG TTTGGTTGAT ATATAATGGC AATAATTAGA CAGCGATATC
 120
 AGGAGCAACT TGATGATTTA ATAAAGGAAT TACGTCGGTT AGGTGCAAAT GTCTATGTGA
 180
 GTATTGAAAA TGGTATAAAA TCATTAAGTA TTGACGATAG AGGCTTTGNA CGACAAACAG
 240
 TTAAAAACGA TAAACATATC AATCAATTAA ATTATGATAT TAATGAGCGA GTTATCATGT
 300
 TAATTACAAA GCAACAGNCC ATTGCGAGTG ATTTGCGTAT GATGATTTCT TCAANTAAAA
 360
 ATCGNCTCCG ATTTAGAAAG AATAGGAGAT AATGCATCGA GTATTGCCAA TATTCGATTG
 420
 CGTACAAAGA TTACAGATGA TTATGTGTTA ACCCGTTTAA AGACAATGGG TAAATTAGCT
 480
 ATGTTAATGC TAAAGGACTT AGATCAAGCA TTTAAAAAGA AAGATACCGT ATTAATAAGA
 540
 GAAATAATTG AGCGTGATGA AGATATCGAT GACTTATATA GTCATATTAT TAACGCAACG
 600
 TATCTTATTG ATAACGATCC ATTTGTCGCT GCACAAGCTC ATTTAGCAGC AAGACATTTA
 660
 GAACGTATTG GTGATCATAT TATTAACATC GCTGAAAGTG TTTATTTTAA TTTAACAGGT
 720
 ACACATTACG AACAAATAAC TTAAAGTTAT TACTATAAAA TCCCTTACGA TAAATATATA
 780
 TTTCTATCAT TCATAAACCC TCAAAAAAAA CCAAGATTCT CACAAATTAG NAATGNGTGA
 840
 AAANCTTNGN GNTATATTTT GGTTCCTACT TATTAAATNG GTCTCGCATC TTAGGNTATT

900
TGGNTTGGTC AATTTTCATCT TG
922

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CCAATCGGTC TTATCTTTCA ACACGTTTGA TTGTANCGGA TATCACCCGG TTCATAAATC
60
CNAATCGTT GTAATATATT TCTCTTTATA TTCATTATTT CTAGGAATCC ACCCCCNCCG
120
TGCGGGCAAG TTTCTGGGAA ATTTAACAGC TATCCAGCCT TTCAACAAAT AAATCTGAAA
180
TTCGATGTTT TAAAATTTCT GCTTCTTGAT GTACTTCTTC CCAATTATAT TTCAATATTT
240
CTATTAAAAA TAATTCTAAT AGTCGATGTC TCTTAATGAT ATCAAGCGTA TCGGTTAAAC
300
CATCCTCTGT TAATCTAACA CCTTTGTATG GTTTTGTTTC AACATAGCCT GCTTTTTTCAA
360
GACGTCCTAC CATTTCACTT ACAGATGGAG GCTTAATATT TAAAAATTGA GATAAGATTT
420
TATTTGTCAC AAAGTTTTTA TCGCCATTAA TTCGTAAGGA TTTGCCTTTA AAATAAGTCC
480
TCTTTTTCTT CAGNTAACAT ACTTTACCT CAACAGACAT TGTCTATATT ATATCACGAA
540
TTTACTTGAC ATGATAAATA TTCTCAGTTT ATTANACAAT TAATTAGGTT AGCCTAAACT
600
TTTAATTAGG AGGTATAAAC GTTTGTTAGA AACANAAGAT TTAAATCTGT TTTTAGGTAA
660
TAAGCATGTA CTAAAAACA TTTCTTATC GATACCAGCA CGAGCGGCGA AATAATTGGT
720
ATCATGGGCC CGAATGGTGC TGGTAAATCT TCCCTTATCA AGTCTTTAAT TGGTGAATTT
780
AATGCTACCG GTACTAAATN GTTNTATAAC AAACCTATAC AACAACAACN GCAACAGATT
840
ACATATATTC CACAAAAAGC ACATATTGAT TTAGATTTTC CTATAAGTGT GGAACAAGTG
900
ATTTTATCAG GTTGCTACAA AGAAATTGGA TGGTTTAGAC GACCTAATAA ATCAGCAAGG
960
GATTAAACTC AAACAGTTAT TAAGCGATTT AGAATTAGAA TCTTTTACGT CATCGACAAA
1020
ATTTCAAGAA TTAAGTGGGT GGGACAAATT ACAACGGTGG TGCTTANGTA GGAAAGAGCA
1080
TTGGATGGTC CCGAAAAGTG AAGGTTTATT TTCTTTAGAT NGAGCCCGGT TGGTCGGGAA
1140
TTTGGATTTT AGGGTAGCGA AAAAATTAAT CAATGACAAA AAATCCGAGA ACTTTAAAC
1200
AACAAAGGA
1209

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GAATTCATNT TATCTATCGG NAATCATTTG TAATACATCT ACTAATTATA GTGTTTTATT
60
CGATAATATA ACTGCATGTA CATCTANAGA AGCCTCTTGC CTNGAAATCG CACCGTCAAA
120
CTTAAACTA TAACCTATTA AATCTGCTTG NGTGNCATTA CCACTCACAG NACAGCGATT
180
AAATGATGCA GTAGCAACCA AATCGTTTCA TGCACTTNCA CATAANTACG ACTGACATTA
240
NGCTGTGTAG ATGTACCTGC TTCTANCTCG CCAAGAACAT CTTGGANTNC GNGNTNGCTA
300
TTTGGNGCAA TGTCANCTTC ATCCATNGAG CGCTCAATAG TGTCAGCTGC CAGAGCGGCA
360
TAACTGCTT
369

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CCTTATTATA AATTAAAGAA AGGTAGTGGT TTCTATGAAA TACAATACTA ATGTTAAACA
60
TACAACTTTA GAAGCGTTTG TCACAACTGT CAATGATTTG GGTATTGAAT TAATTATCAA
120
TGAAGCACTT CGAGAGGTAA GAAAACGACA GCTCATAGAA CTTATAGATG ACGCACTCGT
180
CAATAAAGAT GAAGCAGCAT TTAATCAATA TACGGCAGAA TACAAAAATT TGGAGGCATT
240
TCTCGGTGNA TAACATTGAT TCGAATTC
268

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CTATACAACT AAAGTAATTC ACAATTCAAA CTTTGTAAAG GGTGTACAAA GTGAAAGTAG

60
 CAGTCATTAT GGGCAGTTCT TCCGATTGGA AAATTATGCA AGAGAGTTGT AACATGTTGG
 120
 ATTATTTGGA AATTCCGTAC GAAAAACAAG TAGTATCCGC ACATCGTACG CCAAAAATGA
 180
 TGGTTCAATT TGCTTCTGAA GCGAGAGAAA GAGGTATAAA CATTATCATT GCAGGCGCTG
 240
 GCGGTGCGGN ACATTTACCA GGTATGGTTG CATCATTAAC GACGCTACCA GTTATTGGTG
 300
 TGCCGATTGA AACANAAAAG TTAAAGGGT ATTAGATTCT TTTATTATCA ATTGCTCAAA
 360
 ATGNCAGGAG GGTATTCCNG NTGGAACGAC TTGCAANTGG GTGCAGNAGG GTGCTTAAAA
 420
 ACGCAGGTAT TCTTGGCAGG AAGAATGTTA AGTNTTCAA ANTCTCTTT TGGNNGGANA
 480
 ANTTAATCAA GNTTGATCTT CCGNAATCAA AA
 512

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GAATTCCTCGC ATTTAATTGA ACTTTATAAT ATTTGTAGTC ATCCACAAGC
 60
 AAATATATAC ACTCCCAAAG GTTTACATAA TTCCAAATTA GACACACAAC GGTGGATTGA
 120
 AAAATGGCAA AACCATTGGC AACAATATCA ATTTGGTTAC TTTGTATTGG TGAAAAAAT
 180
 AGATTGTAGT GNTATTGGTA TTTGTGGATA TGAATATCGA CAATTAAAGC AAGAAACAGN
 240
 ACTAANTTTA TTTNATAAAT TACATCCAAG TTTTGGNGGA CAAGGGGTAC GCATGTGAGG
 300
 CTNTTACAGC AATCACAAT T
 321

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GGCAGGACTC GTGCCGCTCC TGCACAAGAT GTAGGAGCAT TTTTATATTT AAATAACTAG
 60
 AGTAATTAAC GTAAAGGCGT GTGATACAGT GAAAACAATT GATTAAATTA ACACCGAAGC
 120
 AAGAAAAGTT TGTGCTAGGA CTCATAGAGG GCAAGAGCCA ACGGAAAGCA TATATTGACG
 180

CAGGGTATTC GACTAAAGGT AAAAGTGATA ATTATATTGA TAGCCGAGCT TTTGAGTTGA
 240
 GTAAGAATAG TGCGGGTTTA GATAGGTATG AAGAATTGCG TCAAGAAGCA GGTGAACAA
 300
 TCAAAATGGA CACGCCAAAA GGGTTTTGAA GAATATGAGT GGGTAAAGAA TGTNGCTAAG
 360
 AATTGACATT GNAATAGAGG GGAGGTAAAG GAAAGGGACA GGTTGATGCA TTCCCCCCTA
 420
 GT
 422

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GGCCCCGAGCG GGA CTTAAAA AGGCCACCAC TGTTGTGAC CTANCCTTAT TTACNTTTAT
 60
 AAATATAAGG AGGAGGTAGT AGTGAAAGAC TTATTGCAAG CACAGCAAAA GCTTATACCG
 120
 GATCTCATAG ATAAAATGTA TAAACGTTTC TCTATTCTTA CTACTATCTC AAAAAATCAG
 180
 CCTGTCGGAC GTCGAAGTTT AAGCGAACAT ATGGATATGA CTGAACGTGT ACTGCGCTCT
 240
 GAAACAGATA TGCTTAAGAA ACAAGATGTG ATAAAAGTTA AGCCTACCGG AATGGAAATT
 300
 ACAGCTGAAG GTGAGCAACT GATTTCGCAA TTGAAAGGTT ACTGNGATAT CTATGGAGAT
 360
 GATAATCGTC TTGTCAAGAA GGGTATTTAA AGAAT
 395

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CTGTGATTTA TCATTGATT GCATGATTAG AGGGAGGGAT TAAACGTGAC ATATCATGAG
 60
 CGTGTTTTAG CATTAAAGAGC AGANAGTAAN AGNNCCGCAT TTGATTTTCG ATTCGGNAGA
 120
 TTTATTTACC NAAGAAGAAT GGCTAAGTAT GTCTCTTGCA GAAAGACNCA AAGCTGANAA
 180
 AGCATTTCTGA CACGNAGTTA AAAATATGGA CGATGTAAGA ATGCCCTTCT CAAGTGTCCA
 240
 TGACGCCCCA AGTAAAATTA TATAATGTTG TATATTCTGA TANC GG CATT AAACGTAATT
 300
 TTAAACNAGC TGAAAATGAA GGATTCTAAT ATCATTTTCGT TTATATATAG CAGACATGAT

360
 AGAATTTTAT ATGTAAATCT TGTAGGTAAT CGTTTTNNAA ATAATATAAG TATGACTAAA
 420
 NCCACATCCA ATATAGGACG GGGCTTTTAG TATCGTTCCA GATTTGTGGG GAGTTAGGGT
 480
 TTACTTAATT AAAGGGGTCT GCCCTCAATT GCTCACCAAC GAGGGCAAGT TACATCAATC
 540
 ACAC TTCAAT TGCCGCCGAC TAGGGGTAGT AATCATTGGC AATAAGAACT AGTTAGTGAC
 600
 TAACGGATTT AC GTTCCATA AGCAAAGTGA TACAAACGCT CAGCATCAAT GTAAGGCATA
 660
 GAATCAATAG TTAGGTAACC ATCTTTGATG TCACCAATTA ATCCTTGATT TACACCAGTG
 720
 TTCACGTAAA TATCATAGCT ACTTACGTCT GAGAAAATAA GCGCTTCAAT CTCTTTTCTC
 780
 ATAATCATCA CTCCAATGTT TATATATTAT TTATATAAAC TCTCTCGTCT CTCTCTATTT
 840
 ATTAAC TTCT TACAAGTCTA ATATTACATG AATTTCCAAA TAAATAAAGA GGT TTGTGAT
 900
 GTATTT CACA AATTTATCAC TATTTTGGAA AATTAAGAAA TAGTTAATTA TATAAAAGTT
 960
 TAATAAGTCA GAAAATATGA TAAATGTAG ATGTTCTTTA GACATTAAAA GCTTCTAACA
 1020
 TGATACGGAA TATGAGG TTC CTGTATCACA TTAGAAGCTT TTTTGTGCG GTGCTTATAT
 1080
 TAATAATGGC ATGAATGAAC GCATGCTGTC TTAGTTTCAG GAATCGGCTA GAATATTAAA
 1140
 CTTCCGTTCT TTGAATATTT NTTAATTTCT TACTAATATC ATCCAGTTCA TTCTTCGCCT
 1200
 TTTTAACCCA ATCTCCTTGA GCTACATTAT CAAATTCACC TTAAATTTT TTGANATGGC
 1260
 TACCTATATT TCACAGCTCA CTTTAGATAT CGAACTTGTT TCTTCAGAGT TACTTGTTAT
 1320
 ATTACCAGGT TTTATTTGAT ATTCAGTTTG ACTCATAACT TGTATCCTCA CTTGAAGTAT
 1380
 AGTG TACAGA ATCTGTAAAA TAAATGTTTT CTTCTTTATT TTCTACAAAG GTAAATTCTA
 1440
 GATTTTTTGA CCCTACAGAT GAGCCTTTTA AATCACCATC NCCTTTTATT AAG
 1493

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TGATGTGATC CAACCAAGTG ATAGCAATGT ATATGCAGTT GGAGAATGTG CAGAACATAC
 60
 CGCCAAAGTT TATGGACTCG TTGCACCACT ATATGAACAA GGTAAGTAA AGCTGATCAT
 120
 TTAACAAATA AAGAAACGAA CGGATACAAG GGATCAACAA CAAATTACGT CATTAAAAGT
 180
 TTCTGGTTGT GACTTG TATA GTGCTGGTCA AAGTTGTAGA AAATGCAGAA ATTAAAGGTA
 240
 TTGAAATATT TAATAGTGTT GATAATAACA ATAAAAAAT CTTTTTAAAA GACGGTAATG

300
 TAGTTGGTGC AGTATCGTGC CAATATGGTG ATATCGATGA TGGTTCACGC TTTTATAACA
 360
 TGATGAAAAA AGGTGAATCC ACTGAAGATT ACACACTTGT ATCATTGCTT ACTAAAGGTG
 420
 GAGAAGAGGC ATCGCTATCA ATTGCTGATA TGGCTGATGA TGAAACAATT TGTGGTTGTA
 480
 ATGGTGTTGA TAAAGGTACT ATAGTAAATG CGATTACGGA AAATGGCTTT ACAACAGTTG
 540
 AAGAAGTAAC GGCTAAAACA AAAGCGGGGA ATTCATGTGG TAAATGTAAA CCGCAAATTG
 600
 CTCAAATATT GCAGCACACC TTAGGAGATG ACTTTGTTGC CGCAAAACCT GCTGGTATAT
 660
 GTGGTTGTAC TGATTTGACA CGCGATCAAA TTGTAACGCA AATAAGAGCG AAAGGTTTAA
 720
 AAACATCTAA AGAAGTTCGA CATGTTTTAA ACTTTAAAAA TAAAGGTGGA TGTCCAAAAT
 780
 GTCGACCAGC AATCAACTAT TATTTAAACA TGGTTTATCC ACATGATCAT GAAGATGAAA
 840
 GAGAATCAAG ATTTGCTAAC GAACGTTACC ATGCGAATAT TCAAATGAT GGTACATTTT
 900
 CTGTTATACC TCAAATGCGT GGAGGTGTTA CAGATGCAGA CCAACTGATT CGTCTAGGAG
 960
 AAGTGGCTAA GAAATATCAT GTGCCACTAG TTAAAGTGAC AGGTTGCGAA CGTGTTGGTT
 1020
 TGTATGGAGG TTAAAAAAGA AGAATTACCA AATATATGGG AAGACTAGGT ATGCGTTCAG
 1080
 CATCAGCTTA TGTAAGAAA ACACGCTCAA GTTAAAAGCT GTGTTGGGTA AAGAGTTTGG
 1140
 GCGATTGGGT ACGCAATACA ACGACAACGA CTTGGGATCC GTTTAGAAAA ACATTTGGGT
 1200
 TCAATCGATC AACCC
 1215

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 760 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

TTACCTCCAA AATCCTTTTA AATCCATGCC CATAGAAGAT GANNCCCAA ATACATTANC
 60
 TAAATCGAAA CATTGCCATC CATAACTACC GTCGAAATCC CATCCTCTAT TCTCTAATGT
 120
 TCTCAAATAA NTTAATGTAC TGCTATTACT ATTACTTTTA TTATTTGAAG ACACTGTTTN
 180
 TGGTNTTGGT TCTACTAATG GTGTCATTGG CACTTTTAAN TTTGACCAA NAAATANTAA
 240
 ATTAGGATTT GCTATATTAT TTGTATTTTG AATATTTGAA ACTGAAGTTT NGTACTTTTA
 300
 ATGCNATAGC ACTAAGTGTG TCTCCTTTTT TTACAGTATA GAGTTGTGTT TTTGGAGCTT
 360
 CTCTAAACCT GTAGTAACCA AAGTAATTAG TAAGTAACNT TAATCGTTTT CTTCTGATAA
 420
 GAATNTTTGA GCTTCCAAGT TTGCAATNTT AANTTCTTNA GTAGGTNCAT TGTANTTAA

480
 TAAC TAGATT GTTACNTGG CTTGAGTTTT TCGGAGTATT TGAAATCTTT ATATCTTGAT
 540
 TAATTTTATT TCCGTTTGAA ATTGCTGATT TGTTGTCTAA CTTTAAACTT GTGTCCGATG
 600
 TTTTAACAGC ACCTTCATTT TTTATTTTGT CTTTGTCTGT ATTTTATTA GCATTTAACT
 660
 CTGATTTTCGC TCGAATACAT TTTGCTCATA CCCTCTTGTA AAATCTTTAG ATTTATCAAT
 720
 TTCATCTGCA TATGCTTNGT TCGACATACC CAATGCCAAG
 760

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ATATGCTGAA AATGTATCAT CAGGATTCAA GATATCAATT AAATGATGTG GAATACCATC
 60
 CATTTCTTCA GGTGTTACTT GTGCAGTTCC AATATTCATA TGTTTGTAAG CTTGCATAGA
 120
 ATCACCGCTT ATGATTTTAC CATTGATACG CTTTCGCGAGT TCTATGCTAA GCTCTGTTTT
 180
 ACCTGAAGCA GTTGGCCCCA CAATTACTAC AATAAAAGGC TTATTTTTTAT TCATATTTAA
 240
 TTCCACTTTC TTTATTTTTT ATAAAATTGA TTCAACCATT TAAACAAGTC TTCCCAAATT
 300
 GTGTCATGAT CTTTTTTTCAA ATAACACTTC ATGACGTTTA TGATGATAAA GATTCACTTT
 360
 TAACAATTTT TAATGCCAGC TTCTCTATAT ATATTCGCCA ATTTTAAAAT CCCTTTACCA
 420
 TAATCACCTA AAGAATCGGC ATATCCTGAA ACTAATAATA TAGGCATGGC ATGATTTAAC
 480
 ATTTTCATAT TTTTAAATTG TGATGTATGT AGCATATAAT AGGCTGTGTG ATATAATAAT
 540
 TGATNTGACA CATTAAATCC ACTATATGGA TCTTTAATAA AGTTATCTAC TTCAATTGGA
 600
 TTACTAGAAA TCCAATCACT NTGTGTACGT AATGGACGTA TTTTTTTATT AAAACTATNT
 660
 GATACTAACT GGTAAACCCA TNCAACTCGT TTCTCAGCAC CATAAATTTG TGTAATCAGT
 720
 TGTAACACTT TAACGGTTGG GTAAACCTTT CCATAATTGA ATACATACCA AGGTCACCAC
 780
 TTTAAATTA GACCATCAAC ATATTTGCGG ATATTGGTTT CTTACAAAAC AATCTTAGTT
 840
 ATACGG
 846

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2854 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```
AAGNTGAATT TTTAGTACAA TTTCCACTGT ATTTATCTGT TANCCACTTT ATACCCGCAA
60
TATTTTCGTTG ATCTTATATA AACACTTTTG GCTGCTTTTC CTTGACCNAG GNTAANATTA
120
NAGATTTTCC TTTGTAAGAG TGTGTTTTGT AGTATCATAA ATATGTAANC TGTATNAAAN
180
TCCACCACAT TTTAGGACCT GGTGANAGAT GTCGNAAAAG AANATTTTAA TATTANCTAG
240
TATTATGTTA ATCATANTAA TTAGTGTTGC AAGTATCNAN TTAAAATGA AATATGACGA
300
AAAAGAAAAC CAAAAATCAA TTTATTATAA AGAACAACAA NCGCGCATT A CACTTTATCT
360
TAAGCATAAT ACTATAGAAC CGAACACAAC CAANTCTGNA CATTTNCNA AATTGGAANC
420
AANTCCTATG GGAAGTGCTG TGATTGAAGG TTACATAAAT GANAATAAAG AAGATGATTT
480
TGTTGCCTAT GCATCACCTG AAAATAACTT TCAATTTGTA GGTGATTTAN TTNNAAAGTG
540
AAAGATTAAG TGAGTTACTA AAACCAGCGC ATCAATTNNA ACATCNCCAG ATGATATNNN
600
NNAAGAACTA AATANNAAGT AGAGTCACTA ANGTTAGGAG TTACTTTAAT GAACAAAAAA
660
CATGTTTTTG TAATTATTGG TGTCATTTTA TGTATATGTA TAGTTGCATC AGTCATTTAT
720
TTAAAAGTGA AATATGACGA AAAAGAAAAA CAAAAAGCA AAATACTATA AAGAACAACA
780
GGAGCGTATT ACACTCTATC TCCAGCATAA TACCAAAGAA CCCAATACCA TCAAATCTGT
840
GCATTTCACT AGTTTAAAAA GAGGACCCAT GGGCGATGCC GTAATTGAAG GCTACATCAA
900
TGAAANCAAA AAAGATAATT TTAGTGCTTA TGCTACACCA GAACATAATT ATCAGTTTGG
960
TGGTGCTATG ATAGAAAGTG AAAGATTAAG TGAGTTACTA AAACCAGCGC ATCAATTAAA
1020
ATCACCTGAC GAAATCAAAG AAGAATTAGA CACCNAAGAA GGCCACTAGG GTCTTCTTTA
1080
TTTTTGATTT AATCTTCCAA TAATCTATGT CATTGCTATC GAAGGTGTTT CGCAATTAAT
1140
ATCAATCACT TCATCATCAC CAATACTTCC CCAGTTTTGT ACAGTACATT AACACAAGCG
1200
AACCCCATTA ATGTAAATGA AATAATAGTT TAGCCATTAT AAAACATTA TATACCGAAT
1260
AACAAATGGCG AGGACGTGAT TTATTGACNA CTATCAAATT TTCTCANATG TGTGTGATTT
1320
TTTATAANNN AGGGTAGAGC AAGGTATAAT ATCCTTTCAA TCGGTTTTCA TATTTTATAT
1380
ATTTTTTAAA TATAAGCGCT AAATGTTTTA ACTAAAGCAT AGATTGACAA GATGTTATAC
1440
AGAAATTTAA ATTCTATCCA ATATTGTTG AAGTGTAAGT TCACTGGANT GGTATTAAAC
1500
AATGTAAAGG AGAGATTGCA NATGCCGTAT AATTACAAGA AACACAATGG AGAGTTAATG
1560
TCTGTAATGA GCCAAGGTGA AAAGTTTATT CATCCAATCC ACCGGTGAAT GATGAACTTA
1620
GTGCATTGAT TAAAGCTATT AATCTCCAAC AAATTAACGG TTGTCATTAT TGTGTTGATA
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1680
 NCCANAANAA AGAAGTAAAG GAANTGGGTG TAACACAACCT GANNATTGAT GAAGTCTTGA
 1740
 NNTTTAGACA TTTAGANTTA TTTACTTGAT CAAGAAAAAG TGACGCTTGA AGTTGCAGAA
 1800
 ATGNTAAATT CAANCAAGA CNTTAAGAAG TTTGAAATTA TTGACCGGCN AAAATCATTT
 1860
 TATGATGAAG AACAANTTAT TGATCTTGTC TTTGTTGTAA ACCAAATTAA CGGTTGGAAC
 1920
 AGACTAAATA TTATTAGTGA TAGACTATAA TTGTTTCATAT AAATGCAGAG TTTTCATCTCG
 1980
 AACGCTATAT CATAACAANT CATGCCACTA TACAGGTCAA ATCTTGTATA GTGGCATTTT
 2040
 TAATTTATCC CTTTGAATAC TGTTATTTAA CGAATATCGG TCCACCTGGT CCAACAGGGA
 2100
 TACCTAATAA GAACCAAATG ATGACAAATA CTGTCCATAC AATGCTTAGC GCGATTGAAT
 2160
 ACGGCATTAA ACTAGAAAGT AAGGCTCCGA GTTTCATGCG TTTATCGTAT TTTTGTGCAT
 2220
 AAGTTAATAA TAAAGGTAAG TACGGCATCA TCGGTGTAAT TGGATTGGTA ATTGAATCGC
 2280
 CTACACGGTA AATGACTTGC GTAAATGCGG GATGAAAGCC GATAAGGATT AACATTGGTA
 2340
 CGAATATCGG TCCTAAAATA CCCCATTTAG CCGATGCGCT TCCGATTAAC ATGTTGACCA
 2400
 TTGCACTCAG TACAATAATA CCTAGTATCA ATACAATACC GTTTTGATGT TCTAATAATT
 2460
 TGGCACCTTT AACAGCAGCG ATAATTCCTA AATTACTCCA CTTTAAATAC GCAAGTAGCT
 2520
 GTGCTGCAA AAACACAATA ACGATAAATG TTCCCATTGA TCCTACAGCA TCGCCGAACA
 2580
 TTTTACCTAA GTCTTTTGTA TTTTAAATTT CTTTGCTTAA AATCCCATAA ACTAATCCAG
 2640
 GTACTAAAA TACGACAAGA ATAATTAATC CGACACCGTT AATTAATGGC GCATCGTCTA
 2700
 GTAAGCTGCC TGTTTTAGCA TTTCTTAAAA AACTATGTTT AGGAATAGCT GTAATAATTA
 2760
 ATAAAATAAT TGTGACTATG AAAGTATAT TTGCCCATTT TAAAGCATGT GCTTCTTTGT
 2820
 CAGTAATATG TGAAGATGCT TCTTCAGGT CATG
 2854

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CTATGATAGN ATCGGAAAGA TGTATAAAGT TATCTAAAAG TTATACGACA CAAGTACACG
 60
 AGGCACATCG CTATGCGGTG TGTCTTNTGG TATGCAATCA AAGAGGTGTA AGAGATGACC
 120
 AAGCATAATA ACATTTATTA GCATGGNCGT AAGTCATATC AATACGATTG GTTCTATCAT
 180
 TCAAAAGCAT GGAAGAAGTT AAGAGAGATA GCATTAGATA GGGATAATCA TCTTTGTCAA

240
 ATGTGTTTAC GTGAAGACAT NGTAACAGAT GCAAACATAG TGCATCATAT TATTTATGTT
 300
 GATGAAGATT TTAATAAAGC TTTAGACTTA GATAATTTGA TGTCAGTTTG TTATAGCTGT
 360
 CATAACAAAA TTCATGCAAA TGATAATGAC AAAAGTAATC TTAAGAAAAT TAGAGTATTA
 420
 AAAATTTTAA TAAAAAATA ATTTATTTTT ATAGCCCCCT ACCCATCGGC TTAAATGTT
 480
 TTTTCGACGG GTACCGGCGG GGGCCCTTCG CTTGCAACGC GGATAAACTT TTATGAAAGG
 540
 GGGTCTTTAT ATGAAATTAA CAAAAAACA GCTGAAAGAA TATATAGAGG ATTATAAAAA
 600
 ATCTGATGAC ATATTAATTA ATTTGTATAT AGAAACGTAT GAATTTTATT GTCGGTTAAG
 660
 AGATGAACTT AAAAATAGTG ATTTGGATGA TAGAGCATAC AAACAAGGCT GGTGCCGAGC
 720
 AATATTGTTA AGAATCCATT AAGCATAGAA CTGACAAAAA CAGNTCAAAC ACTAAATAAC
 780
 TTACTCAAGT CTATGGGTTT ANCTGCAGCA CAAAGAAAAA AGATAGCNCA AGAAGAAGGT
 840
 GGATTCGGTG ACTATTAAAG TTTTAAATGA ACCTTCACCA AAATATTAA CAACATGGTA
 900
 TGCAGAGCAA GTCACTCAAG GGAAAATAAA AACAAGCAAA TATGTTAAAA AAGAATGTGA
 960
 GAGACACCTT AGATATCTAG AAAATGGAGG TAAATGGGTA TTTGATGAAG AATTAGCGCA
 1020
 CCGCCCTATT CGATTCATAG AAAAGTTTTG TAAACNTCC AAAGGATCTA AACGTCAACT
 1080
 TGCATTACAA CCATGGCAAC ATTTTATTAT TGGCAGTTTG TTTGGTTGGG TTCATAAAGA
 1140
 AACAAAAC TGCGAGGTTTA AAGAAGCTTT GATATTTATG GGGGCGAAAA AATGGTAAAA
 1200
 CAACTACTAT ATCTGGTGTT GCTAACTATG CTGTTTCTCA AGATGGAGAA AACGGCGCTG
 1260
 AAATCCATCT NTTAGCAAAC GTAATGAAAC AAGCTAGGAT TCTATTTGAT GAATCTAAGG
 1320
 CGATGATTAA AGCTAGCCCA NAGCTTAGAG AAAATTTTAG ACCTTTGAGA GATGAAATTC
 1380
 ATTACGATGC ACTATATCTT AAAATATGCA CAGGCTTCAG ACAGTGATAA GTGGTTGGTT
 1440
 AA
 1442

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GAATTCAGC CGACCGATGA NGGTTATNTG ANATTACATA AGACGTGGTT TNGTNANTCA
 60
 AAGCTATGTC CAGTTTGTA TCGGAGGCGT GCTATGAAAA NTAGTTATCA CGCTCANANA
 120
 GTGATTGANG ANGTAATTAA GGAAAAGCCA NCAGCACGTT GGTGTTTTTC ACCACTNTCA

180
 CCAANANNTG CGATAGATGG AGATACTTTA GTAACAAAGT TNGANGCATC TAACTAANGC
 240
 ATTTGATAGG TTGAGTAGCA TATNAAAAGG TTAAACANAA TCTNGTTGGA TCTATGCGTN
 300
 CAACAGAAGT TNCCGCCTAC CTAAAAATGA CG
 332

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1070 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CCATCCGTTT NCNTCATCNC ANGACNTTCN ANANTTAATT TTTACNAGGA GTGACATCTG
 60
 TGAATAACAC ACAATCCTCA CCACGCAGTN ATANTATTAT TGCGATTATG TTGTCTGCAT
 120
 TAACATATTG GGTGTGTGNA CAATCATTTA TTAATATAGG ACCTCTCGNN GGNCAAACGT
 180
 ATCAAACCTC TCCTGCCGTG TTAAATTTAT CTATTAGTTT AACTTCCCTC GCCACAGGTA
 240
 TCTTCATGGT GGCTGCAGGT GATATTGCTG ATAAAATAGG ACAANTGAGA ATGACATACA
 300
 TGGGTCTCAT AATCAGNATG TTTGNATCTC TTCTATTAAT TATATCGGAC ATCACTGCAC
 360
 TGCTCATCAT CGGNAGGAAT TTTACAAGGT CTATCAGCAG NTATCTTGGT TACCCTCCAA
 420
 CAGTTGGCGT TTAAATAAT CAATTTAAAG GAGAACATTT AAGACGAGCG ATTAGTTATC
 480
 TAATGATTAG TACTGTTGGG GGCATCGGCC TAGCTGGTGT TATCGGCGGT TTAATTGCTA
 540
 CAAATTTTCG ATGGCAAATG AATTTTCATCA TTAGTATAGT CATTGNTTTC ATTGCCATAT
 600
 TACTTCTAAA AGGCACACCT GAAAAAGTAA GTCAACATAG NCACCGTCAT CCGTTTCGATT
 660
 ACAAAGGTAT GTCGATTTTC GCTGTTATGA TTGGTAGCTT TACATTATTG TTAACACAAG
 720
 GATTGGAACA AGGTTGGTTT AGTACATTCT CATTCAATTG TCTGAGCATT TTTATCATCA
 780
 CTACGCTGAT ATTCATCATC ATCGAACGTC GACATGAAGT ACCCTTTTAT TGATTTCTCA
 840
 GTATTACGCA ACCGNCCGNT CATTGGTGCA TTTTAAATA ACTTTGTTTT AAATAGCGGT
 900
 CTAGGCGTTA CAGTGGTCTT TTTCATATAT GCTCAAACAC ACCTTGGTTT ATCAGCTGCG
 960
 CAATCTGGAT TGNTACATTG GCATATNCCA TAGTGGTAGT TGCGATGATT CGTCTTAGGT
 1020
 GAAAAAGCA ACATTACGGT TCGGGTGGGC AAATTGGATG CTCATCATGG
 1070

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1246 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GAACAANTGG TAAAACCACG ACTTCNAACT TAATTGGACN TACTTTAAAA GCAAATAATA
60
TNCNAATTAT ACNCAATAAT GAAGGTGCTA ATATGGCTGC AGGTATAACT TCTGCATNCA
120
TCATGCAATC AACACCTAAG ACTAAAATTG CGCTAATCGA AATTGATGAA GGTTCGANTC
180
CACGTGTGTT AANAGAAGTT ACACCTNCAN TGATGGTATT TACTAATTTT TTNAGAGATC
240
AAATGGATCG CTTCCGTGAA ATTGATATTA TGGTTAATNA CATNGNAGAG ACAATTAGTA
300
ATANAGGCAT CAANTTATTG CTAAATGCTG ATGATCCATG TGNGAGTCGG GTGAAAATCG
360
CAAGTGANAC GATTGTGTAC TATGGTATGA AAGCACATGC CCATGAATTT GNACAAATGT
420
ACGATGAATG AAAGTAGATA TTGNCCAANC TGTGGTCGCT TATTGCAATA CGATTATATT
480
CATTATAATC AAATNGGTCA TTATCACTGT CAGNGTGGTT TCANACGAGA GCAAGCAAAA
540
TATGAAATAT CANGTTTTGA TGTGGCACCG TTTCTATATC TANATATCAA TGATGAAAAN
600
TNTGATATGA AAATTGCAGG TGACTTGAAC GCTTATAACG CGTTAGNAGC ATATACTGTT
660
TNAAGAGAGC TAGGGTTAAA TGAACAANCA AATTAANAAT GGCTTTGAAT ACGTATACAT
720
CAGACAATGG TCGCTATGCA GTACTTTTAA NANAGAACGA AAAGAAGCGA TGAATCAANT
780
TTAGCTAAAA ATCCTGCAGG AATGAATGCA NAGTCTATCA AGTGGGTGAA CAATTAGAAG
840
GCGAAAAAGT GTATGTTATT TCGCTAAATG ATAACGCTGC AGATGGTCGA GATACTTCAT
900
GGATTTATGA TGCAGATTTT GGAAAAATTA TCTAAGCAAC AAATTGAAGC TATCATCGTG
960
ACAGGTACAC GAGCAGAAGA ACTTCAATTG CGATTGAAGT TAGCAGAGGT TGAAGTACCA
1020
ATTATTGTTG AGCGTGATAT TTATAAAGCA ACGGCAAAGA CTATGGATTA TAAGGTTTCA
1080
CAGTTGCAAT ACCAAACTAT ACATCAATTA GCGCCTATGC TTGACAATTA AACCGTCCGT
1140
TTGAAGGAGG GCAATCATAA TATGCATGAA TTGACTATTT ATCATTTNAT GTCAGATAAA
1200
TTGAATTTAT NCAGTGATAT AGGAAATATT ATTGCTTTAA GACAAC
1246

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 751 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CATTCAAGAA TTATCTATAC TTTAAGCCCG ACTAAAATCT ATAGAACAGC ATTACTAAAA
60
GATAATGACA TTTATTTTCC AGAAGAATTA AAGAGTGCAG AAGATCAATT ATTTACAATG
120
AAAGCATATT TGAATGCAAA TCGAATCAGT GTGTTAAGTG ATAAAGCGTA TTATTATGCT
180
ACAAAGCGTG AAGGTGAACA TATGAGTAGT GCGTATGTTT CACCTGAAGA CTTTTACGAA
240
GTCATGAGAT TGATTGCTGT AGAAATATTA AATGCAGATT TAGAAGAAGC TCATAAAGGA
300
TCAAATCTTA GCAGGAATTT TTAAATCCGN CATTTTAGTT TTTCTCCGTA CGAATGGCTT
360
CTCACTTAAA GTTAAACTTG AAGAGCAACC ACAATGGATT AATGCTCTAG GAGGACTTTA
420
TACAAGCAGT TCCAGAACGT GTAGATGCAT TGGTGATGAG TAAATTACGA CCATTGTTGC
480
ACTACGCGAG AGCGAAAGAT ATAGACAACT ATAGAACTGT AGAAGAAAGT TACCGTCAAG
540
GTCAATACTA CCGTTNNGNT ATTGTAGATG GTAAATTAAA CATTCAATTC AATGAAGGCG
600
AACCATACTT TGGAAGGCAT TGATATCGCT AAGCCAAAAG TGAAAATGAC AGCATTTAAA
660
TTTGGATAAT CATAAAATTG NTACAGGAGC TAACGGTTAA ATGATTTATG ATTGGCGAAG
720
GGACAATTAT GATGTTCAAA GCTTTAAATT T
751

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CCTGTTTGCC CTAATGGANT CGGGTNACAA TNCACGGAGA TCCTTCTTCT CACATCAATN
60
TNAAATGGGG TGTTCACCT CATCTTTGAT CTGATGACGA TGACATGCGC GGCATGCAAC
120
TTGTCCGNTC AATTTGTTCA AGATCATTCG TACGNATAAA ATTAGTAATN TTAACGTGTA
180
TCGGNAATNT TAAATAAATG TTTAATGCTT TTGAGAATAC AGTTCTANCC GNAGACGTCG
240
GGGACACTAA ATCACCGGAG ACGCCAAGGT CTTTTATTAA ACCTTGTTCA CTATATTGCA
300
TATACTGTGG ATACTGTCNC AACACATTGA NTTGATAAGG ATGTGTTGGT AATAAAATAA
360
AATCTTTGGG TATCTCTGAT ATATCTATGT CTGCTAATTG ATACAACACT TTCTCAACCT
420
GATCTTCTTT ACCTTCTACA TAGCGCGTGA GCAGAACATC TGGATGCACA GCTAAATAAT
480
GCAATTGGAA TGATGTATGA CATTCGGGTG CATATTTCTC TAAATCTGCT TCTGAAAACC
540
CACTTGCACT CTTAGGAGTC GGGATGAAAT GGATGACCTA AGTATTNAAG ANTGGTCTGA
600

AACGATATAA CGATCCTCTA CGTAGGCTAT TGTGTTACTT GGGAAAGAAC GCGCCGNGCG
 660
 ATGAATGCTA TTATCGATGN CAAACATAAT TNGCGCCATA TGTTGGTTGC ACTGCCGTTT
 720
 GATTATCTGC ACTTTGAGCC ATATGTGGCA AAATACGCGC AATTGCTTCT TTATAAGTTG
 780
 TTATTTTTTTT ACTTTTTTCCA TCGATAAGCC ATACCTCTGG ATGATACATA TGATGCCCCA
 840
 TCGCAGACCA ATAGCGAAAT TCACCCGTTA AAGTTTCGAG CTCTGATAAT TGTATAGACC
 900
 ATTGATGATT TTGAGGTGGT ACTTGATATA AATTTTCTTC TCTAAAATAT TCATTTAAAA
 960
 TCGGTTTCGAT AGCCGCATAC GCTGCATGTT GTATTAATTC TTTATTTTGC ACTTTTTGGT
 1020
 TTCAACTCCC ATAATTTTCAT TAATGTGTGA TCGGTTGATT TGATTAGTGA TGGTTGAACA
 1080
 AATTAAAAAT AAACACTTA CTGCAAATAC TACGCCCATA ACGATAAACG TAGTAGCTGG
 1140
 TGTAGTATAA CTTGTAATGG CAGCGCCACT AAGACTGCCA ATAATTTGAC CAACAACTAA
 1200
 CATACTGTTC GTCGTTCCAA CAAATGTGCC NTTAAGNTGT TGATGACACG CANTCACGAC
 1260
 AACAAACATG AACTTTTGAA TCNATGCACT AGATGTTAAT CCTGAAGTA TTCTTGACG
 1320
 CATTAAANAC TCTATATTCG TCGCTAAACC TTGCAGTATC GCACTACAAC CACATGCAAT
 1380
 CGTGGCAAAT ATAG
 1394

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ATAATATGTC TAATTGACTA ACTTGTTGGA GTCATTTACT ATTTTATGTA TGACATATTT
 60
 TAAAAAGTGA GGGTCAAGCA TGTCTTATAA AGCATATCCA CTCTTTAGAG ATATATTAAT
 120
 AAATGAATGT ATTTATTTTCG CCTCTAAAAA TAAAAAACTA GTACGCCTAA ATTATAAAAG
 180
 TGAAGCGTAT GTAGGCGTTT GGACAGAAGA AAGTGTGGCC GTATCATTTT TAACAAGTCG
 240
 TGATATTCCA TNTGATAAAG TTGTAAAAAT GGACGTTGAT CCGCCGNGCT ACTTATGAAT
 300
 TAGATGAATT GTGTGATGAA CAAGACATAT TATTATGAAT CAAACAA'GG AAGAAGAAGG
 360
 GCATCTACTA ACGTGGGGCT TGNTACAAAA AGAAGGTGAT GACGGGATTA GATAAAANAG
 420
 ATCAAAGATT TGGGCCCAGA TGTTGCAAAT ATGATGAAG
 459

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```
CTGGTGCCTC TTCTAATGAA TTTAGAGATT TTTTACCAAA TCACCATATG CAGTATACGA
60
TGATGAAGTA TGCACGTGAA CATGGTGCAA CAACTTACGA TTTCGGTGGT ACAGATAATG
120
ATCCAGATAA AGACTCTGAA CATTATGGCT TATGGGCATT TAAAAAAGTG TGGGGAACAT
180
ACTTAAGTGA AAAGATTGGT GAATTTGATT ATCTATTGAA TCAGCCATTG TACCAATTAA
240
TTGAGCAAGT TAAACCGCGT TTAACAAAAG CTAAAATTAA AATATCTCGT AAATTAAAAC
300
GAAAATAGAT TAACGACTGA AATCTGAACG CTCATAAGAC TGTCATTTGC GTTCAGATTT
360
TTTTACACAA TATAGAATGG TTGAGTAAAA TATTTTTGAA TATAGTGAAA GAGGGGGAAG
420
TACTGTGATA AAAAAGCTAT TACAATTTTC TTTGGGGAAT AAGTTTGCTA TCTTTTTAAT
480
GGTTGTTTTA GTTGCTTGG GCGGTGTATA CGAGCGAAGT GCTAAATTGA AATTAGAATT
540
ACTACCAAAN TGTACAAAAA TCCAGTTATT TCAAGTTACA ACAACAATGC CGGGGTGCAA
600
CGCCACAAAG TACCCAAGAT GAAATAAGTA GTAAAATTGA CAATCAAGTA AGATCGTTGG
660
CATATGTGAA AAATGTTAAA ACGCAATCCA TACAAAATGC TTCAATTGTA ACAGTTGAAT
720
ATGAAAATAA TACAGATATG GATAAAGCAG AAGAACAGCT TAAAAAAGAA ATCGATAAAA
780
TTAAATTTAA AGATGAAGTT GGTCAACCAG AATTAAGACG TAATTCGATG GACGCTTTTC
840
CGGTTTTAGC ATATTCATTT CAAATAAAGA GATGACTTGA AAAAGTACGA AAGTACTGAA
900
TGACAATTAA TACCAAATAC AAACGGAGAT
930
```

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 744 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

```
TTTACCTTCC TTAATTGCTT CCAACCCAAT CATCAGCTAA TAATCCACTA CTTTTTCACC
60
CATGCTCTTT CACNAATGTT TTGAACTGCG TTTCCTTTAA CGTCATACCA ACCTGTTTTA
120
CCTACTTTTG TAATATTACT TGCCAACACC ATTTTATTAT TATAAGCGAT TTGGTTAGCT
180
ATCGTGAACA TAGGTTTTAA ACATCGTCTG TGCACCCATA AAGGTATGCC TATCCAGGTT
```

240
 TTTTGATTAC TATCAGTAGC ATCAGATTTT CAAAAACCAT ATTGATTGGC GTTGTCTGCA
 300
 ACAGACTGCA CAGAAGCTTC TTTAGAACT AGATATTCCG GAACATGATA ATTTTACGA
 360
 ATGTTATCAA TTAAATGACT TTCTAAAGTC ACAACCGGTT CTATTTGAAT CGGATCACCT
 420
 ACAGCTACAA CTTTTTTTGA ACGATATAAT GCTCCACAG CTGCTTGAGG TATTGCTTGT
 480
 CCTGCTTCAT CAATAAATAA GTAGTCTATG AAATCTTGTG GTATGCCCCC ATACATAGAT
 540
 TTAAAGCTTG CAAACGTCGN ACTAACTACT GGAAATATNA AATGCATCAC ATTCCATGCG
 600
 TNGTGTNCTT TATCTGGATG NGCATCAATT AATTCCTTC TATCTNAAA ATCATTAATC
 660
 GCATAATAAA TAGTTGGTTT TATTAGCAAT CAATAATAAT TTATGCAATA TCAATNGCTT
 720
 CTTAAAAAGA GCATGGACCG TCTT
 744

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GGCTGGATA AGTAGTACCA GTCCACATAA TCTAACCTAA GACAATTAAG ATTAAGATTG
 60
 ATCGCATGAT TCAATTTATT TAGCTTTGTA ACCCAATCAT ATTGANTAAA TCTTTAGGGT
 120
 GCCAATATGG TGGTGCATAA NCCACNNCAA ACTCAGTTAA CTCATCTACA GTTAGCTGGT
 180
 TCATCATTGC CATCGATAGT ACATCAATAC GTTTATCTGC ACCTTCTTTT CCTACTGCAG
 240
 CTGCTCTTAA AATCTGACGG TTTGAAGTGT CATAATATAC CCTTAAGTGT AAAGGGGAAT
 300
 TTCCTGGGTA ATAATTCGCG TGTGCACCTT GAGTGACTTC CACCATTTTA TAGTCAAATT
 360
 GCTTTAGTTC ATTTGGTTTA ACGCCGACAC TCGCAAATGT ATAATCAAAG AACTTCACAA
 420
 TATTGTTGCC TAAGAAGCCT TTGAATTCAA TAGTGTCATT TCCAGCAATT TGTTCCGGCAA
 480
 CAATACTTGC TGCACGGTGA GCGCCCCAAG CTAAAGGAAC ACTAGCCGGT AGATCGACAT
 540
 GTCGATAATG TGATGTTGCA ATATCGCCTA TTGCATAAAT GTTTGGAACA TTTGTTTCAA
 600
 ATTTATCGTT TACGGTATGA AACCTTTTCG ATCAAGTTTG ATATTTGAAC TTTCGATAAA
 660
 TTTTGAATTG GGGTGAGTAC CGACACCTTC AATAATCATA TCGTAATGTT CAACTTTTCC
 720
 TGATTTAAAT GTAATTTTAT TTCCATTGAT AGCATCAATT CCTCATTTAA CGGTATGGAT
 780
 CTCCGCTATC TATTCAACAA GTATTGGTTG CTTCATGTCA GCATCCATAT TTATTTATCT
 840
 TATCAGATCG ATGATTAA

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1004 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GGAATGCGAT ATGCCTTTTT ATTCATCGTC ATATAAATTG CATTTTCATT TTTACGTGTC
60
ATACGCTGAA AAGGATGCTT CACAAATTGT GGTGTAGTAT AACCAATTCC AATTTCCAAA
120
TACAACACTT TATCATCTTG ATGTTGCTCT AGAAAAGCAT TATAACGTTG NNGNTGNGCC
180
TGAAATTCAG CATCTTCAAC CATGCCAACT TCCGCTTTAC GTTTATTAC TTCCATTGGA
240
GCATCACATT NTGGACATCT TGGAATCATC TCCCAAGGTA TAAGCATATC TTGTTGCGCA
300
ACAACCATTT TACGAATTAA ATCATCATTG CGATACGTGT GAGCATGACA ATGCTGACTA
360
CACTGNTGNA GTATATACTC CCCNTGTATA TGAAATACAT GAGTCATATC ATATTGAGCA
420
GCATCGAAAG CATTGTCTGC ATTCGGAGNT ATGATATGGT ACTGTTTACC CTCCACTAAG
480
GATTTTAATG CGAGATAAGA CTGACCTACA GGTGATCT TAATAATTTA NTGTAATAAA
540
ACGACTCTCA AATGCCCAAT ACTCTTGCCA ACTGCCATAA GGATGTAAAC TCGCTTGCAA
600
CATATCAAAG AAGCGATATT TTTCAATAAA ATCTGGGAAA TTTCCGTAA AACGCTCTCC
660
TACATATGTA AATCCGTCAG ATGCAGACAT GCCTGCACCA ATTCCAATCA CTATCGCATC
720
TGCTTCATCA ATCGCAGTAC GCAATACTTC AGCCTGCTTT GTCTTTTCAT CCATTAAAAG
780
AGACATTGCA TTCCATTTAC TACTCTGCAT CACGGCTCAA TGCCCTCCTTA TACAGTTGGT
840
AAATCCTTAT CTTGGAAATA CATTGAACAC GACTTTCAAT GTTGAATTTG GCTCTGCGAG
900
ATAGCTTTCT TCTGTTGAC AGCATTCTG CTGCTTCATC TTGAGAAAAG CAATACACTG
960
TAGATATACA GCAAAGCGAC ATGATTTAAC TATGTGGGCC AGGC
1004

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ATATTAGCAG CTGTGCTTGÇ TTGTATTTTA GCTGGTGTAC CCTATCAAAG CAATTATTGA
 60
 TAGTTTAACT ACATTTTCAG GAATAGAGCA TAGATTGCAA TATGTTGGTA CTAATAGAAC
 120
 TAATAAATAT TATAATGATT CCNAAGCAAC AAACACGCTA GCAACACAGT TTGCCTTAAA
 180
 TTCATTTAAT CAACCAATCA TTTGGTTATT GTGGTGGTAT TGGATCGAGG GAGATGAATT
 240
 TGACGAACTC ATTCCTTATA TGGAAAAATGT TNCGCACGAT GGTGTATTTC GGACAAACGA
 300
 AAGCTNAGTT TGCTAAACTA GGTAATAGTC AAGGGAAATC GGTCANTGAA GCGAACAATG
 360
 TCGAAGACGC TGTTGATAAA GTACAAGATA TTATAGANCC AAATGATGTT GTATTATTGT
 420
 CACCTGCTTG TGCAGATTGG GATCAATATA GTACTTTTGA AGAGCGTGGA GAGAAATTTA
 480
 TTGAAAGATT CCGTNCCCAT TTACCATCTT ATTAAAGGGT GTGAGTATTG ATGGATGATG
 540
 AAACGAAGAN CGATCAACAA GAATCAAATG AAGATAAAGA TGAATTAGAA TTATTTACGA
 600
 GGAATACATC TAAGAAAAGN CGGCAAAGGA GAAAGGTCAA AGGCTACACA TTTTCTACN
 660
 TCAAAATAAA GATGATACAT CTCAACAAGC TGATTTTGAT GAAGAAATTT ACTTGAG
 717

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 650 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CTCTTCTTCA TCAACATCGA TCATACTTAC TAAATTGTGG ATGTGAAAGC TGTGATGAGT
 60
 ATATGTACTT CTCGNNCAAA ACGGTTTAAT GTNTCCTCCT TTTCTCCAGG GTGGTATAAA
 120
 AATCGCCTTA ATTGCAACCT TAATGTTAAG TATCGTATCT TCTGCAAGAT AAACGGTACT
 180
 CATGCCACCG NCGCCAAGCT TATCTACAAT TTTATATCGC ACATTTATTA TTTTACCTAT
 240
 CATACTTTAT CACCTNCAAT AGCCGCGAGT ATGAAAGTAA CGTTATCTTT CGAATGGTTA
 300
 TCTAATGCCA ATTGCATTAA TTGATCACCA TGATCTTCTA TTGTACCTTC TTTTACTAAC
 360
 AAACGCTTAA TTTCAATTGTC TTAAACATAA TCAGTTAATC CATCTGAATT TAATAATAAA
 420
 TAATCATAAA AATTTAATCG CTTAATAAAC AAATCTGGAC TCACACGTTT ATCTGTGCCC
 480
 ATCACCTTCG TAATAATATT ACGTTGTGGA TGTGTAAATG CTTCTTCCGG CGTAATTTGA
 540
 CCCGTTAAAA CAAGATGATT ACAAATGAGT GATCACTAGT AATTTGCACA ATTGTCTACT
 600
 ATTAATACAT AGGCTCTAGA ATCACCGACA TTTGGTATCA CAACTGATTT
 650

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```
CACCAAGAAC TTACTTATAT TTTAGACAAC ATAAAAGGGA ATAATAATTA TGGTAAGGAA
60
TTTGTTCGAA CCGNTGAAGA AACATTTCGAC ATTGAATAAA GCGGGGTGAA GCACTATGAA
120
TCAATGGGAT CAGNTCTTAA CACCTTATAA GCAAGCGGTT GATGAGTTGA AAGTGAAACT
180
TAAAGGCATG CGCAAACAAT ATGAAGTTGG TGAACAAGCG TCGCCAATAG AATTTGTTAC
240
TGGTCGTGTT AACCCGCATC GCTAGTATTA TAGATAAGGC AAACAAACGA CAAATACCAT
300
TTGGATAGGT TAAGAGAAGA AATGTACGAT ATCGCTGGGT TTAAGAATGA TGTGCCAATT
360
GGTAGAAGAT ATTGATGTTG GCCGCÇAATA TTTTAAAGGA CAAAGAAAAG ATTTTAAAGN
420
TATTGGAGAC CGAGATTATT TCCCGNACAC TAAAGGAAGG TGGGTACCGT CCGCTTCANG
480
TCAATATTGG ATTTCCCAAC TGGACCAATA CAAGGCCAAA ATTT
524
```

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

```
CGTCTATCAT TGTTAACATA TATAGCACCT TCCTTATTTT AATGTTGTTT TAGTTGAATC
60
ACAGTAAAAA GGTGTGTTAAG ATACTCATAC ATTTTATATGT GTAAATATCT ACAAAGTTAC
120
CCANCTACTG ACAATGTTTA TTTNAGATAG TATATGTAAA TTCACAGATA TGCTAATTGC
180
TTAAAAAATG ATTAAAGTGT TGGCTCCAAG CAATGATACT TTAGAAATTT ATTTATCATC
240
TNGACTTTAA AAATTATATT ATAAATGACG TAACTGACAA CAGATATACT TAGTAATGAA
300
GATGTGTAAT GTAATTGTTT AAAATTGATC TCCAAGCAGA TTTTATTTAT CATTTAATTT
360
AAATAGCAAG TGGAGGTACA AGTAATGAAA TTTGGAAAAA CAATCGCAGT AGTATTAGCA
420
TCTAGTGTCT TGCTTGNAGG ATGTACTACG GATAAAAAAG AAATTAAGGC ATATTTAAAG
480
CAAGTGGATA AAATTAAGA CGATGAAGAA CCAATTAANA CTGTTGGNAA GAAAATTGCT
540
GAATTAGATG AGAAAAAGAA AAAATTAACCT GAAGATGTCA ATAGTAAAGA TACAGCAGGT
```

600
TCGCGGTNAA AGCAGTAAAA GATTTAATTA AAAATGNCGA TGATCCGTCT TAAAGGAATT
660
TGAAAAAGAA GAAGACGCAA TTAAGAANGT CTTGAACAAA GACTTTAAGA AAGCAAAANG
720
TACGTNGGGA TAACATGATA TGATGTTAAA C
751

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 785 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

CCTTTGTTTA NCATCCTTAG TCAGTGT CAT AAGGTTGTCC CATCAGAAGG TAGNCCCCAC
60
AATAGTTGAA ATCCTCCCAC AATAGGGGTA GNCTCCTGCA TCTGTAAATA CCTACTGGNN
120
TGCCANATAC TTTTCTGCT GGTGTGTCAA AGAAATTTGT TGTTCATTT GAGAGAACAC
180
TAATAATTTT GACATAATCT GCATATCGCA TATAAATTGT TGC GTTATCA CGATAATCTT
240
CATGTAAATC TGCTAAAGCG TTAATAATAG CATCATACAT GTCTGCTCCC NCAACTTCTT
300
TAACAGATCC ATTATAAAAT GACATGTGTT CTAATCCAGA TTTAGGACTT ACTGCTAAGG
360
CATCTTTACG CTCTTTAGCT GCTAATCCTG ATTGTAGTGC GTTTTCAACC CAGTTTACTA
420
AATCTACATC TGATCCATGA ATTACAGTAT CTGAAATTGC AGCAAATACT TTGAANTTAT
480
TAAGTAGTGA ACTTGACTGT ATCACCTTGT GCTTTTAATT CTTGTGCTGT NTCTACGTCT
540
GTAATGAAAT CATCATCGTC TAAAGTGAT GAAACTCTTG GAATCTCTAA ACCTTTAATG
600
TTAGNTAGAC GAGCTTTTAC ACGTAATTGG GTTNNAGCA AATGGCTCTG AAACAATTTT
660
TTGTAGAAAAG TGGGTTGGGG AAGAGCTTAT CTCCACCTGA ATCATTTCTT GTTGGTAAAG
720
CGTGTAATAA ACGTTGTGCC TCCATTGAAG GTTTTCAAA TTCATTTGGT AAAATCGCTC
780
GTGCC
785

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 924 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CTTNATAAAN ANC NATCNTA TGCCAATTTG ACCATTGTTT GAATCCATAT ANAAACCGGC
 60
 NACGGTTCTT TTCAAATATA ATAGTAAGTG TATAATGAAA ATGTAAATAT TATTAAANAT
 120
 GGGGGTTCAC TCAATGAAAA TGAAACGTTT TATAGCTATT GTAATGGCAT TATTTTTAGT
 180
 ATTAGNTGGT TGCTCTAATT CTAACGATAA TAATGAAAGT AAAAAAGATG ACGCAGACAA
 240
 TGGTAAGAAA CAAGAGATTC AAGTTGCAGC GGCAGCAAGT TTAACAGATG TAACCAAGAA
 300
 ACGAGCTTCA GAATTTAAAA AAGAGCATAA AAATGCTGAT ATTAAATTTA ACTATGGTGG
 360
 ATCAGGGGCA TNAAGAAAAC AAATTGANTC AGGCGCACCN CTTGTTGACG TATTNATGNC
 420
 TNCCNAANTN CTAAAGATGT AGATGCATTN NNAAGACAAG GAATNNAGCG CATTTGATAT
 480
 CATATNAATA TGCGNNNNAT AGTCTAGTAT TAATTGGTGA TAAAAGATTC AAATTACACT
 540
 TCAGTAAAAA GACTTAAAAG NCAATGATAA ATTAGCATTG GGTGAAGTGA AAAGTGTACC
 600
 AGCAGGAAAA TATGCGAAAC AGTATTTAGA TAACAATAAC TTATTTAAAG AAGTCGAAAG
 660
 TAAAATCGTT TATGCTAAAG ATGTAAAACA AGTATTAAAT TATGTTTGAA AAGGGTTAAT
 720
 GCGAAACAAG GTTTTGTGTA TAAACTGAC TTATATAANC AANN CNAAA AATTGATACT
 780
 GTAAAAGTAA TTAAAGAAGT AGAACTTAAG AAACCAATCA CATACGAAGC TGGTGCTACA
 840
 TCAGATAGTA AATTANCAAA AGAGTGGATG GATTCTTAAA TCAGATAAGC TAAGAATATT
 900
 AAAGATACAC TTTGCAGCAT AAGA
 924

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GGCACGAGCT CGTGCCGAAC TTACGGCAGC ACGCGATACN ATAAATACAT TTGTTACAGT
 60
 TACGCTACTA ATCGTTTGTG CTACATCTTT AAAATCAACC GCAATACCTT TGTGTTTGTG
 120
 AAGTAACGTG TTAACTCTC TCGTTTTAGA TAATAAGCTC ATGAATTTCT CTCCTTGTGT
 180
 ATATTTTAT AGAATAAATG CACTTAAATC TTTATNTGTT GAAATTGATT TTAATTTATC
 240
 ATCAACATAT TGTGGGGTAA TATCTACAAC TGCATTCGGC ATACTTGGTG CTTCGAATGA
 300
 TAAATCTTCT AGCATCTTNT CTAAAATTGT ATGAAGTCGA CGGTGCAACA ATGTNGTCTT
 360
 GTATCTTGA TCACTTGA TAAGCAATCT CAAGCTTAAG GCGANTAATT GCTTCCATCG
 420
 GGTAAAGTTT ACAGGNAACT TCTTCTTNTT TGGGAGCAAT GCTTCATATT TGGNNTAATT
 480

AATGACAATG TGGGGTCTGG NCAAAATTCT TACAAAATCT TCCTNCCCGT TANCTA
536

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CTACCTTCAT GTTTTGTAAA GTTGATTAAA GCATTTCATTG CTTGTGTATC ACTTGCATTT
60
TCAAAAGTTA CTCTACCAAT GTCGTGGTAA TAAGAATGTT CAGGCCCAAT ACCAGGATAA
120
TCAAGTCCTG CTGAAATAGA ATGTGCTAGT TGCACCTTGCC CACCTTCATC TTGAATTAAA
180
TACATTTTAG TACCATGTAA TACGCCAGGT GATCCTTTGN CAATTGCAAG TGCATGTTTA
240
TCAGTATCCT CGCCTTGACC TCGGNTTCA ACACCGNATT AATGCAACAT CATCTTTAAT
300
AAATGGATAA AAGGCACGAG ACCGATTGCA TTTGAGCCAC CACCGATACA TGCTACAATT
360
GCATCCGGAA GTCGACCTTC TTTCTTCAAT ATCTGTGATT TNATTTCTTT ACCAATGACA
420
CTCTGAAAAT CTCTAACAAT CGTTGGGAAT GGGTCTGGAC CTAATGCAGA ACCTAATAAA
480
TAATGTGTAT CATCTACATG ACTTACCCAA TATTGCAATG CTTTATTAAC TGCATCCGAT
540
AAAGTCCCTT GANCTTCTAC AACTGCCACA ACCCTTNGCA CCAAGTAATT CCATTCTAAA
600
TACATTAAGT TGGTGTCTTT TAATATCTTC ACTTCCATA AAGACAACAA GTTCCATATC
660
AAATAATGGA GGAACCGGAG GACTAGCTAC AACATGTTGA CCCGCACCAG TTTCAGNAAC
720
AAGCTTCTTC TTGGCCATTC TTTTGTCAAG CAACGGTGAC TAACGCATAT AATTTATGGC
780
GCCGTATGAT TAGATCCTCT CG
802

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CTATTCTTCT ATGTCTTTGA CAAGCGCGAA TATTTTTCGT CGTTGCTTGC CGGTAATTTG
60
AAACGGATCT ATGACGCTTA CATCGACTTC CACATCAAAT CCGTTATCAA GTAGTAATGT
120
TTCTTTATTG CCTAATTCAA CACCCGAGAT GACAACTGTT GNTGTACCGN CATCTTGAGT

180
 GATATAACTA GTAATTATTG GCATCTAATC ATTCCAATCA GAACGGGAGG TCTGAAAAAT
 240
 CTTCTTCACT ATTGTCAAAC GGATTATTGC CAGTTTGAGC TTGTCCTTGT TGTTGATAAT
 300
 TGTTGTTTTG NTGTTGGTTG TTATTCTTCG GTTCTAAGAA TTGAACGCTG TCCGCTACTA
 360
 CTTCTGTCAC AAATACACGT CGCCCTTCTT TGTTATCGTA ACTGCGTGAT TGTAACGTC
 420
 CATCAACGCC AGCCAATGAC CCTTTGGATA AATAATTATT TACATTTTCT GCTTGTTTTTC
 480
 TAAAAGTTAC ACAGTTAATA AAGTCTGCCT CACGTTCTCC TTGAGCGTTA GTAAATGTTT
 540
 TGTTAACTGC GATAGTGAAA GTGGTNACAC TCACACCATN TGGGCGCTGT TCTATATTCT
 600
 GGATCTTTTT GGGTAAGCGT CCCACTTAAT ACTGTTCTCG TNNTAACATT ATTTGNTTTC
 660
 CC
 662

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 656 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CTGGTAAAC AACATTAACA GCAGCAATCG CTA CTGTATT AGCAAAAAAT GGTGACTCAG
 60
 TTGCACAATC ATATGACATG ATTGACAACG CTCCAGAAGA AAAAGAACGT GGTATCACAA
 120
 TCAATACTTC TCACATTGAG TACCANACTG ACAAACGTCA CTANGCTCAC GTCGNGTGCC
 180
 CAGNATCCCG CTGACTACGT TAAAAACATG ATCACTGGTG CTGCTCAAAT GGACGGCGGT
 240
 ATCTTAGTAG TATCTGCTGC TGACGGTCCA ATGCCACAAA CTCGTGAACA CATTCTTTTA
 300
 TCACGTAACG TTGGTGTACC AGCATTAGTA GTATTCTTAA ACAAAGTTGA CATGGTTGAC
 360
 GATGAAGAAT TATTAGAATT AGTAGAAATG GAAGTTCGTG ACTTATTAAG CGAATATGAC
 420
 TTCCCAGGTG ACGATGTACC TGTAATCGCT GGTTCAGCAT TAAAAGCTTT AGAAGGCGAT
 480
 GCTCAATACG AAGAAAAAAT CTTAGAATTA ATGGAAGCTG TAGATACTTA CATTCCACTC
 540
 CAGACGTGAT CCTGACAAAC CATCAAGATG CCAGTGAGAC GTATCTCAAC ACNGTCGGGG
 600
 TCTGTTGGTA CAGGCCCGTT GACGTGGGCA ATCAAGTGGT GAGGAGGTGG GATCAC
 656

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GAATGCCCCAC ANAATGATGC TGGCAATGAT TTTCACTTAG TTATGAGCGG TAATGAATTT
60
TGCGGTAATG CGACGATGTC ATATATACAT CATTTGCAGG AAAGTCATTT GCTTAAAGAC
120
CAACAGTTTA AGGTGAAGGT ATCTGGCTGT TCGGATTTAG TGCAATGCGC AATTCATGAT
180
TGCCAATACT ATGAAGTTCA AATGCCACAA GCCCATCGTG TTGTGCCAAC AACAATTAAT
240
ATGGGTAATC ATTCATGGAA AGCATTAGAA ATTATTTATG AAACATATTG TACATTATGT
300
GATTCCNAGC TAAACAAAGT NACAACCTGA AATTCAACAT TTGGNTGGAA GCATTTGTGC
360
CGTTGANCAA CAAATGGAGT CACAAATATT
390

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GGNACGAGCG CATNATTAAA AACATATCAG GTTATGTATG CGCATAAAAA ACAGCCTTGA
60
AAAACCTTTA TAAATCGGAT TTTCAAAGCG TGTTTTGAAA GGTATTTAAT TAAAACTAAG
120
CATGTTGATG TAAATCATCA AAGTTTGTTA AACGTTGTTG CCACTCATTG TCACTAATAT
180
TATTTGCTTG AACATAACGA TTACGCTCAT GTTTAGCACA TTCATAAGAG CATGCACCTA
240
AATATTTAGT TTCGNTTCT TCAGAACTA ATATTTGTTT ATTACATTCT GGGTTAGCGC
300
AATTAATATT AACGNTCACA TGGGTTTGGC ATCAAAACCC AATCCTTACC AATAATTGTT
360
TTTTCAACTT GGGTTGATAT CAACACTGAT ACGGATCAAC AANTTACAAT ACAATTTNAC
420
CCG
423

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

TTGGTGCACC ACCTCAAAAC TTTGGTACCA TTGATGCATT GTACATTAAT TGCGCCAAGT
 60
 TTTTGTTAAT GCCACCAATG ATTCAGGTAA TAATTGTCCC AAAAGCAGCA GTTACAATTA
 120
 AATCTACATC TAATTGAANC AATTGTTCTA ATTCTTCTGA TCCACTTAAT TTTTCAGGCT
 180
 GATATACAGG TAAATCATAT TTCATTNCAA CTTTTTTAAC TGGTGGTGGT GTCATAACAC
 240
 GTTTACGTCC AACAGGTCGA TCTGGTTGCG TTACGACTGC AATGACATCA TGTTCGCAA
 300
 TAAGCATTTT TAAAACAGTT GTTGAAAAGG CACGAGTACC CATAAATATT ATTTTAGTCA
 360
 TTTATAAAAT ATGCCTCCAC TTCTTTATCT GTTAAAATAC GGTCCGCACG TTCNGTAAAA
 420
 GGGAGACCGT TCATTTGATC TATAATATGC AAAATCATT CTTGCTACATC TTCATGTGCA
 480
 GTTAGTTCAA CTTTGTTCCC ATTGACGTCA TAACTTTCTGA CAACTATCAT TTTACTTCTT
 540
 GTCACTTCGC CGTAAACATC TGGCAATGTA ATTGAACCTT CTAAGTCTGT TATTGTTTCA
 600
 TTTGATTGAC TAATAATTTT CGGATTAACA AGTTGGTAAT AATCCTTCCA TTTCCATATT
 660
 CAATAATTGG CACTTGCGAA TGACTTGATT AATTTGAGGG TGCACATAAG CCAGCAGCTT
 720
 CTTGGTGCAT ACATTGGTAT CTTCTTAAAT CTTGGTAATA ATCTTTTTTA CGAATCACAA
 780
 TTGTTTTAAC TTGCTTGCGC TTTTCCGGT TAAATAGGAT GCGATGCTGG GTACTAACTT
 840
 TTTTAATCGC CAATACTCTT ACTCCTCAAT AAATCAATCA ACTATATACC G
 891

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 652 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GGCACGAGCT ATAAATCCAA TGATGAATTG TAAAAGTGAA TAATTGAGAA AAAGGTTAAT
 60
 ATCAAATTTT GGTGTCATCA TTAATGTAAG TTCCTTGGCT AACGTTGAGA AAGTTGTTAA
 120
 GCCACCTAAA AAACCGGTGA CAAAGAACGC AGGGAACCAT GAGATTGAAA TTGATAGGCC
 180
 TATAGTTAAT CCAATTAAAA AACTACCAAC TAGATTTACT ATCAATGTTG CGATAGGTAA
 240
 CTTTGAAGTA AATTTATGAT TAAAATAATC AGTAATGGCA CTTCTAGCAA TTGCGCCAAA
 300
 ACCGCCGCCA ATCATGACTA AAATGATTGA TATCATGATA AACCACCACC TAGTTTTATA
 360
 CCGACGTAAC ATAACAAAAT CCCAAAGACA TAACTTGTTA CAGCATATAG TAGTAAAGTT
 420
 ATAAATTGTT GATGATCAAA CATATGTATT AATTCTTAAT TGAAATGTTG AAAAAGTCGG
 480
 CTAAGCACA AGAAAACAGT CGTAATAGCT TTTTITAGGG TCGGATGGTT TGAAAAAATG

540
CAATCGTTAA GCTGTTAGCA TCCCATTACA AAGGCACCAG TCAATGGTAT CAGTGTCCGA
600
TGGAACTCCG CAGTATCAGA AAGATGAGGT ACGTATAAGG CTAAGCACAC CG
652

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GAAACCATCC CCNCGTGCTC GTCACTGATT GTTCCGCCAC CACCTTGTGT TCCACCACTT
60
GATTTGATCA GCAGGATTGA AAGTACCTCT NCCACAGTAA TACCCATTAT TAGTCCCACC
120
AAACCTGTA CATTACCTGC TGATGCTCCT TTCACCCATG GGCTCGTATT ATNACGACGT
180
GTAAATGTCG TNACCACATT TCCATTACGT TTAATAACTA ATTTGTCAGC ATATGTCGTA
240
ACATTACCAG CATGAGTATT GACTGTTTGG TTCGCACCAG GTGCAATTGT AATCGCTCCT
300
GCCGCTGTTT CAGTGACAGT TGGTTTCGCT GGTTGAACAT CTTTACTAC AAATTTGCT
360
GGTAAAGATG TTGCAAATGT ATGTCCATTA TAGATGACAT CATATTTTGC ATTAACGACT
420
TGTGCAGTAT TTGGTTTATT CATTGCTGCC CAGTTTGCAT CGTTTGTACC CGTAGTATCA
480
CGATTCCATT TATACGTAAA TCCATCTGTT GGTAACCTG AAGCGTTTTG CATATGTGCA
540
TATCCTGATG CTTGCGTACC ACTTGCTAAA GTGCCACCAA CTGTTGTTGT ATAAGTAGTT
600
TGAGGGAATT CCAAATTGAT ATACGTTTAC AGTTACAGGA ACTCGTTTAG CAGCTGAAAT
660
ACCTGGATAT GTGACATCGA CATTTAAATG TTGAACGCCT GCTTGCTGGT TATTTGGTTG
720
TTGTCTATTT GCCCATGCTG CTGTAATACC ATTCGTATTA GTATTTGGAT CAAATGTAAT
780
GTAATCAATA GCGTTTGTAC CATGTGTCAA ATTTTGACCT TTCACATCAC GTGATGGCGC
840
CTTAGCATTG GCAACTGGAT AAACCTTGAC TGGAACCTCA ACATTACGCG TACCTTGACC
900
ACTAGGTAAT GTTACAACCG CAGTTTTATG TGTGTTGGCG ACTGTATTCT TCCATGTATC
960
TGGACTATCA TGCCATGCGA CCGCTGGCCC ATGTGGNGGA TTTTGAATA AATCGTCTTC
1020
ATGACCGAAA TCAAACCGN CGCACCTTTA ATAAATACAG CGCTTCAGTA GTTGCTTGTA
1080
TTGTGGGGTT ACTGTACAAG AAGCACTATC ATTTGATCAC AGATCAATCT TGGTNNNTGA
1140
AC
1142

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GGNANTNGAG GAANCAAANC NGCCCTTCNA CNCGGATTAA AACCTGTTNG AANCTGNNGA
60
AGNGTGGGNC NAANNCCTTG ANTGCAAGGT GCGANGGNCG NNTGCAAGNT GTNNAACNGC
120
NNGNGANCGN TTGNCNGTGC ANTGNNAAG ANTGGTGAAA ACCCNTGTGN TANATTGTGC
180
GNCCNNCTTG GTGANGNTGN GTTGNGCNGN NTCTTCAGNA GTCGCANCTG CAGNGTGTCC
240
NATAAGCGCT NTNTGNACGG TTGCTGGTGT TGCNNANTCA TCTATCGCAA CATCGNTAAT
300
TGTTGTATCT CCAGTAATAC CTTGAATATC AGCAACTGCT TGATCATTAA TTTGCGTAAC
360
ATCATTAGTT GNTTGTGCAN TTAAGATATC TTGANACGCT TTTTCTTTAG CTTNTAAAAC
420
TAAATCTTTT GCTGCATTTT TCTCTTCAGT TGTAGCGCCA GTTGTATTAT CAATTGCTTG
480
ATTTTGAGTT GTCACAGCTT GATCAACTTC ATTTTTCGCA TTCGATTAA CTGCTGNTGC
540
TGGTTGTGTG CTTTGAATTA NAGAAGACTC AAGCTTGCAT GCCTGCAGTC GACTCTAGAG
600
GATCG
605

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1778 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

AAATTCATAA TAAAGNCTTT TGNCATTAAA GTTNNAAGA AGATAAAGAA NCTGCTNNAA
60
ATTGACGTAT CNNAAGAAG TAAAGAAGT TTAAATANTC AAATAATAAA TCNACAACAC
120
AAGANATTTT TGAAGAACAA AAAGGTGAAT ATCAAAGAAA GTCAGAGGCA TTAAAAGAAA
180
GATTTATAAA CAGACAAAAA TCTAAAAATG AGTCTGTGGT TTCACTAATC GATGACGAAG
240
ACGACAACGN AAACGACAGG CAACTTGTGG TTTCTGCGCC ATCAAAGAAA CCAACAACAC
300
CGACTACATA TACTGAAACA ACGACTCAGG TANCAATGCC TACAGTTGAG CGTCAAACCT
360
AGCAACAAAT CGTTTACAAA ACACCCAAAA CCATTAGCTG GATTAAATGG TGAAAGTCAT
420
GATTTACAA CAACGCATCA ATCACCAACA ACTTCAAATC ATACGCATAA TAATGTTGTT
480

GAATTTGAAG AACGTCTGC TTTACCTGGT AGAAAATCAG GATCACTGGT TGGTATAAGT
 540
 CAAATTGATT CTTCTCATCT AACTGAACGT GAGAAGCGTG TAATCAAGCG TGNACACGTT
 600
 AAGAGAAGCT CCAAAAGTTA GTTGATAATT TATAAAGATA CACATAGTTA GAAAAGACCG
 660
 ATTAAATGCA CAACAAAAAG TAAATACCTT AAGTGAAGGT CATCAAAAAC CGTTTAATAA
 720
 CCCAATCAAT AAAGTANCCA TGCCAATAAT ATTAATGCAT GGCTGCAAAG CAAATAATGA
 780
 GTTTGTCGTA AAAATACCAA CATTTAACT AGCAATAAAT AATATCCAAG TCATCATTTT
 840
 ATTGATGCAA TCTAGTATAG TCCACATTCT AAACAGGTGT GGACTATTAC TTTTTTCACT
 900
 TTATATTACC GAAAAAATTA TTATGCTTAA CTATCAATAT CAATAATTAA TTTTAAGCTG
 960
 AAAACAATA AAAATGTTAA GACAACGTTT ACTTCAAGTT AATTATTATA CTGAAAATTC
 1020
 TGGTATATAA TGCTGTTAGT GAATATAACA GGGAAATTAT ATTGGTTATA ATATTGAGTC
 1080
 TATATAAAGG AGAAATAACA GATGAAAAAG AAATTATTAG TTTTAACTAT GAGCACGCTA
 1140
 TTTGCTACAC AACTTATCAA TTCAAATCAC GCTAAAGCAT CAGTGACAGA GAGTGTTGAC
 1200
 ACAAATTTG TAGTTCCAGA ATCAGGAATT AATAAAATTA TTCCAGCTTA CGATGAATTT
 1260
 AAGAATTCGC CAAAAGTAAA TGTTAGTAAT TTAAGTACA ATAAAACTT TGTAGTTTCT
 1320
 GAAGACAAAT TGAATAAGAT TGTAGATTCA TCGGCAGCTA GTAAAATTGT AGATAAAAAC
 1380
 TTTGCCGTAC CAGAATCAAA GTTAGGAAAC ATTGTACCAG AGTACAAAGA AATCAATAAT
 1440
 CGCGTGAATG TAGCAACAAA CAATCCAGCT TCACAACAAG TTGATAAGCA TTTTGTGCT
 1500
 AAAGGCCAG AAGTAAATAG ATTTATTACG CAAAACAAAG TAAACCACCA CTTCATTACT
 1560
 ACGCAAACCC ACTACAAGAA AGTTATTACT TCATNCAAAA TCAACACATG TNCATTAACA
 1620
 TGTNNATCAT GCAAAGGAT TCTTTTAATA NACACTTTAT TGTTACACAT CAGACTCGCC
 1680
 TAGATATACA CATCCATCTC AATCTTTATT ATCAAGCATC ATGTGCAGCT CCTGGATATC
 1740
 ACGCGCATAA TTTGGTACAC AGGGCATGCT AGCATTA
 1778

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GTGCTTTTGT TCAAGCTTCT GATCAATTTT TTATCGTCTT TTGTAATTC GCGAATGTCT
 60
 TCAAACATTG ATAAGACAAT CTGACCCACA TTTTGTAAAT CTTTTTGAGT TTCTTGTAAT
 120

GCAACACCAG GTGCGTGATA AACAAAGATCT TTGTGTAAGT GCTGAGGNNT ATAGTCANCA
 180
 GCNATATCTT TACCTGGGAC AAGCTTTGTA NCTATCCATG CTAAACCTGC TACANATGGT
 240
 AATTGAATCA NAGTATTTGT TATGTTGAAG ATACCATGTG ATACTGCAAT CGTCATCGCT
 300
 GGGTTTAAGT GCCATACATC TTGTAACANA CTAATCAAAT GAATCACAAC TGGCAAGAAA
 360
 ATTGTGNAGA TAATTACCCC GANTAAATTA AAGATGACGT GTACAAGCGC CGCACGTTTT
 420
 GCAGCGATTG ANCCGGCTAA ACTAGCTAAG ATAGCTGGAA TTGTGGGACG AGACAATGTT
 480
 ATCACCTAGG AACACAGGGA TTGCTGCGTT TNAGCTGATT AAATCTTGTT GATAAAATTC
 540
 TTGTAAAATA CCAATCGNCG GACTTGAANT GTTGANCTAG TGCTGTTACC CCTGCGCCGA
 600
 CAATGACACC AAGTATTGGA TGTGATGACA ATATCAAGCA TTAATTGNTT AAAATCCATC
 660
 TAATGATGCT AAGGGGTTTA NCGGCATCCA CCCCATAAAT TCTAAGACCG AAGAAAAGAG
 720
 ACCCCGAACC CGATAGTATG CGGCCAATGT TATTGATTTT AAGAGCGTTT AAAAGAAAAA
 780
 GATTAAAAAT GCACCTAATG CTAAAATTGG CATTTGCATA TTCGCCTAAA TCTAATNCCG
 840
 ATAATAAATG CAGTTACCGT TGTTCCGATA TTGGCACCCA TTATCACTCC AATAGCTTGT
 900
 TTTAACGTCA TAAATCCAGC TGTTACCAGT CCGATTGTGA TAACGGTCGT ACCTGAACTA
 960
 CTTTGTATTA AAATAGTTAC AACGATACCT GCAATAACAC CTAATACTGG ATTTGATGTA
 1020
 AATTTGTTTA AAATATCTCG TAGCCTGTCT CCTGCTGATG CTTGAAGCCC GTCTCCCATG
 1080
 ATTTTAAAGC CGTAAAGGAA AATACCTAAA CCACCTAAAA AGGAGAAAAT GACTTCTGTA
 1140
 ACCGACATTT CCATTATTTT CACCTCAAAT AAGCTTTATA TTTAGATTAT CGCTTATAAT
 1200
 TGTAATTTA ATGTTAAGAT TAGGTAAAAT TATTTAACAA TATATGTTAT TTGTANATGA
 1260
 CTTGTAAAAT ATCGTCACTT ATTATGTNAA TTTTCAGTGT GAAATGGCAG GTNTGCAATA
 1320
 ACGTGTTTAA CAAAATGATG CAATCAATCA TGTAATTATG TTTCATCAAA AAAATCATGT
 1380
 GAGTGGGATA ACGAAATAAA GTTTGTGAAC ATATCATTTT TATCCCACTC CATGATTTGA
 1440
 AATCACCAAA TAAAAATCTA TTAATGGTTT TCGTTATAAC AATTTGTGTT CTTTAAATAA
 1500
 TGTCTCAATG TACGTACCTT TTATCTTTTT AAGGAATCCT GCTAATGCGA GTTTCTGCAT
 1560
 TTTCGAAT
 1568

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

ACCCCATTGA TTCCTGAATC CCCTGAAAGA AGTTGAATCA CCTTGAAGAT CCTGATTCCN
60
CCTGTACTTT GTGAACCCAC TGAAACTTAT TGAAGAAGAA TCCCCTGANC CTGTCTGATG
120
TTGATAATGA TGCCGACACC GATGTGCTTT GTGATGCCGA TGTACTAGCA CTCATTGACA
180
TTGATGTTGA TATCGATGTA CTTAAGGAAC CAGATGCACT TGTACTTGTT GACTGCCTTG
240
TGACATTGAA TCACNTAATG ATGTAGATGT GCTTGTTGAG CTCGAGTCAC TTACACTTGT
300
TGAACCTGAT ATTGAGTCAC TTAAACTTGT CGATGTTGAA ACTGATACGC TTCCGCTCAT
360
TGAGTCAGAT GTTGAAAGTG ATGTACTCGT TGAATTTGAT CCACTGATGT TAGACGAATC
420
ACTTGTAGAC ATTGAGTCGC TTTCTGATGC ACTGATGCTC ATAGAGTCAA ATTGACTATT
480
ACTTGTTGAG CTTGACTGCG AATCGCTCAC ACTTGTTGAC GTTGATTCTG ATCCACTCAA
540
ACTTTGCGAG CTA CTCAATG ATTTTGAATC ACTTAATGAA TCCGAAGTGC TAAGACTTGT
600
GGAACCACTT AAAGATATTG ATCCACTTAA TGAGTCGGAG TCACTTGAC TAGTAGAATC
660
ACTCATTGAT ATTGAATCAC TTAGCGAGGT AGACTCGCTT ACGCTTTCTG AACCCTTAA
720
TGATGTTGAG GTACTCAATG AACCAGATGT ACTTGTTGAA GTCGAACCAC TTGTTGATTT
780
TGAATCACTT AATGAATCAG ATTCCTCAC GCTTTCTGAA CTTCTTAGTG ACGTCGATAC
840
ACTTAATGAT GACGAATCGC TTGTGCTTAC TGAATCGCTC ATCGATTGTG AGCCACTCAA
900
TGAACCTGAC TCGCTTACAC TTTCTGATTT TCTTAATGAC GTTGAGACGC TCAATGAGCC
960
AGAATCACTG ACACTTGTTG AGCCACTCAT CGATTTAGAG TCACTTTCAG AATTAGATTC
1020
ACTTACACTT TCTGAATCAT TTACAGATTC TGACATACTT TGTGAATCAG ATATGCTTGC
1080
GCTCATTACT TCACTAGCCG ATGTTGATGT ACTTGTCGAA TCACTTAACG ATATAGATAC
1140
ACTCATCGAA CCAGATGTAC TCGCACTTGT TGAGTCTGAT GTTGAATCAC TCACACTATC
1200
AGATAATGAC GTTGAATCAC TCATACTTGT TGATGTACTT GTTGAAAGCG ACATACTTTG
1260
TGAATCACTA GTACTTGATC GCATCGAAGT ACTAGTTGAC AGCTGATGTC TCGTGCC
1317

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CCCAAATTGG CGATAGCTAA TATTTGATAA TGATGCGCAT TTCATACAAT TTGTGACTTG
60

GCAATTATTG AATATTTTATA TAATTTTTTTC TCGTAATAAAA CACAACCTTTG ATAGCGCTAA
 120
 AACAGCTGTG TTAAGTTATG AGTTAACGAA TTTAACACAT TTTACTAGGG CGGCATTTAA
 180
 GAATATTTAT ACGTTTTTAN CGAATATTTA TTTATTGTAA NACGCTACCA AAAAGTTAGA
 240
 CTTCCCTCCC ACTAAAGTNC CACTTTTTTTC TTTCAACTTT TTTAANAAAC GGATATGCAA
 300
 CTTTTAGTAT TGGTATCAAA ATGATTGTGA GGTCATATTC TATCAATATA TTTTCTAAA
 360
 GAATTGCTTT TATTAACCTT CAATTATGTA CCTAACCTAA AAAGAAGCCA AGGCAACGAA
 420
 TGTACCTTG ACTTCTAATA CATATTCAAC TAACTATATA TTCAATCATA CGCGCATGCG
 480
 AGAGTGATTG TTGTACATCT ATAATGCGTT GATTTAAAGA ACCTTTATAT GGTAAATCAG
 540
 GTTTGAATAA GTGTTGTATA AATAGACCAT CGACTAAAAC GTCAATGTAT GATAATAACT
 600
 CTCGACGTTT TGTACAATCA TTTGCTAAAT ATTCATATAA AAATCCAGTC CATACCCAAA
 660
 TTGTCTTTGT ATTTCCAAAA CGTGCTCGAA ATGCTTTGAC AAGATTTAAT GTAATATCCA
 720
 AATTACAAAA TGGTTCGCCA CCTAATAGAC TTAGCCGAGA TATATAATCA TGATCGCAAT
 780
 CATCTAATAT TTCTGCTAAT ATTTTCATCAG TGTATTTCTC GCCATATCTG AACTTTTGTG
 840
 AGGCTTTGTT ATAACATCCA ACACAATTAA ATGGACATCC TGATACATAA AACTGTCATC
 900
 TTACTCCTTC ACCGTCAACA AAGCTATTTG AATCCTATTT TAGCAATATA ACCTTGTCTT
 960
 TGTTTAATGT CCTAAAAGTG TCATCCTTTA GGCGCCTTCA TATGTTTTAC TCGTGCGCAA
 1020
 ATTTCTTTAT GACGGCCTTT AATTACTGGA CGTTGAACTG GATTGCCTAA GTAACCCACA
 1080
 TGTTTCGTTTA ACGACATCAA CTGTTTTAGG ATTATCATTG NCACAAGTTC GGGCATTTAA
 1140
 ATCCTTTTTT AGNTGCTTCA AAATCTCCAT CCGNNATCAC ATTCAATAAC AATGGANCAA
 1200
 ATCGGNATAT TTGGNNCCTA AGGTAAACCA ACTTNGGCAA TAAGAGTNGG GCCCAATACC
 1260
 CGNTTCTAGG GCTTTCAAAT TGTGTTGCAA TTTCGGATAC TCACAATAGT GAATGAAACC
 1320
 ACCACTCGCA TAATAAGGAT AATCTTTTTT AAAATCTAAC TTTTCAAAG GTGTAACATC
 1380
 TTTACGTACA TCATAATGGA AAGAGTTTTG ATAATATCCT TTATCTGTAA TGTCTTTAAT
 1440
 ATCTCCAAAT CTCTCTTGGT CTAAACGACA AAAACGATCC GTTAGCGANN CACTCGGCGT
 1500
 ACTCGTAAAT ACTGANCCAA ATGTCATATA ATTCTGNCCA TNGCGTGTGA TAACGTNTCA
 1560
 TTTCTTTAAG AATNACAAGC GTAAATGCTT GNGCTTCTNG AGATGTCTCC CAGTCTGGAC
 1620
 CATAGAAAAC AGNAGCTGTN TCATACAACC CTATCTAGCC CATTGAAATC GTTGCACGTT
 1680
 TATTTTTAAA TAACTCAGCA ACATCATCTG TTTCTTTTAA TTTATAGTTA AAAGCGCCAC
 1740
 TTTTATATAA AATTGGTGCG TTATTCGGTA CAGNATCTTT CAAACGATTT ATACGATAAA
 1800
 GTAATGCATC ATGTAACACA TCGATACGTT CATAAAAGAT TTCCCAGAAT TTCGTATAT
 1860
 TACCGGCAGA TTCTAATGCC ATTCTAGGTA AATTAAGTGT NACAACACCA AGATTACAAC

1920
 GACCATTATT TTCAAATGA CCTTCCGCAT CTTTCCAAC TGGGTAAAA TGAACGACAA
 1980
 CCCATTGGNG CTTTGAAATC ACCTAATATT TCTACGAGTT TGGTCAATAA TTTAAAATAT
 2040
 CTGGATACAT ACGTTTCGGN GGAACAACCT TAATGCTAGT TGTTTAATGT CATAGGTCGG
 2100
 ATCTTGGGGG ACTAAAGTTG GGGTCCCNTC TCTATTGGAA ATCAAA
 2146

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1015 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

ATTGTCCCAC ACCATTTACT ACAAGANACG AGCGTCCTCC ACATTGTTAC NTTGTGCNAT
 60
 CAATNCTTCT NGTTTGTTTT GAANNNAAGA CCGAAGCATT TGTANTCTGC TGTGTTTCGCA
 120
 GCCTTGTTTC GCACGTTCTA AGGTATTGAA TACCGTTTAA TGCAGTATTG GCTTGTGTAA
 180
 CAGCTTGCAT TGCTCTATCG ACATCTGCNT TAGGTGTATT TCCTCCAGCT GTTTTATNTA
 240
 AAATAGTTGC TGCTGCATTT ACTGCTTGAG AATAAGCCGT TCGTTTAGCA TCATCAGCAT
 300
 CTTGATAATT TTGACTTTGT AACGTCGTGT CTTTATCACG AATTGATGTT TCTAATTGAC
 360
 CCATAGCACC ATCTAATTGT TGCGCTTTGG CTTTAACTGT ATTAACACCT CAACATTTGT
 420
 TGCTNGTGTA ATTTCAATTAT CTAACGCATT ACGTTGTGCA TTATTAATGT GTGTTAATGT
 480
 ACCTAACGTT TGTTTCGCAG CAGCTTTAGC TTCATTTAAT TTCGCATCAC CGCNCAACGC
 540
 CGTCTTCGTA CTGTNCACAT TGTGTAATGC TTGNNAACCT GCTGCTTTGT CTACATTGTG
 600
 ACCACTAGCT TTTGTTAAAA TTGCTTTTGC TGCATTTACT GCTTGATCAT AAGCTGATTT
 660
 CTTACTTGGC TCAGCATCTA GGTATTTCTG AGTTTGTTTT GGTTGTGTCT CATCATTGAT
 720
 ACCATTTTGT AACTTGTGC ATTGCGTTAT TTAATTCTTG TTGCTTTNGC AGGTTCTTGG
 780
 ATTTACACCA GCTACTGTAG GTGGNACCAT CAATGTTAAG CGTTAACGCA TCTTTTTGTG
 840
 CATTGTTAAT TGATGTTAAG TTATTCAAGT TTGTTTTTCG CTGTTGTCTT AGCTTGAGCT
 900
 AAGTTTTGGC GCACCATTTA ATGCATGTTT TTTAGTNGGT CACTTGTGAT GTTGCTTGGC
 960
 GTAATAGTAT TNGGGNTCCA TCCNNTGGNT TCCACGTTTG GATTAATGAT TGCTT
 1015

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1550 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

```
GGCACCAGCT AGAGCGAGTT TTTATATATA CAACACGAAA GAAGACATTG ATCAGTTAAT
60
AAATGCCTTG AAACAAACGA AGGAGTTTTT CTCTTATGAA TTTTAATAAT CTAGATCAAT
120
TATATAGATC TGTCATTATG GATCATTATA AAAATCCTAC AAATAAAGGT GTATTANATA
180
ACGGGTCTAT GACAGTAGAT ATGAATAACC CGACATGCGG TGACCGTATA CGACTAACAT
240
TTGATATAGA AGACGGCATT ATAAAAGATG CTAAGTTTGA AGGTGAAGGT TGTTCGATTT
300
CAATGGCAAG TGCATCGATG ATGACACAAG CTGTAAAGG GAATCCANTT GGAGAAGCAA
360
TCCAAATNGA CCCAAGGAAT TTACCGNAAA TGATGCTTGG TTGGAAGCCT ANTGTGATNC
420
AGGGAAGAAT GGGGAGATAT TGAAGCATTC CNGGGTTGAT CTCAATCCCA GCTCGTATTA
480
AATTTGTCCA CATACTTGG AAACATTGGA AAAAGGGTCC TTGTTCTTAA AGGAGGGTAA
540
AACAGGAGGG TCCGGCTTGA AGAAGAAAAG ATCCTGTAA TCATAAGATG ATTTTGATAT
600
TAAGACATAT NNAAGTATNN NAATTTTTAA TAAAGATGTC ATGTCATTGT AATAAATATG
660
GTTTACATCA TTGAATTAAA AACTTACGCA CCGCCGTTGT AAATATATTT TTAAGGAGTG
720
ATTGAAATGG CTAAAAAAGC ACCTGATGTT GGGGATTATA AATATGGATT CCCC GCCGAT
780
GATGTATCCA TTTTCAGATC AGAACGTGGT TTAAGTAGA ATATCGTTAG AGAAATTTCT
840
AACATGAAAA ATGAGCCGGA ATGGATGTTA GATTTCCGTC TTAAATCATT AAAATTGTTT
900
TATAAAATGC CAATGCCTCA ATGGGGTGGC GACTTATCAG AATTGAATTT CGATGACATT
960
ACTTACTATG TAAAGCCTTC AGAACAAGCT GAACGTTTAT GGGATGAAGT GCCAGAAGAA
1020
ATTAAGAGAA CTTTCGATAA ATTAGGAATT CCTGAAGCTG AACAAAAATA TTTAGCTGGT
1080
GTTTCTGCTC AATATGAATC TGAAGTTGTT TACCATAATA TGGAAAAAGA ACTTGAAGAA
1140
AAAGGTATTA TCTTTAAAGA TACAGATAGT GCTTTACAAG AAAATGAAGA ATTATTCAAA
1200
AAATACTTTG CTTCTGTAGT ACCTGCAGCA GATAACAAAT TTGCGGCGTT AACTCAGCA
1260
GTATGGTCAG GTGGNTCGCT CATTTATGTA CCTAAAAATA TCAAACTAGA TACGCCACTA
1320
CAAGCTTATT TCCGTATTAA CTCTGAGAAC ATGGGTCAAT TTGAACGTAC ATTAATCATT
1380
GCTGATGAAG GTGCTTCTGT ACATTACGTA GAAGGTTGGT ACTGCACCAG TTTATACAAC
1440
TAGNTCTTTA CACTCTGCTG TTGGTGGNAA TCATTGGGCA TAAAGATGCG CACNGTCCGC
1500
NTTATTCTTA CGAANCAAAA CTGCGGGACA ATGTTTTCAA CTNNAGGTAC
1550
```

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

```

TGATAATACT GCTTAATACA ACATTTATTG CAATTAAAAG TGCAGTAATA GCCAGTTTTT
60
CNTTGANTTC AAAATGANTG TCCTCCNTTT TTGTTTGTA NTAAATCACTA TGCTTGGCTT
120
TATTATGGTC ANNTAAACGT GTTTCATTT GTTGATACTA ACATTTTCAA TAATTGATTC
180
GCTTCATATT GTGAAGTTTG AAAGTGTTC NCTATGGGCA ATGTATTTAT TTCTGCTTCT
240
ATACTTTGAN TGGTATGTTT CGACTGTTCT AGCGCATTTT GTTTCCTGTA ATTTTGAAAG
300
TTTACTGCTT GTTTTTGATG CTTTTTTAAC ATATCCATTT TAGTCTTTAT CGTTTGCTTC
360
TGATGAATCT GTGCTTCAAT TTGTTGATAT GTTTTGATAG AANCCCAAAT TTTAATTTTA
420
NTTGCAATAT AACCCGCTTG TTCCAAANCG TCATCTTTAT AAAACAATTT ATTTGAATCA
480
CCNATTTTCG GCTCCTACTT CCTTTACCAA ACTTGCCATT TAATGGAATA CTGTTTAGCT
540
TCATCTATTC GTACTTCCAC TAGTTTACCC AATCATTTCT TTAGGTGCTT TGAAATTAAC
600
TAGCTTATTT TTATCAGTGT AGCCAGCAAG AACCTGATCA TCTTTTTTAC TACTACCTTC
660
ACAAAGTACT GTTACAGTTT GTCCTTCGTA CTTACTCATA GCTATTTGTG AATAATGACC
720
AACTTTTTTA TTCAAACGTT GCAATCGTTC CTTTTTGACA TTAAAGGTA CATTATCTTT
780
CATTTTAGCA GCAGGCGTAC CATCACGTTG TGAATACAAG TACGTATATG CATGTTCAAA
840
ACCAACTTCA TCATACAGAG TTAAAGTTTC TTCAAATTGT TCCTCTGATT CATTTGGATA
900
CCCTACAATA ATATCTGTAG TTAATGCTAC ATTAGGAAGT CTATCTTTGA TTCGTTTTAC
960
TAAATCCAAA TAACTTTCTC GTGTATATTT TCTACCCATT ATTTTAAATA CTGCATTATT
1020
TCCAGATTGA ACTGGCAAGT GGATATGAGG AACGATATTA CCACCCTCTG AAATAACATC
1080
AATCATGTGA TCTGTAAAGT CCCAAGGATG ACTTGTTGTG AAACGAACTC TTGGAATCGC
1140
TATTTTAGAA ATTGCTTGTA AAAGATCTCC TAAGTCATAT TCTATATCCT GTAAATCTTT
1200
ACCATAAGAA TTTACATTGT GACCTAAAAG CGTTATTTCT TTGTAACCTT CACGAGCAAG
1260
TTCACGTA CTATCTATAA TGTCTTCAGG TCTACGGGTC CGGTCCTTAC TCCTTGTTAA
1320
TGGAACAATA CAATATGTAC AAACTTATC ACAACCATAC ATAATATTGA CCCATGCTTT
1380
ATGTTGCTTC ACGGACTTGT GGNAGATTAC AATAACGTCT NCTTCTTTTA GACATACTCA
1440
CAACAATGT
```

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GAAAGTGT TT CAGAACGTGG AGCAAAAGGC TTCGGAAGTA GCGGAGTGTA AAGACATCTT
60
AGATCGAGTT AAGGAGGTTT TGGGGAAGTG ACGCAATACT TAGTCACAAC ATTCAAAGAT
120
TCAACAGGAC GACCACATGA ACATATTACT GTGGCTAGAG ATAATCAGAC GTTTACAGTT
180
ATTGAGGCAG AGAGTAAAGA AGAAGCTGAG CGCAAATACG AGGCACAAGT TAAGATAAGG
240
AGAGATGGAG ATGCCAAAGA AAACGGNAAC GATTGATGTA GATGAAAAC TATTAGTAGT
300
AGCTAGTAAT GAAATATCAG AACTATTATA TGAATATGAC AGTGAGTTAA TCNCAGCTGG
360
ATGAAGATGG CGATAATAGA GATATCGGAA GGAAAAAAGA GGACGCATTA AAACAAGCTA
420
TACAAAATTT CTCGATAAAT TACATGGGGG TGTTTAGTG
459

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2005 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GGCACGAGCT CATAATCGC TAGTAAGAAT AATAATCTTA GTATTTGTTT AGTCATTCCC
60
CACACTCCCT TATATTTTCA AACAACTGAC TCACTTTAGC ATAATTCCAT CTCTCCTATC
120
TTAACCTTGT GCCTCGTANT TGCGCTCAGC TTCTTCTTTA CTCTCTGCCT CAACAACTGT
180
AAACGTCTGA TTATCTCTAG CAGTAGTAAA ATGTTTCATGT GGTGTGCCTT GTTGAATCTT
240
TGAATGTTGT GACTAAGTAT TGTGTCATTC CTCATAGCTC CCTTGAACCTT GTTTGAGCTT
300
ACTCATAAAA AACATTACTA AAAATGCTAT TAAGATATGC GTCTTTTGAT GTTTATAAGC
360
AAATGTAGAT ATCATAAAGA TAGTAGCAAG CATTAAACATT TCATATATGT TTGTGTGTAT
420
AGTCTTTTTA CTCTTAAGAA AAATAATTGC TATGCGATAA AAGAGATAAA CGCCAAACCC
480
TATTAAAAAT ATTTCTAACA TGTCGCTCAC TTCCCCAAAA CCTCCTTGAC TCGATCTAAG
540

ATGTCTTTAT ACTCCGCTAC TTCCGAAGCC TTTTGCTCCA CGTTCTGAAA CACACTCGAA
 600
 TTCCTCCACT TGCTTTAGTT CAGGTGTCCA TATAGGCACG ATAACCAATT GAGCTAGTTT
 660
 GTCGCCTTCG TTGATTTGAT AAGTTCCATA TTGTCTTATG GCGTCACTCA AATCGATTTC
 720
 TCCTTTAATA TCAAAAACAC CTGGTGTGAT ATAACCATTG GATGCAATAG CGTCATTCTT
 780
 GATATTAATC CCTAAATTGC CGTGATATCC CGCGTCTATC TTGCCTGTTT CAATCACTAA
 840
 ATGCGTTTTA CTACTTACAC CACTACGACT AGTTAATAGT CCGACATAGC CCTCTGGTAT
 900
 ACTCACAGCT ACATCTGTTT TGATCACTGC TTTTCTTGT GGTTCGAGTA CGACAGTTTC
 960
 AGCTGAGAAT ATGTCATAAC CTGCATCCGT CTTATGATTT CGTTCGGGCA TTCTAGCATT
 1020
 TTTTGATAAT AGTTTTACTT GTAATGTGTT AGTCATTTTC CTATTCCTCC TCATATTTAT
 1080
 AGACAACCTG ACCTGCCATA ATCCCTACTG CTTTCATCAAG TTCAATACCT CNTTTAACTG
 1140
 AATGTTGAAT AGCATTGTGC ATTCCCTCAA GTATTTTCATC AAACGCTTGC GCTTCTTAT
 1200
 ACACGTCCTC AATCTCTTTT AGCAACCCCT CTGTGTCATT ACCGTATACG CACTAGCACT
 1260
 AATAACGGAC TGTTGATTTT TTTGCGGATT ATTCATTGGT GTCATCCTCC ATAAAAATTT
 1320
 TATTGTTTAA TTCCATTCCG AATTTAACTC TTTCATCATC GTTACCGAAT TCGTTTATTA
 1380
 AATCTTTTTT AACGCTCTTG CAATACCTAT CCCATGCGCT TGCTTTCTTC TCCAGTTCTT
 1440
 TGTTACAATC TCGTAACTTC GCTATATCCC CAATAAGCTC ATCTCGTTGC TTCTTGTAAT
 1500
 CTTACGATC TTTTAATGCT TTGTGAAGTT TATCTAATAA CTTGTTAGAG TTAGTACAAA
 1560
 GATTTTTATA TTGTTTCATCT GATAAGGTGA ACGTCATCTC ATAACTCCA ATAGCATCTC
 1620
 ATTTTCAAAA ATATTTCCAA CAATTTCAAT AATATCGGCA TTTTCACTTA GTAATTCAGT
 1680
 TACATTGCTA AAAGTTATAT AAAAGGCTCC TTCTTTAAAC TCGATAAAAC TTAATTCTCT
 1740
 CGAATTAACA ATCTTGAAC AATATCCCCT TCATAAATCT CCACAACCGG GCACATCTTT
 1800
 TAAATCCTGT GTATTGGTAA TAGGTTTTAC TTCAATTGAA ACTTTTATTA ACCTGGTGGA
 1860
 AATCAAAATG TACCCACTTA TTAATAATCG GATTTGGGNC AATAATACTC AATAACTTNN
 1920
 NNTATCTTNA TCCCAAGCTT TTAATTTCAA CATCAATCTT ACCAACTCCC CATCTTTCCA
 1980
 AATCAATGTC AACCGGCAAN GTCAC
 2005

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 796 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GGCACGAGCT GTTTTTTATT TGCTTCGTTA CAAAGCATT A TTGAATTTAT TTTACGTGTT
60
CATATTTTGA AACATCAAAG CCGTCTTGCT TAGCTTTGTT GATAATGTCT TTGATTGAAT
120
GTAGTCCTTT ATCGGCGAAG TATGATCTTA AGTTGTCTTT TGTAGCTTGG TCAGCATTCT
180
TATCTAATAA CACATCGATA TAGCTTAATT CATGTTCTAA GAAGTTTGCG TCATCATGTA
240
GTACGAGTCC ATTTTGAGAA TAAACTTTTCG CATCTGCTTG ATTACCATAT CCAACAACGC
300
CAGTTGCTAA TACACCTACC ATTGCCGTAG CTAATAAAAC CTTTTTAAAT TTCATATCTA
360
TCACTCCTCT AAAAATTGTA CTCTATCATA AACTTTGAAT ATTAAGAAAA TTACGGNTTA
420
TTAAGTCGGA CTTNANTAAT TCTTAATAAA TAGNTAAACT GACAAATATT NGCTNAAATG
480
CAATTANTCT TNAAAACCGG GGTTTATGGA TTTTTCCTAC TAAACCTTG ATTTCAAAAA
540
GGGTTTANCT CAAATGAAAC AATAATAAAA AATAATGCAA CATAATAATA AGTACAAATT
600
TANTTAAGAA ATTAAATTGA TTGTATATGT ATATTNTGGT AACGTNAAAG AGAAATATNC
660
AANATAATTA ATTATTTATT TGAAAAGAGA ATATTAATGA AGTATTAAAC AAAGAGACGT
720
GAAACGATGC GATATTTAAA AAGACTTTCA TGGNACATAA GCATCTTAAT TTTAATAGGT
780
GGTATTGCTG GGTGGG
796

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

AACTTTGAGT NTTTTGTTN ATATGGAAC TTAAGATTT GGAAATTATN TAGATGGAGA
60
TATATCATAT AATCCAGAGG TGCCNAGTTA TTCAGCTAAA TATCAATTAN CTAATGATGA
120
TNACAATGTA AAGCAATTAC GTAAAAGATA TGACATNCCA GCAGAATAAA GCACCCAAAG
180
TTATTTGTTG AAAGGGTACA GGGTAATTTN AAAGCCTCAT CAGTTGGATA TAAAGACAGT
240
GAATTTACTT TCGTAGAGAN NAAAGGTGAA AATATATACT TTAGTGATAG TCTACATCTT
300
GANCCAAGTG AGGATAAATA AACGTGACCA ATAAAGAGTA TGAAATCGAA CCCGGAAAAA
360
GAGAGTGTGA AATGATGAAA CGATTAAATA AATTAGTGTT AGGCATTAGT TTTCTGTTTT
420
TAGTCATTAG TATCACTGCT GGTTGTGGCA TAGGTAAAGA AGCGGAAGTT AAGAAAAGCT
480
TTGAAAAAAC ATTGAGTATG TACCCTATTA AAAATCTAGA GGATTTATAC GATAAGGAAG
540

GCTATCGTGA TGATCAGTTT GATAAAAATG ATAAAGGTAC ATGGATTATA AATTCTGAAA
 600
 TGGTTATTCA ACCTAATAAT GAAGATATGG TAGCTAAAGG CATGGTTCTA TATATCGAAT
 660
 AGAAATACCA AAACAACAAA TGGTTACTAC TATGTCTGATG TGAATAAGGA CGAGGATGAA
 720
 GGAAAACCGC ACGACAATGA AAAAAGATAT CCGGTTAAAA TGGTCCGATA ATAAATCAT
 780
 TCCAACAAAA GAAATTANAG ATAANAACAT AAAAAAAGAA NTCGAAAAC TTAAGTTCTT
 840
 TGTTCAATAT GGAAACTTTA AAGATTTGTC GAAGTACAAA GATGGAGATA TTTCATACAA
 900
 TCCAGAGGTG CCAAGTTATT CACCAAATA TCAAGTAACT AATGATGACT ATAATGTAAN
 960
 ACAATTNCGN AAAAGATATA GATATACCGA CCGAATAAAG CACCANAGCT ATTGTTGANA
 1020
 GGTACAGGGA ATTTAAAAGG TTCATCAATT GGCTACACAA AAATTGAATT TACTTTCGTA
 1080
 GAGAAAAAGG GAGAAAATAT ATACTTTAGT GATGGGCTAC AG
 1122

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 652 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CGGTGGTCTT CTATTCCCGT TTTGCCATCT CNAATTTCTT ACCATGGCCC ACAAAGTATT
 60
 GTNACGTTTG AGCTGATCCT TATTTAATTT TNAAATTGAG AAAAATGTCT CCAAATCCTG
 120
 TACCTNCCCC ATATTCCCGC AATACAAATA AAATTTTGTC GTATTTGCTC NCCGGTAAGC
 180
 TTTAAATGTG GTCATTATAA GANCGGATTG TCTTGTAATT GACCGCATGT CATACCAGTT
 240
 AGGAATCACA TGGATATTGT CAGCATTTTT AAGAAATTTG ATGATTTAGT AAGTAGTTTT
 300
 TCATTTCCGT ACCCAAGGAC AATGACATTT TCAGCATTTCT TGTAGACATG TCTATTAATG
 360
 TAACGCATCA GCTTATCAAT CATGCTACCT GGACGAGTTG CACCTGTCTT AATCGCATTA
 420
 TCAGGTGCTA TATCATACAC CACAAAAGAA TATTTTTTCT TAAGCAGTCT GTGTAAAACG
 480
 TCTGGTATTA ATGGCAAGAT TGGTGGATTA GAGTAAACAA GAATCTGATC ATATTTCAAC
 540
 ATTTTAGGTA TATTAATCAC GAATTTTGAA AATAAACTAA AGAAATTGAT GATCCTTCCA
 600
 ACCTTACTTT TGTTATTAAA CCTCGAATAC TTGAGACGTC GAATGCCAAN TC
 652

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GAATTCCTT CAAAAGCACC TTTGATACCG AATAAATTAT GGTTTGGTGA CTTAGATAAA
60
GAACTAGCGG GAAGATTTTA ATCGCAAGAC TGGTGCGAAT GTGAAGTATA TTGAAGCACC
120
TTATGAACCG CATAAGTTTG TGAAAATGGT GAAGGATAAA GAATTAGCTG ATGAAAAGA
180
AGGCGGCTTA CGTNGTACCG CTTGTTTTGA AATGCGTTTG GATATTGTAG CGAAAGCAGC
240
TGTAGAACAT GGCTATGATT ATTTTGGCAG TGCAATCACG TTATCACCTA AAAAGAACGC
300
ACAATTAATC AATGAACTTG GTATGGATTG TCCAAAAAAT ATACGATGTG AACTTATTTG
360
CAAGTGATTT TAAGAAACT AAGGTATTGA GC
392

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3797 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

TCAAATGCAG TCAGGGAAGC AATAGGACGA TATGCATAAA GGAGATGGTA AAGTGAACA
60
GTGACAGAAG GTAAAGACAC GCTTCAATCA TCGGAGNCAT CAATCAANCA CAAAATAGTA
120
AAACAATCAG GAACGCAAAA TGATAATCAA GTAAAGCAAG ATTCTGGAAC GACAAGGTTT
180
TAAACAGTCA CACCAAAATA ATGCGACTAA TAATACTGAA CGTCAAAATG ATCAGGTTCA
240
AAATACCCAT CATGCTGAAC GTAATGGATC ACAATCGACA ACGTCACAAT CGAATGATGT
300
TGATAAATCA CAACCATCCA TTCCGGCACA AAAGGTATTA CCCAATCATG ATAAAGCAGC
360
ACCAACTTCA ACTACACCCC CGTCTAATGA TAAAACTGCA CCTAAATCAA CAAAAGCACA
420
AGATGCAACC ACGGACAAAC ATCCAAATCA ACAAGATACA CATCAACCCG CGTGCCTCAA
480
ATCATAGATG CAAAGCAAGA TGATACTGTT CGCCAAAGTG AACAGAAACC ACAAGTTGGC
540
GATTTAAGTA AACATATCGA TGGTCAAAAT TCCCCAGAGA AACCGACAGA TAAAAATACT
600
GATAATAAAC AACTAATCAA AGATGCGCTT CAAGCGCCTA AAACACGTTT GACTACAAAT
660
GCAGCAGCAG ATGCTAAAAA GGTTCGACCA CTAAAGCGA ATCAAGTACA ACCACTTAAC
720
AAATATCCAG TTGTTTTTGT ACATGGATTT TTAGGATTAG TAGGCGATAA TGCACCTGCT
780
TTATATCCAA ATTATTGGGG TGGAAATAAA TTAAAGTTA TCGAGGGAAT TGAGAAAGCA

840
 AGGCTATAAT GTACATCAAG CAAGTGTAAG TGCATTTGGT AGTAACTATG ATCGCGCTGT
 900
 AGAACTTTAT TATTACATTA AAGGTGGTCA CGAGCGTAGA TTATGGCGCA GCACATGCAG
 960
 CTAATACGG ACATGAGCGC TATGGTAAGA CTTATAAAGG AATCATGCCT AATTGGGAAC
 1020
 CTGGTAAAAA GGTACATCTT GTAGGGCATA GTATGGGTGG TCAAACAATT CGTTTAATGG
 1080
 AAGAGTTTTT AAGAAATGGT AACAAAGAAG AAATTGCCTA TCATAAAGCG CATGGTGGAG
 1140
 AAATATCACC ATTATTCAC TGGTGGTCATA ACAATATGGT TGCATCAATC ACAACATTAG
 1200
 CAACACCACA TAATGGTTCA CAAGCAGCTG ATAAGTTTGG AAATACAGAA GCTGTTAGAA
 1260
 AAATCATGTT CGCTTTAAAT CGATTTATGG GTAACAAGTA TTCCGAATAT CGATTTAGGA
 1320
 TTAACGCAAT GGGGCTTTAA ACAATTACCA AATGAGAGTT ACATTGACTA TATTAAACG
 1380
 CGTTAGTAAA AGCAAAATTT GGACATCAGA CGATAATGCT GCCTATGATT TAACGTTAGA
 1440
 TGGCTCTGCA AAATTGAACA ACATGACAAG TATGAATCCT AATATTACGT ATACGACTTA
 1500
 TACAGGTGTG TCTTCACATA CTGGTCCATT AGGGCACGAA AATCCTGCCG AATTAGGCAC
 1560
 GAGACATTTT TCTTAATGGA TACAACGAGT AGAATTATTG GTCATGATGC AAGAGAAGAA
 1620
 TGGCGTAAAA ATGATGGTGT CGTACCAGTG ATTTTCGTCGT TACATCCATC CAATCAACCA
 1680
 TTTATTAATG TTACGAATGA TGAACCTGCC ACACGCAGAG GTATCTGGCA AGTTAAACCA
 1740
 ATCATACAAG GATGGGATCA TGTCGATTTT ATCGGTGTGG ACTTCCTGGA TTTCAACACC
 1800
 GTAAGGTGCA GAACTTGCCA ACTTCTATAC AGGTATAATA AATGACTTGT TGCGTGTGGA
 1860
 AGCGNCTGAA AGTAAAGGAA CACAATTGAA AGCAAGTTAA ATTCATCTTC TGAATTTAAT
 1920
 AGGCTATGTA AATCGTGCTG TTATCATGGC ACATCAGATA TAAGTAGCAT CACAGTGTG
 1980
 AATCTCAAAA TAGTAAAGTG AAATAAAGCG CCTGTCTCAT TAGCGAAAAC TAAAGGGACA
 2040
 GCGGTATCTG TTTATGAGCT TAATAAATTG TATGAATAAT ATGGTTGATC GAATAACTGT
 2100
 TTATCATTGA TGATAAATTT GAGTTTTTTT AAAATAATTG ATATATTACA CCATTGTTAT
 2160
 AGCGTTTAAA GAAATCAACC CAACTTTACG ATAAATAGTG ATTGCTTCGT CATTAGGTCT
 2220
 ACGATCAAAA TCATGCTCGT TTTTATTAC GCGTTCAAAT GTTGAATGTG GAACATGATT
 2280
 CATGATATGT TCGCTTTCCT CAACGGGAAC ATCATAATCG CCATTACAAT GCGCAATGAA
 2340
 AACAGGTGGA AGTGTTTTAA GNTCATCTGG TGCAATATTA TATTTTGAAT CAGTATAATC
 2400
 ANCAATGTTA ATCATATTTA TCCATTTACC TGTGCCACGT GCATAAACGT AGAGTAAAAA
 2460
 ACGTGTGCGA TTTGATCTTG ANCAACCGGT GTTGGTGAAG TGAGTTGTCC AATCATTGTT
 2520
 TCGTTTATGC TTTGAGCTAT TTTTGCGTAA TACCTATTAG TTGTTTTAAA AGGGTTCAGT
 2580
 GTTGATGCGA CTATAACCAT AAAAATCAAT AACACCATCA ATATCTCTGT CTCGTGCAAT
 2640

TAATAAGACT TAAATATGCA CCTGATGATC TGCCAAAGGT AAAAATAGGG CAATTAGAAT
 2700
 ATTGTGATTG AATCGCATCG AATGATGCGT AGACATCCTC AATAATGCAA TCGAGACTTA
 2760
 CTTCTGGTAA TAAACGATAA CTTAGTTGAA TTAAATCGTA ATGTTCCGTA AGGATATCGA
 2820
 TATACTGTGG GGATAAATCG TTAGCTTTAC CGAACATTAA TCCACCACCG TGGATGTAGA
 2880
 CAATAACGCC TTTTGTGGT TGATTTTTTG CTTAATAAT TGTGTAAGGT AATGCAAATG
 2940
 CATCTTTAGT AATTACTTTA TATTTAATTT CAGTCACGAT TTAATAGGCT CCTTAGGAAT
 3000
 CCGATATTGA TGTCATTATA ACACTGTCNT NAATTTCCAT GNAAAATAGT CTTAAGACGA
 3060
 TGAGTCATGA TAATTCTGTT CCAATTGACG TAAAGCGTCN CGGGTATGCT TCTTTAGACC
 3120
 TTCCCCATAA TCCATCATTT TAACAATATC TTTAAAAGCA GCATGTGGNA TGGCTAAATC
 3180
 TTCTAAATCT GCCATAGAAA ATTCAAGATT GATATCATGT GGTCGCTGTT CAGCAAGTTT
 3240
 ATGCACAAAG TCAGGTTCTG TGACCAAAGG CGAAGACATG CCGACCATAT CTGCATGTTG
 3300
 TAAAGCATCT AAAGCAGACT CTGGAGAATT AATCCCGCCA CTTGCAATTA AAGGGATACG
 3360
 ACCTGCTAAA TGTTCATAGA CAATTTGGTT AACTGGTCGA CCGAAATGAT CACCTGGTGT
 3420
 ACGAGACGTA TTTTGATAAA TATGTCGACC CCAGCTAGCG ATTGCTAAGT ATTGGATGTT
 3480
 TGAAACGTCC ATGACCCAAT CGATTAATTG GTTGAACTCG TCAATGGTAT ATCCTAAATC
 3540
 ACTGCCTCTG GTTTCTTCTG GCGTTGCTCG AAATCCTAAA ATAAAATTGT CAGGTGCTTC
 3600
 TTTATCAATC ACTTCTTGTA CCGCACGCAT AACTTCTAAA CATAATCTTG CACGATTTTT
 3660
 TAATGAGTCG GCACCGTAAT GGTCTGTACG TCTATTTGAA AAAGTTGAGA AAAATGTTTG
 3720
 AATCAGCAAA CGTTGTGCAA TCGAAATTC CACACCATCA AAACCTGCTT TAATCGCGCG
 3780
 TGCATCGAGC TCGTGCC
 3797

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CAAGCCAGTT CAACTNACCG ACCCGGTATA TTTGGGGAAT ATACGAANCN CNNTCAGATG
 60
 ATCNAATAT GANTGANACN CGGTNGCGTT CTCNAGNCAN AACAGNGTTA AATAANCGTA
 120
 AGTCGGCAGT TATGTCANAT GAGATTACTT CTNCTGATTG GGNAGTTACG NNTCCACACG
 180
 AGANNATATC ANNTGGTGAN NCAGNCAGAG TAAAACATAG AGATTTTGAC CCGCCATTGT
 240

ATGTAGAGGC AGAAGTTATT GCCGAAGAAT ATAACATAAT TTCAGAAAAAT AGCACATATA
 300
 CATTTCGGTCA ACCTAAAGAG TTCAAAGAAT CAGAATTACG AGAAGAGTTT AACAAAGCGAT
 360
 TGAACATAAT ACATCAAAAAG TTAAACGATA ATATTAGCAA TATCAACACT ATAGTAAAAG
 420
 ATGTTGTAGA TAGTGAATTA GAATACTTTG AACGCAAAAT ACACAAAAGT GATACACCGC
 480
 CAGAAAATCC AGTCAATGAT ATGCTTTGGT ATGATACAAG TAACCCTGAT GTTGCTGTCT
 540
 TGCGTAGATA TTGGAATGGT CGATGGATTG AAGAAACACC AAATGATGTT GNAAAATTAG
 600
 GTGGTATAAC AAGAGAGGAA AGCGCTATTC AGTGAATTAA ACAATATATT TATTAATTTA
 660
 TCTATACAAC ACGCTAGTCT TTTGTCAAGA AGCTACAGAA TTAAGTGAAT AGCGAGTACT
 720
 TAGTAGATAA TGATTTGAAA GCGGACTTAC AAGCAAGTTT AGACGCTGTG ATTGATGTTT
 780
 ATAATCAAAT TAAAAATAAT TTAGAATCTA TGACACCCGA AACTGCAACG ATTGGTCGGT
 840
 TGGTAGATAC AAAAAGCTTTA TTTCTTGAGT ATAGAAAGAA ATTACAAGAT GTTTATACAG
 900
 ATGTAGAAGA TGTCAAAATC GCCATTTTCAG ATAGATTTAA ATTATTACAG TCACAATACA
 960
 CTGATGAAAA ATATAAAGAA GCGTTGGAAA TAATAGCAAC AAAATTTGGT TTAACGGTGA
 1020
 ATGAAGATTT GCAGTTAGTC GGAGAACCTA ATGTTGTTAA ATCAGCTATT GAAGCAGCTA
 1080
 GAGAATCCAC AAAAGAACAA TTACGTGACT ATGTNAAAAC ATCGGACTAT NAAACAGACA
 1140
 ANGACGGGAT TGTTGAACGT NTAGATACTG CTGAAGCTGA GAGAACGACT TTNNAAGGGG
 1200
 AAATCAAAGA TAAAGNTACG GTTANACGAA TATCGAAACG GATTGGAAGA ACAAACAA
 1260
 TATACTGATG ACCAGTTAAG TGATTTGTCC AATAATCCTG AGATTAAAGC AAGTATTGAA
 1320
 CAAGCAAATC AAGAAGCGCA AGAAGCTTTA AAATCATACA TTGATGCTCA AGATGATCTT
 1380
 AAAGAGAAGG AATCCCAAGC GTATGCTGAT GGTAAAATTT CGGAGAGAAG AGCAACGCGC
 1440
 TATACAAGAT GCTCAAGCTA AACTTGNAGA GGCAAAACAA AACGCAGGAN CTTAAAGGCT
 1500
 TAGANACGCT GAAAAGANAG CTAATGTTTA TACAGACAAC AAGGTCAAAG AAAGCACAGA
 1560
 TGCACAGAGG AAAACATTGA CTCGCTATGG TTCTCAAATT ATACACAATG GTAAGGAAAT
 1620
 CANATTAAGA ACTACTAAAG AAGAGTTTAA TGCTTCTAAA AGAACACTAT CAAGAGTGTT
 1680
 AGCAGACATC ACTGTAAATG CTATGAAAGG CATCTATTTA AGGTATGACG AAAATGGGGC
 1740
 GATTACTTCA CATACTATTG ATAAAGATGG CGTGAAAATT AGTGGCGATA AAGTTGATAT
 1800
 AACAGCGAAT AGAGAATTTA ATGTATTCGC AAATAATATT AATAACAAAG TTGGTAAAAA
 1860
 TGACATTGTT AATAGCCTAA ACTTATCAAA TGAAGGTCTT GACATCAATG TGAATAGAAT
 1920
 TGGTATTAAA GCGGGAATG CTAACCGTTA TGTACAAGTT CAAAATGATT TTATTGAACT
 1980
 TGGCGGAATC GTACAACGAA CTTGGAAAGG CAAACGATCA ACCGATGATA TATTCACACG
 2040
 TCTTAAAGAT GGACATCTAA GGTTTAGAAA TAATACCGCA GGCGGGTCAC TTTATATGTC

2100
 ACATTTTGGT ATTTCAACAT ATATTGATGG AGAAGGCGAA GACGGAGGTT CATCCGGTAC
 2160
 TATTCAATGG TGGGATAAAA CTTACAGTGA TAGCGGTATG AATGGCATAA CAATCAATTC
 2220
 TTATGGCGGT GTAGTCGCTT TAACATCTGA CTACAATCGA ATTATTATCG ATTCATATGC
 2280
 TTCAGCTAAT ATTGAAAGTA GAGAAGCGCC GATATATTTA TCTCCGAACA CCCAAAAATT
 2340
 AAACCTGGNT TTAANCCGAT TCGCATTAC ATTATCAAAC GCTGATAGGT NCATTACGAA
 2400
 ACTGGCGGTT ATATCATGTT GGGTTCAAGA TGNAANCTAT AAGTNCGGTG CTGGATTAAG
 2460
 ATTTTCTAAA CGTACCAATA AAGGATTGGT TCAAGTCGTT AATGGTGACT ATGCTACAGG
 2520
 CGGAGACACT ACAATTGAAT CAGGTATGGC CAAATTCAAC TTAGTTAANC GGAAGAGATG
 2580
 GAAATAGTTA CGTTAGCATT CAAAGTTATG ATTTATTGGC GGTAGGTTCT GATAATGCTG
 2640
 GCGATAGAGT CGCTTCTAAT TCTATTTATA AGCGTACTTA TTCAGCACCT GCTAACTTAC
 2700
 ACATTACTTC TGCTGGAACA ATTGGGCGTG CTAATTCTGC CAAAAAGTAT AAAATTTCAA
 2760
 TCGAAAACCA ATACATCAAT GAAGACGATC AGTTCAGTCA TTCAAAGAG ATTTTAAAGC
 2820
 TTCCAATTTC TACATGGTTT GACAAATATG AATCGGAAAT AATGGCTAAA GAATTGGAAA
 2880
 GTGGTAAAAA GTTATCTGAT GATACTTTTA AACTTAGTCG ACATACTGGC TTAATAGCGG
 2940
 AAGAGGTTGA AGAATTAGGA TTTAATGAAT TTGTTATTTA TGATGACAAC GGAGAAATCG
 3000
 AAGGTATCGC ATACGATAGA CTTTGGGTTT ATCTANNACC TATTATTACC CNAAAACCAN
 3060
 CANTCAAANA NCGNAAAACN TANTGGNGGN NTTAACNTCT NATNGACNGC AACCAGGGTC
 3120
 CNCATNCCAC CTCCACATTA TACAANTCAC TTTCTCNCGT CACTA
 3165

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

AAAACAAGCG ATTATCACAG CAATTATTTT AATAGCACTG AGCTTGATTT TACCTGCATT
 60
 TGCAGTAGGT AATCACATTT CAATCTTCGT CATTTCTATG ATATTCTTTG CAGGTAGCTT
 120
 TGCTTTAATG TATGCACCTT TACTTAACGA AGCCATTAAA ACAATAGATC TTAATATGAC
 180
 AGGTGTGGCT ATTGGTTTTT ATAATTTAAT TATTAATGTG GCGGTATCTG TAGGTATTGC
 240
 GATTGCTGCG GCTCTAATCG ATTTTAAAGC ATTAAATTTT CCAGGCAATG ATGCATTAAG
 300
 TTCACATTTT GGTATTATTT TAATTATTTT AGGTTTAATG AGTATTGGTC CGGATTAGTT

360
 TTATTCCGNC ATCTTTAAAT CCGGTGGGAC AACAACTCTG AAAAAATAAT AGATATTAAA
 420
 TCGCGAGATA TATCCGTATT TTATTGGTAA AATTAAATTA AAGAGATTAT ATTACACGAG
 480
 GAGTAGTAAG TATTGAAATT GGAGAAATAT ATAGATCACA CTTTATTGAA GCCTGAGTCA
 540
 ACACGTACGC AAATCGATCA AATCATCGAT GAAGCGAAAG CATACCATTT TAAATCTGTA
 600
 TGTGTGAATC CAACGCATGT TAAATATGCA GCAGAGCGAC TAGCTGATTC AGAGGTGCTC
 660
 GTTTGTACGG TAATAGGATT CCCATTAGGT GCGTCGACAA CTGCAACGAA AGCATTTGAA
 720
 ACAGAAGATG CAATTCAAAA TGGTGCAGAT GAAATTGACA TGGTCATCAA CATCGGCGCA
 780
 TTAAAAGATG GACGTTTTGA TGATGTACAA CAAGACATTG AAGCAGTGGT TAAAGCTGCG
 840
 AAAGGTCACA CAGTAAAAGT GATTATTGAG ACGGTATTGT TGGAACCATG ACGAAATTGT
 900
 AAAAGCGAGT GAATTAACAA AAGCGGCTGG TGCGGACTTC GTTAAACTT CAACAGGTTT
 960
 TGCAGGTGGC GGTGCGACTG CAGAAGACGT TAAATTAATG AAAGATACAA GTAGGTGCTG
 1020
 ATGTAGAAGT AAAAGCATCA GGTGGCGTAC GTAATTTAGA AGGATTTCAA TAAAATGGTT
 1080
 GAAGCAGGTG CGACACGTAT TGGGCGCGAG CGCAGGCGTT CCAAATTATG CAAGGTTTAG
 1140
 AAGCAGATTC AAGATTACTA ATATATATAA AATTTGGGAG TGATAGCTAT GACAAAGACC
 1200
 ATTTAATCGN GTTCATTTTA TCCGTATGG
 1229

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1066 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GGCACGAGAC GTAAATGNAA AGAAAACCGG CCTNCNTGAT TAAGANATTT AGAAAAGTGT
 60
 TTGTCATNAC GGTGTGCCA GTGNTNAGTA TGTCCAAATA NAGGAAGTGA NAACGATGGN
 120
 ACCGTATTTT TAAAANAGGC AGNACATANC ATTTTAGATA GGAAGTGATA ATATGAATTT
 180
 GGCTAAACGC ANATTACAAG GGGAACNATT AACAANAGAG ACTGTAGTGA AAATTTATGA
 240
 GGATACTAAT ATTGATACCT TAGNTTTATT AAATGAGGCG NACATCTTTA AGNANACATT
 300
 ATTTTGGTGC NATNAGTCAA ATTAAACATG ATTTTAAATG CTAAAAGTGG NATATGTCCT
 360
 GAGAATTGTG GGCNCGAGAC TGTGGACAAT CACGAGATAT TAAACAANAA CAGCGATATG
 420
 CTTTAATTCC AGAGGAACAA ATTATCGATN GANCANAGGT GGCACATGAT AATCATATTG
 480
 GAACATATTG TATTGTTATG AGTGGTAGAG GACCGAGCGA TAAAGAAGTT GATCATATTA

540
 GTAATCCTGT AAGAACGATT AAATCTCAAC ACCCGCAACT AAAAATCTGT GCATGTTTAG
 600
 GATTAACGGA TTGCCGACCA AGCTAAGAAA CTTAAGTCAG CTGTTGTAGA CAGATATANC
 660
 CACAATATTA ATACCAAGTG AAAATTACCC ATTGATAACC GTCGTGCCAA CGCATAGTTA
 720
 TNAAGATAGA ACAGATACGA TAGAACTAAT GAAAGCGAAT AATATATCAC CATGTTCTGG
 780
 CGTGATTTGT GGTATGGGAG AATCTAATCA AGATATTGTT GATATGGCAT TTGCTTTAAA
 840
 AGAAATGGAT GCCGACAGTA TTCCGATTAA TTTTTTGCAT CCAATCAAAG GCACAAAGTT
 900
 TGAAGCATG GATGATTTAA CACCAATGAA ATGTTTAAGA ATCGTAGCAT TATTCCGATT
 960
 AATCAATCCT ACGAAAGAAA TTCGTATTGC TGGAGGAAGA GAGGTCAACT TACGTTCGTT
 1020
 ACAGCCATTA GCATTAAAAG CGGCGAANTN CAATATTTGG GCGGGG
 1066

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3222 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

CCAAGTAAGT ATAGAAGCAG CATCCTTAGA AAAGAAAAAT GTAGATTTGA ACGAATTATT
 60
 ACAGCGTCTC AATGACGTTG AACAAACGGA ATACACCAGG TTCGCTTNAC CCTAAATTTT
 120
 TAAATGTTTC GTCACCTTATT CAATATATTC AAGCAGCATA TCATGAACCT CTTAGAGAAG
 180
 AATTTAAAAA TTTAACACCT TATGTGACGA AATTATCGAA AGTACATGGA CCTAACCATC
 240
 CATATTTAGT CGAGTTAAAA GAAACATATG ATACATTTAA AAGTGGCATG TTAGAGCATA
 300
 TCCAAAAAGA AGATGATGTT GATTTTCAAA ACTAATTAAA TATGAACAAG GTGAAGTAGT
 360
 AAACGATATT AATACAGTGA TTGATGATTT AGTATCTGAT CACATTGCAA CGGGACAATT
 420
 GTTAGTGAAA ATGAGCGATT TAACATCTAG CTATGAACCA CCGATAGAGG CATGTGGTAC
 480
 GTGGCGACTC GTTTATCAGA GATTAAAAGC ACTTGAAGTG TTAACACATG AGCATGTTCA
 540
 TTTAGAGAAT CATGTTTTAT TTAAAAAAGT ATCATAAATA ACGCGATTAG AACTGTTGG
 600
 CAAAGTAATG TCAGCAGTTT TTCGCTATAC TTAACAGAAA TTTAGTGATA TGAACAGCAT
 660
 TATTTGAAAA GAAAAATGGT CAACTTAGCA TAAAAATTGA TATGAAAATT TAATGGTATA
 720
 GATAATTAAA TAGTAGCGTG TTTTTTTAAT AATTTATTCA TGAATTTTAC ATGCACTATT
 780
 ATGATAAAAT AAACATAATT ATAATTCAC T GAGGTGCTAT CGTGCTATCG CTAACAATGT
 840
 TATTACTTGA GCGTGTAGGT TTAATTATTA TTNTGGGCCT ATGTGTTGAT GAATTATTCC

900
 ATATTTTTTAA AAACCTTTAAT GAATCCGTCG ACGCTACATG GAAAGCACGT TGGCAATTAT
 960
 GTATTATTTT CAGTTTGTTT GCCTTAATGT TCTAATTTAA CTGGTATCGT CATCGATCAT
 1020
 CAACATAGTT TGTGAGGAAG TGTGTACTTC CGTTTAGATG ATGATGTATC TTTAGCTAAC
 1080
 ACACGTGTAT TAACGATAGG TGTGCGAGGA TTAGTTGGTG GCCCTTTTGT AGGTCTATTT
 1140
 GTTGGCGTTA TTTCAGGTAT TTTCAGAGTG TATATGGGTG GGGCGGATGC ACAAGTTTAT
 1200
 CTTATCTCAT CTATATTTAT CGGNATTAAT TGCTGGTTAT TTNGGGCTTA CAAAGCTCAA
 1260
 AGGACGCAAA GCGGTTACCC GAGGTATTTG GCGAAAAAGT GGCCAATGAA TTGGGANTTG
 1320
 GTTATTGGGA AATGAATCAA ATGTNGGAGC AATTTTAAACA TTTTTCCTCA CGACAAAGCA
 1380
 TATTGCGGTT GACTCATATC ATTAATTGCA CTACCAATGA TTATTGTTAA TAGCGTTGGT
 1440
 ACGGCGATTT TTATGTCTAT TATCATTTCC AACATTAAAA GCAAGAAGAG CAAATGAAGC
 1500
 CTGTTCCAAA CACATGACGT ACTGCAATTG ATGAACCAGA CATTGCCGTA TTTTAAAGAA
 1560
 GGATTGAATA GAGAATCGGC ACAGCAAATT GCGATGATTA TTAATAATTT AATGAAAGTA
 1620
 TCTGCCGTAG CAATTACAAG CAAAAATGAA ATCTTATCGC ATGTAGGTGC AGGTAGTGAT
 1680
 CATCACATAC CAACAAATGA AATATTAACA AGTCTGTCTA AAGATGTATT GAAATCAGGA
 1740
 AAGTTGAAAG AAGTGCATAC TAAAGAAGAG ATTGGTTGTA GTCATCCGAA TTGCCCGCTT
 1800
 AGAGCAGCTA TCGTGACACC ACTTGAGATG CATGGTTCTA TCGTCGGTAC ATTGAAGATG
 1860
 TATTTTACAA ACCCTAATGA TTTAACTTTT GTGGAACGTC AACTTGCAGA AGGATTGGCA
 1920
 AATATTTTTA GTAGCCAAAT TGAAC TTGGT GAAGCCGAAA CGCAAAGTAA GTTATTGAAA
 1980
 GATGCTGAGA TTAAGTCATT ACAGGCACAA GTGAGTCCAC ATTTTTTCTT CAATTCAATT
 2040
 AACACGATTT CAGCTTTAGT TAGAATAAAT AGCGAAAAGG CACGAGAGTT ACTATTAGAA
 2100
 TTGAGTTATT TTTTCAGAGC GAATTTACAA GGCTCAAAGC AACATACGGA TTACTTTAGA
 2160
 TAAAGAGTTA AGTCAAGTGC GTGCATACTT ATCACTCGAA CAAGCACNGT TATCCAGGAA
 2220
 GATTTAATAT CAATATTAAT GTTGAAGACA AATATCGCGA TGTGCTTGTA CCACCATTTT
 2280
 TAATTCAAAT TTTAGTTGAA AATGCCATCA AACATGCGTT TACGAATCGA AAGCAAGGTA
 2340
 ACGATATTGA CGTGTGAGTG ATTAAAGAAA CTGCAACACA TGTACGTATT ATTGTACAAG
 2400
 ATAATGGTCA GGGTATTTCT AAAGATAAAA TGCATTTGTT GGGAGAAACA TCTGTAGAAT
 2460
 CAGAATCTGG AACTGGTAGT GCTTTAGAAA ATTTAACTT ACGCCTAAAN GGATTATTTG
 2520
 GAAATCCGC AGCATTACCA ATGTGAATCC GACATCGAGN GGTACCACTT TTTGGTGTGT
 2580
 ACCTTCCTTA TGAAAGACAA GAGGAGGAAT AAATATGAAA GCATTAATCA TAGATGATGA
 2640
 GCCATTAGCA CGCTAATGAA TTAACATATT TATTAAATGA AATTGGTGGT TTTGAAGAAA
 2700

TTAATGAGGC AGAAAATGTA AAAGAAACAT TGGAAGCACC TACTTGATCA ATCAATATGA
 2760
 CATTATATTT TTAGATGTCA ATTTAATGGA TGAAAATGGG ATCGAATTAG GAGCTAAGAT
 2820
 TCAAAAGATG AAAGAGCCAC CTGCGATTAT TTTTGCAACT GCACATGACC AATACGCAGT
 2880
 ACAGGCATTT GAATTAAATG CGACAGACTA TATTTTGAAA CCGTTTGGTC AAAAACGTAT
 2940
 TGAACAAGCA GTCAATAAAG TGCGTGCGAC TAAAGCCAAA GATGATAATA ACGCAAGTGC
 3000
 AATTGCGAAT GATATGTCCG CGAATTTTGA TCAAAGCTTA CCTGTTGAAA TTGACGATAA
 3060
 AATTACATG TTAAAGCAAC ANAATATTAT TGGGATTGGC ACACATAATG GTATTACAAC
 3120
 CATACATACA ACGAATCATA AATACGAAAC AACAGAGCCA TTGAATCGTT ATGAAAAACG
 3180
 ATTGAATCCC ACTTATTTTA TACGTATTCA TCGTTCATAT AG
 3222

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

ATCAATGTAA CCTAATAGTT TATGTCTATC TTGTGTACCA ACTACTACAT CGACACCAGG
 60
 AATTTCCATA ATTTTCAGCTG ATGAAGTTTG CGCATAACAA CCTGTTACAC AGATTACAGC
 120
 ATCAGGATTG TGTCTTATTG CACGTCTAAT TATTTGACGA CTTTTTTTAT CACCTGTATT
 180
 CGTTACTGTA CAAGTATTAA TAACAAATAC ATCAGCATTG GCTTCAAAGT CAACGCGCTC
 240
 ATAGTTTGCT TCTTTAAATA ATTGCCAGAT TGCTTCAGTT TCATAATGGT TTAATTTTACA
 300
 ACCTAATGTG TGAAACGCAA CTGTTGACAT AAATATTCAC CCCATTAATT CTTTTTCATA
 360
 ACTTATTGCA CTTAACGCAT ACAATGGCGC AGTTTCTGCC CGTAAAATTC TCGGTCCAAG
 420
 ACCAACAACT GTACTAGTAT TACTAAATAA TGAAATTTCA ATTTCTGACA AACCACCCTC
 480
 AGGACCAAAA ATCATCAACA CTTTATCCTG AGCCTTGAAT TGTTGTAAAG TNTGCTTGAA
 540
 ATTGCTTAAC TCACCATCTT TTGCTTCCTC TTCATATGCA ATAAGAATAT AGTCNTAATT
 600
 ATCAATAGTA TCACAAATTA ATTTTAAATT CCGACTCCGA ATTGAATAGA TGGAAATCCAC
 660
 TAAACGAATA GCTTTGTTCA GCAGCTTCTT TAATTATTTT TTGCCAACGC TCTATCTTTT
 720
 TGACAACTTT CGCCTCCGTT TAATTTAACA ATTGAGCGTT CCATGCTCAC AGCTATAAAT
 780
 GATGAAGCAC CCAATTCATA GCTTT
 805

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

```
GGCACGAGCG TAGATTTAGC ATTTTCAAGA GACCAAGAAC ACAAAGAAAT ATGTACAGCA
60
TCGTATAATG GAAGAAAGTG AACGTTTCAA TGAATGGATT GAGCAAGGCG CAGCAATCTA
120
TATTTGTGGC GATGAAAAAT GTATGGCGAA AGATGTCCAT CAAGCCATTA AAGATGTATT
180
GGTAAAAGAA CGTCATATTT CTCAAGAAGA AGCAGAGTTA TTATTGCGAC AAATGAAACA
240
ACAACAACGC TATCAACGTG ATGTTTATTA GCGATTGGTG TTAAATATTT TAAGGTGTAA
300
TGATGTAAAA AGATATAAAG GATGTTGCTC AACATGAATA TGCCATTAAT GATAGATTTA
360
ACAAATAAAA ATGTCGTCAT AGTTGGNTGG AGGCGTCGTT GCAAGTCGTC CGGGCACCAA
420
ACATTAAATC AATACGTTGA ACATATGGAC GGTCAATCAGT CCGACAATCA CTGAAAAACT
480
TCAAAATATG GTAGATAACG GTGTCGTCAA TATGGAAAGA AAAAGAATTT GAACCAAGCG
540
ATATTGTAGA CGCGTATCTA GTTATTGCAG CAACCAATGA GCCACGTGTC AATGAAGCGG
600
TAAACAAGC CTTACCTGAG CATGCCCTTT TTAATAATGT TGGAGATGCA TCAAATGCCA
660
ATGTTGTATT TCCAAGTGCA CTACACCGCG ACAAGCTAAC TATCAGTGTA TCAACTGATG
720
GTGCGAGTCC TAAGTTGACA AAATCAATTA TGGCAGAGCT TGAGGCGTTA TATCCACCAT
780
CATACAGTTC GTATATCGAC TTTTATATA CTTGCCGACA GAAAATAAAA GTACTTGATA
840
TAACATATAT ACGAAAAGCA ACAGTTACTG TCACAAATTG TGTCACAAGA ATATTTAAAT
900
CATGACAAAC AAGCTCAATT TTTAGCGTGG TTGGATGTAA GATAATAATA GCGGACCGTC
960
TAACCGTCTA AGGTAAGTCT TCTTATTTTA ACTTTAACGC TTAATCATTG AAATTAAGAC
1020
ATGGGTGGCT TTGTGAATAG TCTAATAATG AAGGATTTAA GCGATAATGA TATGCGTTTT
1080
AAATATGAAT ATTACAATAG AGAAAAAGAT ACGTAGAACA AACTTAATAA AATAGATGGA
1140
TAAATTGAAA TCTGGTTGAA GTCGTTACTA TCATAGCGAC CTTTAGCCAG ATTTTTTGTG
1200
CAATAGAAAG CAATAATAAA AATGATAGAT CAANATGAAA TACAGGACAG GATATACAAG
1260
GATTAGTCAT GCCATGTTAT CAAGTAGGAA AATCAAACCT CACTATTGAT AGTTACGCAN
1320
AAAGATTTTT TTGATAAAAT GAGATAACTT AAAGATAAAA AATTATATTA ATTATAATAT
1380
TTAAGTTAAA GAGGGGGATT ATGTAAATTG TATTTAAAGT GGAGGGAGAA AATAATATGA
1440
ATAGTGAG
1448
```

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

```
CGACATGGAA GAACNTANAC CCTCGTNNAG GAGGCCCAAG AAGGNAGCNT NAAGNNAAAT
60
TAAGNNAAGC GAAAAGCACC AACAATAAAA CCTGATGGCA GCATCATTCA ATGCGTGCCA
120
CCAGGTTTTT ATGTTTTGTC AAGAAAATTA AATAAATCAT TAAATGATTC GGCCCATCGT
180
AGGATGTGAA TAAATACTAT CTCGTAATAC GGTATATGGA ATGTTTTGAT CAATCGCAAG
240
TTTAATTATA TTAATTAATT CTTCAGATTG CTTACCATAT AATGTAGCAC CTAAAATCAT
300
ATTATTTTCA TTATTAATGA CTACTTTAAA TAAACCTCTT GGATCATTGT TAATTTTGTG
360
ACGAGGTATA GCACTTACTA AAAGTTGATG TTCAGTGTA TCATAATGTT GAGCGGCAGC
420
TTCTTTACTA GTTAATCCAA CACGTGATAA TGGTGGATCT ATAAATACTG TATAAGGCAC
480
GCTACCTCTA TTGTCAGTCG TACGTGACTG ATTACCATAT AACGCTGATT TGATAATTCTG
540
ATAATCATCT AAAGATATAT ACGTAAATTG AAGTCCGCCT TTAACATCAC CTGCAGCATA
600
AATATGTGGC ACAGATGTTT GAAGTTGAGC ATTGACTTTA ATTTTCGCCTC TATCACCTAA
660
TTCGATATCA GTATTTTCTA AAGCTAAGGC TGTATTCGGT TTGCGCCCGA TAGCCAAAAG
720
TACTGCATCA GCCTCANAGT TGCCAACATT AGNACGGACT GTTGTATGAT GATCGTCAGA
780
TGACAATTCA GTCGTTTCAA CATTTGTATG CAATGCAATG CCTTTATTTT CTAAGTCAGT
840
AATAGCATGT GCANCGACAT CTTGATCTTC GCCGTGGCAT AAATGATTCA CCACGTTCTA
900
ATACNGTTAC CTTACTACCT AAATTCGCAA ACATTGAAGC AAATCTAAG GCAATATAAC
960
CGCCACCTAC AATAACGAGA TGCTTAGGTT GATAGCTAAT GTTTAATAAA CCTGTTGAAT
1020
CGAAGACATG TTTAGCTTGA TCAAGGCCTT TTATGTTAGG AATGATAGAG GTAGCACCGG
1080
TATTAATAAT GATATGAGGT GCAGTAATAC TAGCGACGAT ATCGCCG
1127
```

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GAAGANATAN CGTGGTNTTG AAGATTTGGG ANGTTAATAG ATNAAGGGGA ATATGCANTT
60
ATTACCGGGA GNNNAGTATC CAAGNAAATC TAGAGTCAAT AGGTTAATAA TCTTATGCCT
120
TTTTAATTTT GAATAAAAGT GGGGTGGTGT AATGTTTGA TTTACCCANC CGACCCGAAC
180
AAGATTGNCG TTTNACGCGA TTAGAAGNAA ATGATAAGCC TATGTTTGNN AAATTCGACA
240
GAATAGAAGA CAGTCTGAGA ACGCAAGAAA AAATTTATGA CAAGTTAGAT AGAAATTTTCG
300
AAGAACTAAG GCACGAGCGA CAAGGTAGAA GATGAAAAGA ATAAAGAAAA GAATGCCAAA
360
AATATTAGAG ACATAAAAAT GTGGATTCTA GGATTAATAG GGACGATCTT CTAAGTACGA
420
TTTGTCATAG CCTTACTAAG AACTATTTTTT GGTATTTAAA GGAGGTGATT ACCATGCTTA
480
AAGGGATTTT AGGATATAGC TTCTGGGCGT GCTTCTGGTT TGGTAAATGT AAATAACAGT
540
TAAGAGTCAG TGCTTCGGCA CTGGCTTTTTT ATTTTGATTG AAATGAGGTG CATACTGGG
600
ATTACCTAAT CCGAAAAATA GAAAGCCAC AGCTAGTGAA GTGGTTGAAT GGGCGTTATA
660
TATCGCTAAA AACAAAATAG CTATTGATGT ACCTGGTTCT GGAATGGGAG CACAATGCTG
720
GGAATTTACC TAATTATTTA CTCCGATAAA TATTGGGGAT TTAGAACATG GGGAAATGCT
780
GATGCTATGG CTCAGAAATC CAATTAATAG AGGTAGAGAT TTCAAGATAA TTAGAATCAA
840
AAGACTTGGT ACACAACCAG GCGACTGGGT TTTTGG
876

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GGCACGAGCG GCACGAGCGT GTTGATCAAA GATTTTGTAG GCAGTTTTAC AACGTCCGAT
60
TCAGCAAGTT ATGCACAAGA TTTTAAATCT GAGGAAAACG CTAAAAAGAT TGCTGAAACT
120
TTAAATCTTT TATATCAATT AACAGGCAAT CAAAACGGTG TGAAAGTTGT GAAAGAAGTT
180
GTGGATAGAA CTGACTTGTC ATCTGATAAA TCAGTTGATA GCGAAACAAT GTAACATAC
240
TAAGTTATGA GCATTACGCT CATAGCTTTC TTAGAAAAGTA GGTGTAGTTT TGGATGATAT
300
TCAGAAAATA AAAAAAGAGC TTTCTGAATT AGTTGAACGT GTTGATGATG TTGAAATACT
360
AGCAAACGAA ACAGCTGATC ATGTGCTTGA ACTTAGAGAG GAACATAAGC AACATCATAA
420
TGAACATAAGA GAATCTCATA AAGAACTTAA AGATAAGCAA GATAAAGTTG TAGATGAGAA

480
 TTTAGAGCAA ACAAAGATAT TAAACAGAAT TGAAGAAAGA TATCANACGC AAGTAGNTGT
 540
 TGNGCAAAAA AATGAAGAAA AGACACTCGC CCAAAATAAA TGGCTCGTAG GTGCCATATG
 600
 GGCGCTTGTA ACAATTGTGA TGATTGCAGT CATTACTGCA TCAATTNCTG CGTTATTACC
 660
 TTAAGGGAGG TGGACATAAT GAGTTGGGCA AGATGGTTAT CATGTTATTT GTNTGGTCGT
 720
 AAATGTAAAT AATGTTTTTG GTCAGTGCAT CGGCACTGGC TTTTATTTT GATTGAAAAG
 780
 AGGTACGTAC ATGGTATTAC ACAGCTCACA AGACAGGAAG CATACTCCAA GTGAAGTTGG
 840
 GAAGTGTTGT TAATACCAAG TAAGTAGGAT ATCTGANATG TATAATAGAG TAAAAATGAA
 900
 ATCTTTTTTAT TATAGACACA TATAAAAAGT GTATAGTAAT ATATGTATGT ATAATTAAAT
 960
 GATAATCATT TCATAATTAT TGTATATAAC TAAATAACTA CTTAACANAA ATAATTATGC
 1020
 TTTAGAGNTG ACCANNATGA NNNANNCCAG CATTTACATT ACTTTTATTC ATTGCCCTNA
 1080
 CGTTGACNAC AAGTCCCANT TGTAATGGT AGCGAGAAAA GCGNAGNAAT AAATGCGAAA
 1140
 GATTTGCGAA AAAAGTCTGA ATTCCAGGN ACAGCTTTAG NCAATCTTAN NCANATCTAT
 1200
 TATTACNATG NNANAGCTAN AACTGAAAAT AAAGAGAGTC CNCGACCACA TTTTACAGC
 1260
 ATACTATATT GTTTANAGGC TTTTTTACAG ATCATTCGTG GTATANCGAT TTATTAGTAG
 1320
 ATTNTGATTC NNAGGATATT GTTNATAAAA ATAAAGGGNA AANAGTAGAC TTGTATGGTG
 1380
 CTTATTATGG TTATCAATGT GCGGGTGGTA CACCACACAA AACAGCTTGT ATGTATGGTG
 1440
 GTGTAACGTT ACATGATAAT AATCGATTGA CCGAAGAGAA AAAAGTGCCG ATCAATTTAT
 1500
 GGCTAGACGG TAAACANAAT ACAGTACCTT TGGAACGGT TAAAACGAAT AAGAAAAATG
 1560
 TAACTGTTCA GGAGTTGGAT CTTCAAGCAA GACGTTATTT ACAGGAAAAA TATAATTTAT
 1620
 ATAACTCTGA TGTTTTTGAT GGGAAGGTTT AGAGGGGATT AATCGTGTTT CATACTTCTA
 1680
 CAGAACCTTC GGTTAATTAC GATTAATTTG GTGCTCAAGG ACAGTATTCA NATACACTAT
 1740
 TAAGAATNTA TAGAGATAAT AAAACGATTA ACTCTGAAAA CNTGCGTAG
 1789

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

CGATCTACAT TCGCTGCGCC AATACACACA ATAGGATAAT CTTCAATTTAA AACATATGCC
 60
 TTTCCCATAA CATATTCCTT TTGTATTAAT CCTGAAATAA TGTTTGCTAC GCTGGGTCTA

120
 GATAATCCAA TTGCCTCAGC AAGTTCACGT TGTGAAATAA NCGGATTATC TTTAATTCTT
 180
 TTTAAAATTT CTTTCTCAGN ATCGCTCATA ACCATCCCTC CTCATATTGA CTTAAAATAC
 240
 TTGAATCAGT GAATTCACCA AAAATATCGT AGCATGCTGT TATTTCTGTT GTAAACGCTT
 300
 ACATTTTNCC GTTATATCAA TGATATTTGT TTATAAAATA CGCATAATTT CGTAAAAAGT
 360
 AAGTTCATTG CCATCGTGTA AAAGNTACTC GAGCAAATGA TAAATGTTTA TACAGTATGA
 420
 TATTTGTCGA CAATAAATTA TGACATTTTT ATGTCTTATA TTTTCTATA AAAAAACGTG
 480
 ACTCATTATC GATTTTTTCA TCGACTGAAT CACGTTACGA TGTTTTATTT GTTTTNCTA
 540
 TTCAATATGA TGATGCTATG CGTCCAACGT CACCTCGATT AATCATGTCT TGCTTAGTAA
 600
 CAATTGGATA TTTTTTAAAT ACGGATTGAA CCAAGATAA CCCTGCAAGC GCACCCTACA
 660
 ATCGCCATTA CTACACCATA AATTACAATA GTCATTGGAT GATTAAATCC ANACATTACT
 720
 AAAAATCCTN CAATCGGTGT AGCTGTACCT GTCGCATCGT TAATTAAACC TGACATAGCA
 780
 ATAATTAAAC CAGCAATCGC ACCACCAAAG AAATTTGTAA TATAGATTGG AATTGGATTG
 840
 GCTGATACAA TATCTGCTTG TGATAAAGGT TCAATACTTA CTGCAATCGT AGACTTACGA
 900
 TCACCTAATT TTAAGCGATG GAATAGCGTC CCATTCATAA ATGCCGAAC TAAATGCTGCC
 960
 ATGGCACCAA TAGCCATAGG TACACCCGTT AAACCTAATA ATGCTGTCAA TGCCATTGAA
 1020
 CTCAATGGCG CTGTGCCGAC AACCGTGATA ATACCACCTA AAATGATACC CATGATAATT
 1080
 GGATTCGTAT TCGTACTACT TTGGATAATA TCACCAATTC GAATCAATGT ACTATTCACT
 1140
 ACTGGCGTTA ATAATACTGC AATAAGACGA GCTAATGGCG CTAAGATGAC AATCGGATCC
 1200
 AATTAAAGTCG ACAACCATCC GGGCACATAT TTCTCTTGTA TATTTTCATCA CATATCCAAT
 1260
 CAATATTTAA CCCGNAAGG AAACCTGGGT AATAAATCCA TACCACCGCA ACGCTCGGGC
 1320
 CGGTTATTAA CTTAATGGAT ATTCTGGGGG ATACAACCGA TTAGGTAAAT GCTTGTTGAA
 1380
 TCCCAGGCGG GAGGGGACAA CAACCTAGGA
 1410

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 926 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

AATTATCCG GTTTCGCCGT CTTTGTGTTGT GGCTATGTTA CATTCAACAA TAGATTTGCC
 60
 AGTGATACTG TCATCTTCGT CACGGTTATA ATAATCATCA CGGTAAAGTA GCATTGCTAA

120
 ACTTGCATCG GCTTCTATTC CGCCTGATTC TTTCATGTCT GATAGCATTG GTCGTTTATC
 180
 CTGCCTAGAT TCAACACCAC GATTTCAGTTG TGAAAGTAGT ACGATGATTG CGCCTGTCTC
 240
 GTTAGCGATT ATCTTTAAGT CACGTGATAT CTTTTCTACT GCTACACGTC TATCAACTTT
 300
 CGCATCAGTA TCCATCAGTT GAAGATAATC TATAAAAATA ACTTGGTTGC TCGGTCTGAA
 360
 TGCCTCATTG GTTTGAGCTC GCACATCTTG CGGTGGTAAT ATTTACTTTT GGTCAAGAAA
 420
 TATCAAATAC CTAAC TTCAA TGATTTGGAT CCCATTGCAT TTGT TAACTT CGTTAAGTCA
 480
 TCCGGTGTTA AGTTCCTGAT TTCTTTTATC TTGGTTAACT CAATACCAGT AATTGTTGAT
 540
 AACATACGTT TCAATACTGA TGTGCCAGTT GTTTC AAGAC TAAAGAAAGA TGTTTTATAT
 600
 CCATTTTCGTG CTATGTTCAA CATCATGTTT AATGCAAAAC CTGTTTTACC CACTGAGGGA
 660
 CGCGCGTGCC ATGACGATTA ATTGCGACGG CTCTAATCCC CCTATTTTGT AATCCATGAG
 720
 CTTATAACCC GTCTTAATTT GCTTCTTAGG GCTATCGCTG TATAACTCAT CAACAACTC
 780
 CTCAACAAAC TTCTTG GTTC CATCTTCTTT TTTGTTAGTA ATCGTTTTTA AATCCTTGAG
 840
 TTCATCAATC AAGTTGTTAA AGTTTTGGTT CGTAGGTTGT TGTTTAACT CAGTTACCAA
 900
 TTCGTTAGCT TTGTTGAGCT CGTGCC
 926

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CCAATAATCC ATTNCAAGGC TTTTTCGTTG CCCCAATNAA GAAGCACGAG ACCCATCCCC
 60
 GCTATTAAAT ACCTGCAATT TGAAATTTGC CAAGGGCACC ATGGTGTGAC CGACAAGTAT
 120
 TAAAATCCTG CACCAGCGAA AAGCATTACC TAATGAATTA TTATCATTA TCGATATTAT
 180
 TGTGCCAAAC GAAACAGAAG CCGAATTGTT ATCTGGGATT AAAGTAACTA ATGAACAATC
 240
 TATGAAAGAC AATGCCAATT ACTTTTTATC TTTAGGCATT AAGACTGTTT TGATTACGCT
 300
 AGGTAAGCAA GGTACATATT TTGCTACTAA AAATCAAAGC CAACACATCG AAGCTTATAA
 360
 AGTAAATGCG ATTGATACAA CTGCTGCAGG CGACACATTT ATTGGTGCAT TTGTCAGTCG
 420
 CTTAAACAAG TCGCAAGATA ACTTAGCAGA TGCTATTGAT TTTGGTAATA AAGCGAGCTC
 480
 ACTCACTGTA CAAAAACAC GGCGCGCAAG CATCTATTCC TCTACTAGAA GAAGTAAATC
 540
 AAGTTTAAAT GAATCAAACA CAGCTATGAT ATGAAGGTTT AGCATATAAC ATGCAACATT

600
 CGTATATCAT GGCTGTGCTT TTTTATCTTT ATAAACATC ATCTATTAGA AATAATTTTC
 660
 CACTAAACCT ATGCTTGTTG ACTCATGTTT AGTTATAAAT GAAGTGACAA TTTTTTGTAA
 720
 TCTTTTTAAC TTCCAAATTA TTGCATATAA ATATGCTATA TTAATGATAA TAATTATCAA
 780
 TTAAAAGGAG GTTATGCTAT GTCTAAAGAA GCTGGTCATA CATTTTTAGC TAAATTAGGA
 840
 AAAACTCGTC TACGCCCCGG TGGGTAAAGA AGCAACAGAT TGGNTTAATA CANCAAGGGG
 900
 CATTTTCACA AGATAAACAA GTGTTAGAAG TGGCATTGTA ATATTGTGCA CAACATCTAT
 960
 TTATCTAGCT CATACATATG GCTGTCACAT TCAAGGCGTT GGATATAAAT AAGAAAGCAT
 1020
 TAGAAAAAGC ACAGGAAAAT TTCCAGCAGC AGGTCTTGAA TCATATATTC AAGTTCAACA
 1080
 AGCGAATTGC TGTTAAATTG CCCTTTGATG ACAATCAATT CNATGTCGTT TTAAATGAAG
 1140
 CAATGTTAAC AATGTTACCC ATCGCCATAA AGGAAAAAGC ATTACGCGAG TNCTACCGAG
 1200
 TCATAAGCC NGGGGGTNTN TTGTAAACCA CATGATNTTG TCATCGTTAA TGAATCANAT
 1260
 NCCACANATG TTGTAAATC ATTATCTGCA GCAATTAATG TCNATGTCTC ACCGCAGACG
 1320
 AAACCTGGCT GGTTAGATTT ATATCATCAA AGCTGGTTTT AATCAGGTGC ATTATCCATA
 1380
 CTGGTCCATG AGTTTAATGA CACCAA
 1406

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GGACGTAATN ATACGCCTTT TCTGATTATT TCTTTACTAT TCTAAAACT GTTGTCTAC
 60
 TAATACCTAC CATTTTGAAA TTTCATTTGG CGTGTACATT CTACTTGCGA ATAATTGTTT
 120
 AATATATTTA CGTTTATCTT CAGAAAGTTG AGGTCGTCCT CCATACCTAC CACGTTCTTT
 180
 TGCAGATTCT AGACCATTTG TTGTTCTTTC TTTTAATAAT ATATTTTCTG AATCTGCTAA
 240
 CATTTTAAAT ACTTCAATAA ATGATTGTCC TTCTTCACTA TTAGTATTTA TGCCTAAATC
 300
 AAGCACTTCT AAATGGATAT CATATGGTAA TATTCTACTT TCAAAAAATT CCATGAGTTT
 360
 TTTTGGTGTG AATCCTAGTA CTTTAAATTT TTCTATCACT AATGTATCAT CTGTTTTCAA
 420
 CTCGTCTAAA CAATGCTCAA GTTCTAGTTG TTCTTTATAA TAAACATTTA CTGCTCAGA
 480
 ATAAACTAAG TCACAACCAT TTATTAAGAG TTTCGTTAAT TGAGTATCTA GATTTTGATC
 540
 AGGATATGCT ACACGTGCGT AACCAATTTT CCTCATTTTA TACACCCTTC CAGCTTATTC

600
ATTTTCTCCG ATTAATAAAC CTTGCTCGT GCCGTTTCAA CAAGTCGGGC CCTG
654

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GCAAAGGCTT TGAAGATATG AGTGGTAAAG AATGTACCTA AGGATGACAT TGAATAGAGG
60
GAGTAAAGAA AGCGACAGCT GATGCATCCT CGCTAGTTTG GACGGCATGA ATAGAATGAC
120
GTTAGGAAAT GAAGTTCTGA CTAACAAAAA GATTGAAACT GAAATCAAGA TGCTTGAGAA
180
AAAAATTGAC CAAATGGATA AATCAGAAAA TAATTCACAA GAAGCAGAAG TTGCTAAAGC
240
ACTTATTAAG TTAGCGGGTG TTAATAATGA TTAATGAAAT GTTAAACCCG AAACAACAAG
300
AAGTCTGGAC CTGCTTTATA AACGATAAAC CCAAAGTATT AATAGCGAGT GGTGCCAAAA
360
GGGCAGGTAA AACATATGTG TTCATCCTGC TTTTTTTAAT GCATATAGCT ACTTATAAAG
420
ACAAGGGGCT TAACTTCATT ATTGGAGGAG CAACACAAGC ATCTATAAGA CGTAACATAC
480
TAGATGATAT GGAGTTAATA CTAGGTAGAG AGTTAACACT CGACAAATCT AACGCAGTCA
540
AAATATTCGG TAATAAAGTG TATGTATTCG ACGGACAAAA CTCGGATGCA TGGAAAAAAG
600
CGCGTGGTTT TACTTCAGCA GGTGCTTTTT TAAATGAGGG AACAGCATT AACAATATGT
660
TTATTAAAGA AGTGTCTCA CGTTGTAGTT ACAAAGGCGC GAGAATATTA ATTGATACCA
720
ACCCCGAAAA CCCGATGCAT CCAGTTAAAA AAGATTACAT TGATAAGAGT GGTCAACGGT
780
TATCGAATGG AAGACTAAAT ATCAAAGCAT TCCAATTTAC TTTGTTTGAC AATACATTTT
840
TAGATGAAGA ATATATTGAA TCGATTATCG CAAGTACACC AACAGGAATG TTCACAGATC
900
GTGATATTTA TGGTAAGTGG GTTTCTGCTG AAGGTGTTGT ATATAAAGAT TTCAAAGAAA
960
AAGTTCATTA CATCACAGAA GAAGAATTTA AACTAAACA AATAAAAAGG AAATATGCAG
1020
GCGTCGACTG GGGATATGAG CATTATGGTT CTATTATGGT TGTAGCGGAA GACTTCGACG
1080
GAAACAAGTA CGTTATTGAA GAACACGCAC ACAGACATAA AGAAATAGAT GACTGGGTAG
1140
CTATTGCAA AGAGTTATAA AAGCATGGCG ATATCCTTTT TATGTGATAC GCTAGACCTG
1200
ACATATTGAC ATT
1213

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1141 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

CATTATTATT TGTCGTTAAA TACAATAGAA AATACTATAC CTGTATATGC AATTCGACAA
60
TAGATAAATT ATTAAATATG CTTACAACAA TCTTAATATC CTTTAACGCA CTACAATAGT
120
GCTCTGATAA TAGGTTATAA ATGTACGTAA AACCATTGTC TCAATAAAAA TGAAAACGTA
180
TACTTCAAGA AGGATGGGTT ACTTAATATA AACAAGGGGG TAACATATAT GACTTTATAT
240
TTAGATGGTG ANACACTAAC AATTGAGGAT ATTAACATCAT TTTCACAACA ACACTCAAAG
300
ATTGANATTA TTGATGATGC GTTAGAACGT NTCAAAAAAA GTAGAGCGGG AGGTGAACGT
360
ATTATTGAAA ATGANGAAAC GGGNTTGACG GGTATCACTA CAGGGTTGNG GGGTTTATTT
420
AGTGATGTAC GTATTAGCAC CCGACGCAAT ATNATGAATN ACAAGTGAAT CTGATACGCT
480
CACATGCCTG TGGACTAGGT GAGCCATTTT CAAAAGAAGT AGCATTAGTC ATGATGATTT
540
NACGATTGAA TACATTATTA AAAGGTCATT CAGGTGCCAC TTTAGTAATT AGTGAGACAA
600
TTACAATTTT TTATAAATGA ACGTATTATA CCGATAATCC CACAACAAGG CTCTCTCGGT
660
GCATCAGGAG ATTTAGCGCC ATTATCACAT TTAGCATTAG CATTAAATTGG TGAAGGGAAG
720
TATTGTACAG AGGGGAAGAA AAGGATAGTG ACGATGTATT AAGAGAATTA AATAGACAAC
780
CTTTGAACCT TCAGGCTAAA GAGGGTTTAG CATTGATTAA TGGTACGCAA GCTATGACAG
840
CTCAAGGTGT CATTAGTTAT ATAGAAGCAG AAGATTTAGG TTACCAATCT GAATGGATTG
900
CTGCATTAA C GATCAGTCT CTTAATGGCA TTATAGATGC ATATCGACAT GATGTGCACT
960
CTGTTTCGTAA TTTTCAAGAA CAGATTAATG TGGCAGCGCG TATGCGTGAT TGGTTAGAAG
1020
GATCAACATT AACGACGCGA CAAGCAGAAA TACGTGTACA AGATGCATAT ACGTTGCGTT
1080
GTATACCACA AATCCATGGC GCTGGTGCCC AAGTATTCAA TTATGTTAAA CAGCAATTAG
1140
A
1141

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TTTGTGCTTC GTCAATCTTG TCACCANCTA ACTCTAAACG CTTTCCTTTT GTCGTTTTTCG
 60
 GGNTCCCACC ACAATTAATC TGTTTTGATT TCTGACATAT CAATCTTCCT AGTTAACCCA
 120
 AGCCAAATCT TTACCATACT CAATTTCTTT ACCTTGGAAC AAGCTGTTTT TCTTGTTGAG
 180
 TACCACATAT CTACCTTTGA CGGTATTAGA ACTAAGCTCT ATATAAAAAT CCAATGCCAT
 240
 TTTATAGGTT GTACATAATT GCTTTAAAC TTCATATCTA GTNTGATAAG AAGTCCATGA
 300
 CGTAGTACGT AAGCCATCGT ATTCGGTNTG TTCAGAACT TCCCAACCTG TATCGCTCAA
 360
 CACATCTTTC AATGCTTCTG AAGTTGTCTT TTTCTCAAAT TTGCCTGGTG CATACGGTTT
 420
 AGCTGTTGTT ATATCAGCAA GATAAGACGC TATACATTCT ATCTCTGTGT AGCCGTCCAT
 480
 CGTATCTTGA ACCCAGTTAA TAATAAATTC ACGCCATTGT TTGTTTGAAT CCCTTATAAT
 540
 AACACGATGT CGTTCACGGA ACNTTTCAGC TCTTCTGAT GATATGAGCA GTTCAAGCAT
 600
 TTCTGAATTG TCATTAACAT TACGTTTATG AATCGCTCTA ACTAAGGAAG GATCATCAGT
 660
 AGAAAGGAAA TCTATAATCT TGTCGTTAAA ATCTAAAACA TGTATCACAC TCTCATCTCC
 720
 TTTCTATAAA TATCTATCTT GCCATTTAAC CGTCGTATCA AAGACGTTTT CAGGTTGTAT
 780
 GATTAATTCA CTGTACCCAG AATCAACATT GAAATAATTA CTTCCAAACG ATTTCTCGCT
 840
 CCAACATTGG TTCCTCATTT GATGACAACA CTTNNNGCTT GNATATCTAT TTTCATAAA
 900
 TCACCTTTTT GTATAATGAC ATCCCTTGCG CCTTTCGGNT TCGGTAGAAT CTCCGTATTG
 960
 AATGAACCTA ATCCATTCAT CTCCATCCAC TTATAACCGT NATACTTCGC ACTATAGATA
 1020
 GCTATGATAG AAGCTGGACG CTGATAAAAC TTACCGCCAT CTATCCACTC TTTCTCATCC
 1080
 ATATCAATAG GTTTACGTCT ATCTGGGTCT TTAATGTGAT CAAATTTCCA AGTTTAAATA
 1140
 GAAATTTAT TACCTACTCT TCTGAGCCGC ATATAAACAN CGATTCTGTC CAAGTTATAC
 1200
 ATTATCGGTT TATTCTGATA GTCGTATATC TTTTGGGGT CTCCTTTTTG GTTATACG
 1258

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

TCGAATTTGG TGTTGNCCGT TCCTGTATNA CATTCTGNCT TATCTAATGG GGGACGTTAT
 60
 GATGAGTGCC CACNNATTAG GGATGATCGT NCGAGAGTAA GTGTTGGTGC AAGGTCAAGT
 120
 GTGTTGCGAC CTTTCACAA ANTTAGGGTT AATCATCATT GATGAAGAAC ATGAATCTAC

180
 ATATAAACAA GAAGATTATC CGAGATATCA CGCTAGAGAA ATTGCCCAAT GGCGAAGTGA
 240
 ATATCATCAC TGTCCAGTCA TTTTAGGAAG TGCAACACCA TGTCTTGAAA GTTATGCACG
 300
 AGCTGAAAAA GACGTTTATC ATTTGCTATC ATTACCAAAC AGAGTGAACC AACAAAGCTTT
 360
 ACCTGAAATT GATATAGTAG ACATGCGTGA AGAATTGAGT GAAGGTAATC GGTCAATGTT
 420
 TTCAAAAGAT TTACGTGAAG CCATACAATT AAGATNAAGA TCGACAGGAA CAAGTTGTTT
 480
 TATTTTTTAA TCCGACGTGG TTATGCATCG TTTATGTTAT GTCGGGATTG TGGATATGTA
 540
 CCGCAATGTC CAANCTGTGA TATTTTCATTA ACGTATCATA AAACGACAGA CTTATTAAAA
 600
 TGTCACTATT GTGGTTACCA AGAGACGCCA CCGAATCAAT GTCCAAATTG TGAGAGTGAA
 660
 CACATTGAC AAGTAGGTAC TGGTACTCAG AAAGTTGAAG AACTATTGCA ACAAGAATTT
 720
 GAAGATGCGC GCATAATTAG GATGGATGTA GATACAACCT CAAAGAAAGG TGCACATGAA
 780
 AAGTTATTGA CTGAATTCGA AAAAGGTAAC GGTGACATTT TACTAGGTAC TCAGATGATT
 840
 GCGAAAGGAT TAGATTATCC AAATATTACT TTAGTTGGTG TGCTGAATGC NGATACAATG
 900
 TTAAATTTAC CTGATTTTCG GGCGAGCGAA CGTACTTATC AACTATTAAC GCAAGTGGCT
 960
 GGTAGAGCTG GTCGTCATGA AAAGGCAGGT CAAGTCATCA TTCAAACGTA TAATCCAGAT
 1020
 CATTATTCAA TATTGGATTG TTCAAAAAAA TGATTATTTA ACATTTTATC GTCAGGAAAT
 1080
 GGAATATCGT CAAATTAGGA AAGTATCCAC CGTATTTATT ATTTGGTTAN TTTCACAATC
 1140
 TCACATAAAG AAATGAAGAA GGTATGGAA GCATCGCAGC ATGTTCATAA AATTTTATTA
 1200
 CAGCATTTAC AAGAAAAAGC GCTTGGTACT AGGTCCATCC TCCGGCAGCA CTTGCGAGAA
 1260
 TCAACAATGA ATTTAGATTC CCAAATTTTA GTGAAATATA AAAGTGAACC TGGATTATTA
 1320
 CAAGCCANTC AGTTTTTAGA TGACTATTAC CATGAAAAAT TTATAAAAGA AAAATTAGCA
 1380
 TTGAAGATTG ATATTGGANC CACAGATGAT GATGTAACAT TACTAATTAT TAGAAACAAG
 1440
 NNCAAGTATT GTACGAGTAT TTGAACCCAG TGTGTGAATA TTTACTTNAN GNACAAGAAA
 1500
 AAGGGCAGAA TATACAACTG TTAACATTTT AAATTAGCAG TTTATATTCT GTCTTTTTAT
 1560
 ATGGCTTTAT AACTTACGTG ATTTTGGTTT GATAAGGAAT TTATTAGTAT TTTCATTTAC
 1620

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 875 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

AATTGGGCAC GGGTANACAG TTGTAGCGTT ATTAAGNATT TTAAC TTTTG CGAAGTTAGC
 60
 AACAA TTTNC CAATGATGTT ATTTTATCAA TGTTACCTCA AGCAGCAACT ACAANCGATT
 120
 GCGTTACCAG TATCAGCTGG TATCGGTGGT ATAAAAGAAT TAACATCATT AGCAGNTATT
 180
 TTAAATGGTG TCATTATTTA TGCCCTAGGT AATAAATTCN TGAAGCTTTT CCGAATTACT
 240
 AACCC TATTG CCCGAGGATT AGCACTTGGA ACNAGTGGTC ACACATTAGG TGTAGCACCA
 300
 GCCAAAGAAT TAGGACCTGT AGAAGAATCA ATGGCAAGTA TAGCTTTAGT GTTAGTTGGT
 360
 GTAGTTGTTG TAGCAGTTGT GCCTGTCTTT GTAGCAATAT TCTTCTAAAA CGAAAAACCT
 420
 AAGCAAGATA ATAGCAATTT GAGCCATTGT TATTATCGTA AAAAAACGTC TATACTCCAG
 480
 TTTATAACTG GGATATAGAC GTTTTTATGT ATTTATTACT TTTTACTAGG AATATAAAAC
 540
 TGTGCATGNC GATAATGAAA TACGATGTCA GACGAATCAA AGGGTTTGCC AGTCATTGTA
 600
 TAAAAAGTCT GGTGGTAACG TAAACATGGT TCACCTGTAG ACAATTGTAG TAATGAAGCT
 660
 TCACTTGAAG TGAGTTTATC TACATTAAAG AAAATATCTG AAAAACCAAT ACGAAGTTTC
 720
 ATGTTTGATT CTAAATAATC GAAGATAGAG CCCTTAGCAA TATCATCATT TAAATATTTT
 780
 ACGATTTCTT TATGATAATA AGAATATTCG ATACATAAAA CATCATCGTC CACGAATCTT
 840
 AATCGCTCTA AATAGTAGAC GGTATCACTC GTGCC
 875

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CAACTAGTGA TTCAGGATAT AGGAATTGTA TTGTCGGAAT TCANACAGGT GGATATGGTC
 60
 AAGATTTAAA AAGATTATAA CTTGGCCCAA TTATNACGGN GATCTTGAAA ACGATTANTG
 120
 GATTAGAACG AATTCGAATT TCTTCAATTG AAGCAAGTCA ACTTACAGAT GAAGTAATTG
 180
 ACGTTTTAGA ACGTTCAACA AAAGTTGTGC GTCATTTGCA TATTCCATTA CAATCTGGTT
 240
 CAGATACAGT ATTAAAACGT ATGAGACGTA AGTATACAAT GGATAGATTT TCAGAACGAT
 300
 TAACAAAATT GCATAAAGCT TTACCAGACT TGGCAGTTAC GAGTGATGTA ATTGTTGGTT
 360
 TCCCAGGTGA AACTGAAGCA GAGTTCCAAG AAACATATGA TTTTATCGTA AAGCATAAGT
 420
 TCTCTGAAC TGCATGTTTT CTTATTCTC CTAGAATTGG CACGCCAGCT GCAAGAATGG
 480
 ATGACCAAAT TGATGAAGAA ATTAAAAATG AACGCGTGCA TAAGGTTAAT TACGCTTAAG

540
CAATCAACTC GGAAAGTTAT ATGCGTCTTA AATTGGATCA AAGATGTGCT TGGANGGTNA
600
TTCCCTGAGG GAACAAGGGT GGACACAAGA AGGGTACAAT TAGGTGGRRD CTNS
654

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

CTANCNAANG GAANTTCAGC ATCCTTAAAA ATACCTATTT GACTGTAGAA ACCTTTTGNT
60
GCGTACAATA TCTAAACCTT GTCGTGCTGC TGGAACTGCA CCTGAACATT CAACAACAAC
120
ATCTGCACCG TAACCGTCTG TAATTCCATT GATATACGTT TTTAAGTCTG TGTGTTGTAA
180
ATTGACTACA TAATCCATGT GCAATGCTTC TGCTTTATCT AATCTGACTT NGTGGCANTG
240
TCCAATCCAG TTACCACAAC AGGTGCGCCT TTACTTTTCA ACACTTGTGC TACAAGTAAT
300
CCGATTGGCC CAGGTCCCAT TACAACTGCT ACATCGCCAG AGTTCACCTG AATCTTAGAA
360
ACGCCATGAT GTGCACATGC TAATGGTTCT TGTCATAGCT GCAGACTGAT ACGATACTTC
420
CGCTTCTGGA ATATGATNCA AACTTTCTTC ACGTGCAATG ACATAATTAG TAAATGCGCC
480
ATCAACTTGT GTTCCAATAC CTTTTCGATG GTTGCATAAA TGATAGTTTT TTGATTTACA
540
GGAATCACAC TCATTACANA CCATAGAATG TAGTTTCAGA AGTGACNCGG TCACCAACTT
600
TAAATCNTT AACGTCTGCT CCCAACTTCA ACGATNTCAC CAGAAAATTC ATGACCTAAT
660
GTCACTGGAA AATTAACCTN ATAATGCCCT TCATAAGTAT GAAGGTCTGT GCCACAAATT
720
CCTGCATAAT GTACTTTAAT CTTTACTTTA TCATCTAGCG GTGTTGCAAC TTCTTTATCA
780
AGAAGTTCTA AGTTGCCATG TCCTTCTCTT GTTTTTACTA AAGCTTCCAC CACAAACACN
840
TCGANTTTTT ANTTGNAATA GACTNNATAG NTTNAAGATA AGATAGTTAN CGATATTNCC
900
ACCTTGATCA ATACTTGANA TTTCAGATGA ACCTTTTGNC ATTTGTACAT TCGTACCTTT
960
CGCCATATCT GTGAAAATGG GTGCTACGTC TGTTGCAATA TATAATGAAA TTGCAATCAT
1020
AATCGTACCC ACAATGACAG AATGAATAAT GTTTCCTCTT GCTGCACCAA CAATAAACGC
1080
GACAACAAAT GGTATAGTTG CTAAGTCACC AAAAGGTAGT ACTTGTTTTT CTGGTAAAAAT
1140
AACGGCTAAT AAAACAGTGA TAGGTACTAA AATTAATGCT GTCGAAATAA CCGCTGGATG
1200
ACCTAATGCT ACAGCCGCAT CCAATCCAAT ATAAATTTCA CGTTCGCCAA AACGTTTATT
1260
TAGCCATGTT CTTGCAGACT CTGAACTGG CATTAAACCT TCCATTAAGA TTTTTACCAT

1320
TCTAGGCATT AAGACCATTA CTGCAGCCAT TGACATTCCT AAATTAATGA TGTCTCCAGG
1380
TTTGTAACCT GCTAACACAC CAATACCTAA ACCTAAAATT AAGCCGACAA ATATAGACTC
1440
TCC
1443

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CTTAGCAACT CAAGAAAACG TTAATTTATC AATTCGCGGA ATTCCTAAAG AAGTAGTAGC
60
ACGTGGTGCA CATCCATGTA TTATTTCTAT GGAGGGTCTT GAAAAAGAAG GCGACACTTA
120
TGTCATTCCT CATGTACATG AATTATTGAC ACCATTAGTT TCAGTAGTTG CATTACAATT
180
GATTTTCATAT TATGCAGCAT TACACAGAGA TTTAGATGTG GATAAACCAC GTAACCTTGC
240
TAAATCAGTT ACTGTAGAAT AATTCACTTT TTTAGAATCA ATCATGTATT AAAATTAAAG
300
TATATGGCAC CCTTTTAGAT TAATCGACTA GAAGGGTGCT TTTTLAGGTC GACTTAGCTT
360
TTACTTCATC TTAATTTGGC AGAAATGCGT NAAAAGGAAG TGTTTTATTT ATTTAAATAG
420
TCTGACAATT AAGGGTGTTA TGTTAATATG ATTTTATGAG AAGTATGGAG TAGCNATAGA
480
GGGGTGACCT CGCATGTTAA TTCAATTAAG ATCCACATTG GGCGANTGAA GCAAGGAAAA
540
ACAATTTTAA AAAATATTTT TGCCACATT CCTAAAGGTG ATAAATGGAT ATTATATGGG
600
TTGANTGGTG CTGGTAAGAC AACGCTATTA AATATATTAA ATGCATATGA GCCTGCGACA
660
ACTGGCGGTG TTAATCTATT TGGTAAAATG CCAGGCAAGG TAGGGTATTC TGCAGAGACT
720
GTNCGACAAC ATATAGGTTT TGTATCTCAT AGTTTACTGG AAAAGTNTCC AAGAGGGTGA
780
AAGAGTAATC GATGTGGTGA TAAGCGGTGC TTTTAAATCA ACTGGTGTTT ATCAAGATAT
840
TGATGATGAG GTACGTAATG AAGCACATCA TTTACTTAAA TTAGTTGGAA TATCTGCTAA
900
AGCGCAACAA TATATTGGTT ATTTATCTAC AGGTGAAAAA CAACGAGTGA TGATTGCACG
960
AGCTTTAATG GGGCAACCTC AGGTTTTTAA TTTTAGATGA GCCAGCAGCT GGTTTAGACT
1020
TTATTGCTCG TGAGTCACTA TTGAATATAC TTGACTCATT GTCAGATTCA TATCCAACGC
1080
CTTGCGATGA TTATGTGACG CAC
1103

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1095 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

```
CTGACATATT TAATGTTTAC ATCTAGTGCA TCAGGTTACG CCGTNTGTAT AGCGATGTTG
60
AGACGTTTAA CTGGATTAACTAATATCATT GGTAATTTTT ANCCAAAANA TATTGNTNGG
120
GTTTAATTGG CCCGAGTACT TTTACCANTA TCATGGTTAA NTAATTTTTT GNTGTGACTC
180
NAGGTGTACC NCCCAAACCG TTGCATGCTA ATTTAATGAT TCGGACTTTA AGCGGACATA
240
TCCAACATAT TGCATTTGGA CCTATTGCAT CACTTGAATC AATAAAACAT CTTGGTACGA
300
ATGGTGGAGG ATTTTGTAGCA GGAAATTCTG CAACACCTTT TGAAAATCCA AATATTTGGA
360
GCAATTTTAT AGAAATGGGC AGTATGATGT TACTTCCTAT GTCAATGTTG TTCTTATTTG
420
GTCGCATGTT AAGTAGACAT GTTAAACGAG TACATCGTCA TCGGTTGATA TTATTTGTCTG
480
CAATGTTTTT CATTTTTATA GCAATTCTTA CATTAACTAT GTGGAGTGAG TATCGTGGTA
540
ATCCAATACT AGCGAATTTA GGCATTTATG GACCGAATAT GGAAGGTAAA GAGGTACGGT
600
TTGGAGCAGG TTTGTCAGCA CTATTTACAG TTATTACGAC GGCATTTACA ACGGGTTCTG
660
TTAATAACAT GCATGATAGC TTAACGCCTA TAGGTGGATT AGGACCAATG GTATTAATGA
720
TGCTAAATGT TGTATTTGGT GGCGAAGGCG TAGGACTCAT GAATTTATTG ATATTNNTCT
780
TACTGACGGT GTTTATATGC AGTTTGATGG TTGGTAAAAC ACCAGAATAT TTAAATATGC
840
CAATTGGCGC CCGTGAAATG AAATGTATTG TCTTAGTCTT TCTCATACAC CCAATTTTAA
900
TTTTAGTATT TTCAGCACTT GCTTTTATGA TTCCTGGAGC AAGTGAAAGT ATAACGAATC
960
CGTCTTTTCA TGGTATTTCA CAAGTTATGT TATGAAATGA CATCAGCTGC TGGCGAACAA
1020
TGGATCAGGG TTTGAAGGAC TGAAANGAAT GAATNCAACA TTTCTGGGAA ATATCTCTAC
1080
AGGAATCATT AATGT
1095
```

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 913 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GGTGTTGTTT TCCTCCAATT TTTGGATCTT TTTTGCTCTA AAATCTCATC TTTTTTAATC
 60
 TAAATAGATC AAGAGTGCGC TCTAAGTTTT CTTCCTTTTG AAGAAGTCGG GTTTCCTTGT
 120
 CTNTGAAGAT CNCAACGTCT TTCTCGNAGT TCTGCTTCAG TNTGTTCTCT TNGGAGTTGG
 180
 TNTTCTTCTT TTGCNTCAAG TAATTTCTCT TTTTGTGATAN TGTCAGCTTC TTTATGTGCT
 240
 TGATNAACAA TATCNTCGGC AGTTTGTCTA GCTTGTGATT GCTTTTGAAG CANCANATTT
 300
 CGGGCNACAA CATACCCTCC AACAACTCCT AGAATGATCC CCANCACATG AGTAGGAGGC
 360
 TTAATAAATT CACACACACA CCTCCTTTTC TAGGGGTTTG CTCCTTTAAT ATGAAATCCA
 420
 ATATGACTTT ATGAAATTAA AAATAAATCA AACCAAATTA ATTTGTGCGG TTTAATAGGA
 480
 GATAAGTGTC AAGTTATCAA TTTGCACTTT TGCATATAT TGAATGCTAT TTCTACTATT
 540
 TTCTAAAGTT TTGAAGCTCG ATTATAAAAC TATTGATAAT GTAATAATAA ATAAAATAAA
 600
 AACCTTATA GTCTCGATTT GTAGTGTATC CCATAAAGTT AGATATTATT CTAGCTTTAT
 660
 GAGATGAATA TCACTTTCAA TCAATCCTAT AAGGATATTT GCTAAGTTTA ACTATAGATA
 720
 TAAATTTGTG TACTATTCTT CGTCAAATAA TGACTTTGGT GCATCTTCTG TTTCTTCAAC
 780
 ATCACCATCA GATATACCTA ATTTTTCTCT CAATTTACGA TCAATTTCTT CTTTAATTTG
 840
 TGGATTTTCT TTCAAGTACA TTTTAACATT TTCCTTACCT NGACCCATTC GTTCGCCATN
 900
 GCAAGAATAC CAG
 913

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 970 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

TGANGTAAAT TTGGTTGTGG CTCANTCGCA TCTGCGAAAG NGNAGTGCCC NGAGACCGCC
 60
 TGTAATGTTT ATGACGACCC TAGAATAATA ATAACTAAA AGCGCCGCCT NATGAAANTG
 120
 AGCGCCTTGG ATGNAATCAC TCCAAACGGA CACCNTCGAA NCCACCTNGA GATGTANANG
 180
 AAATACATAG TAAACCTACG AGTGATCCAN CGATATAAGG GTTCATGTCT GATACAGATG
 240
 TGATTGCTAA TGTTGGTAAG TAGATAACAA TTGCAACACG CCCTAAATGG TAAACGACAA
 300
 ATAATAATGA GCCANTGACA CGTATGCTAG GGCCAAATCT AGCTTCTAAA TATTCATATG
 360
 CAGATGTTAC CTTTAACTTT TTAAAGAAAG GGACATAGAA ATAAATAAGT AATGGAATAA
 420
 TTGCGACGAT AGCAATGTGA CCAGCGATAT ATGACCAATC TGTTAAAAAT GCTTTCCTCT
 480

GGTGTAGACA TAAATGTAAT CGCACTTAAC GTAGTAGCAT AAATTGAAAA GCCAACTACC
 540
 CAAGATGGCA AGCGACCACT TGCGGTAAAG AACTATTGG TACTTTGGCT CGCGCGCTTG
 600
 GTAAAATAAA CGCCAATGAA CAACATAGCT AGTAGATAAA TGATAACGGC AACCCAGTTT
 660
 AGTGTGCCAA ATCCAACCTC TTTCATGGGC AACATCCCCT TTACAATGTA TTGATTCTTT
 720
 GATGTCTATA AATCGTATTT TGCAATGAGT TGATCTACAT GTTCGTCGAT GTGCTTCGTT
 780
 AAAAGGTTTG AAAGGTCTTT TCGGTAATCC TGCATCAATG TCACGATGAC GTAATATTTT
 840
 TTTCAATGTT GGATAAATCC CCATNGATNA CAACTGTTTC GATAATGTCT TTTGAATCAT
 900
 GTTGTAGTTG GTAAGCTTCT TGAATTTGAC CTTGTCGTGC TAAGTCGAAG ANTTCTCTAG
 960
 CGCTCGTGCC
 970

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GAAGACATGA ACGCATACGA AGATAGTTAT GAAAACCGAA CTAAAAAAC AACTGCTGGC
 60
 AGTAGCGATT TAAGTATGTA ATTAACGAGG GCATTAGCCC TCTATTTTGT TGTACAAAAT
 120
 AACGATAAAC GAGGTATTTA ATATGACTGA AACAACTTTT AATCCAATTA CATCATTAAC
 180
 AATTAACAAT GAAGAAGTGA AAGCAAAAGC AACATTTATG TTCGATAAAA CCGCTAAAAA
 240
 ATTTGCAACT GAACAAGAAG ATAACAAAGG TAGAAAACAA ACGATTTTCAG GATTTACTAA
 300
 TGTTTATNAC GCTTTATTAG AACGTGACAC AGTGGCAATC GTAGACTTTT GGGAAATGTGC
 360
 AACAGCTTAT CTAGGTAAAA GCGCGCCTAA AAGAGAAGAT ATTGAAGCGG AAATCATGGA
 420
 AATCATCGAA AGAGAAAACG ACACGTTGAT CTTTACAAAG GTGCGTTGGA CGTAATGAAT
 480
 AATAGCGGTT TTTTCAAGCA GAAATCACGT CTATTCTGGA CACAGATGAA CCAAGCGCCA
 540
 TCGTTAGCCA AAGAAGACGA GAAAGAGGGC GCGAAAGCTG GTATCGAGAT GATGAAGAAC
 600
 AACTACAAAG AAATCATGAC CGTAGCACCT TATTAGACTA TTCGGAAATA AGGCAGATGA
 660
 CAAGTCGTTA CATAGGTTAT ATGAGTAATG ACGAGCTAAT GAGCATGCTA CCTGCCGAAT
 720
 GGAATGACTG GATTATTGGC GCTAGACAAG CATTGATTGA CCAAAGGGAC NTCGCTCGTC
 780
 CCGCTCGTGC C
 791

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 820 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```
GGCACGAGCT AAAATATATG AAGCTAAAGG CCGTCCATCT GACAATCCGC TTATTGTTCA
60
TATACACAGT AAAGTTCAAT TAAAAGATTT TACATATACT TTGGCACGAG CGTAGAAAAG
120
TTAATGCAGG CATTCTGGCC GGGCCCTATT TCGTTTATAT TGCCGCTAAA GCCAGGCTAT
180
CTATGTCGAA AAGTTTCTGG AGGTTTATCA TCAGTTGCTG TTAGAATGCC AAGCCATTCT
240
GTAGGTAGAC AATTATTACA AATCATAAAT GAACCTCTAG CTGCTCCAAG TGCTAATTTA
300
AGTGGTAGAC CTTACCAAC AACTTTCAAT CATGTATATC AAGATTTGAA TGCCCGTATA
360
GATGGTATTG TTCAAGCTGA ACAAAGTGAA GAAGGATTAG AAAGTACGGT TTTAGATTGC
420
ACATCTTTTC CTTATAAAAT TGCAAGACCT GGTTCCTATA CAGCAGCAAT GATTACAGAA
480
ATACTCCGA ATAGTATCGC CCATGCTGAT TATAATGATA CTGAACAGGC AATTGCACCA
540
GGTATGAAGT ATTAAGCATT ACTCACCCAA TACAACACTT ACAATTATTA CAGATATTGA
600
GAGCAAAATT GGAAATGACG GTAAAGATTG GTCTTCTATA GCTTTTATTG TGCCGAGTAA
660
TAAGGTGGCG TTTATACCAA GTGAAGCGCA ATTCATTCAA TTATGTCAGG ATGACAATGA
720
TGTTAAACAA GCAAGTCATA ATCTTTATGA TGGTGTTACA TTCACTTGAT GAAAATGAAA
780
ATATTTTCAGC GGCATATATA TACGGCTTTG AGCTCGTGCC
820
```

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

```
GTGACTTGAA AGATATAGTA TATCGGATTT GTAATGCGCC GTTAATCAAT TATGATGCCA
60
TTAAGATGAC CCGACTTAAA ATACNCAGTC CGACACAAGA TTGCTATGAG TTTTTTGGGT
120
GGAGATATTG AATTATATAA TTATCACTAT TAATACCTAC ATCAAAGGTA TGCTATTGAT
180
TTAGTTATTA AAGNAAATCA TAAAACATAT AAGAATCAAG GAAAAGTAAA TACTGATTAT
240
TTTTGTTTTG GAAAAGATAT CATTGCGCCA GCAAATGGTA CAGTTGAAAA AGTAGTGAAT
```

300
 GGGGTTCAAG ACAACAGTAT TGGAAGTACG AATGAATCAC AGTTTTTAGG AAATTATATT
 360
 GTAATTAAGC ACGCAGAAAA TGAGTATAGC TTAATAGCTC ATTTACAACA ATATTCAATC
 420
 ATTGTGAATG AGGGGCAAAA TGTTAAATAT GGTGACTTCC TTGGGAAGGT TGGGAATTCT
 480
 GGCAATTCTA CTGAACCTCA TATACATTTT CAAGTAATGA ATGATAAGAA TATTGAAGCA
 540
 TGTACGTCTT TGAAAATTCG ATTTTTTAAAT AATCTAGAAC TTATCAAAGG GGATGTGGTC
 600
 TGCGGATTAC AAGGTGAATG ATGGCGATAC TTATAAAATC TCGACACTAT AAAAATGGTA
 660
 TAGTGTGCGAG ATTTTCTTGC TTATTTAGTT AATTCAAAGT GTACGCCGGA TTCATTAGAA
 720
 GTTGATGTAT TTGTGTTTGT AATAGAGTAT CCAGTTATTG AAATTTTAGA TTCAATATCT
 780
 GAAGCGGTAT TTGTAGATTC GGGATTATAG AAGCTACATT CATAAGTGTT ATCATCTNTG
 840
 GTNTTCNAAG AATTAAACAT TCCCTTTGGC TTTTAACTTC CGACTTTAGT GGTGGGNTAA
 900
 TGNCAAAAAG TNTGGAGNTG CTTATTACTA TTAATTAACA ACCCAGCCCA ATTGGGNCAC
 960
 CCCCCAACGG ATTTGGACCA ATCCTCAACT TACCTGCTTA TGAATCCCTG GCTCCCAACC
 1020
 CCCGCAAATT TGCTAAACCC AAAATCCACT TCCAANGTTT CCAAACCTAC TTTCTTCCAA
 1080
 GNTAATTTCT TCAAGGATTT TTTTTGG
 1107

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

AAGTTTGATC CACCCACCNT AAACCCATCG CCTAACAATA AANCCGAANN TCACCTCCTG
 60
 CCTGTTGATC CAATTGTTCC CATTCCAATA ACCGCCACCT CTTTTTCTAG AACACCCACA
 120
 CCTATCGTTC TATGGTTAAT ATGTTGACA TCTGTATGCG GTATAGCGAC CGAACATAGA
 180
 TGTGTTGGTA AACCAGTANC NAATTCTTTT TCTCTGTCGA TGAATGCATC TTAAACGTT
 240
 GACTTCACGA ACCCATTTTG AAATAACACA TCTGACATTT GNGACAATAC GGATTCTTTA
 300
 TCAGTTGCCG ACNAATTGAG CATTATATTT TCTTTATGCA CCTAATTGCT TGTCCCATCC
 360
 ATTTTCCCTC GCTTCTTTAT TTGAATAATT TTTTAAATC TCATTTACAT CAGAATTTTT
 420
 GCGACTTTGT ATGATGCGCT TAATTGCGTC ATTGTCTTGC GCCACATCTC TCAATTGTAG
 480
 TAACGCTCTT AAGTGTGTCA CTTTATCAAC AGCAGCAATA GGTACAATAA TATGGATTGC
 540
 TGTGCCATCT GACATGTATA TTGGTTCTTG TAATATCAAC ATACTCATCG CTGTTTTATG

600
 TACATGCTTT TCAGAGTATG CATGTGGAAT AGCAATATTT TGCATGATAA CCATATACGA
 660
 ATCANCANAT ACCNNGGAAT TCCATCTCAT GAATATATTT AATATCAATA AAATGATTAG
 720
 CAACTAACAC AGCACGNGCT TTAGCAATAG CTTTCATCAAT ATTTTCAACA GGAGGCNTNC
 780
 TTTNCACGGG CCTGGCCGGT ATCAAGGCAG CTAAATCTAA TGTCTTATTT TGTGTGACAA
 840
 TCGATCCATT AATGGTTGAA ATTGAATTAT AATTGGCAAT AAAATCTTCT AAACCATCAC
 900
 GTAGTTCTGT AATGTCATTA ACTGTCGTTG TCGGTTCAAT TAATGCCATT AACTTGTTTA
 960
 TTTCTTATC AATGTCAGCC GATTCCTTAT TAATGTACTT CATCACTTCT TTACGTAAC
 1020
 TTCGTTGCTC ATTTTCAGAT AAAGCTACTT TTGTGATAAA TAATTTTTTA TGTGTTAGGA
 1080
 CAAACATTGG TGAAAAGACG AAGTCATAAT CTAATGTGTA ATTTTCAAAT GTTCT
 1135

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 973 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

CGTGCGAGCT GCTTTTGGTA AAAACGGCGG TAATATGGGT GTATCTGGAT CAGTTGCTTA
 60
 TATGTTTGAT CATGTGGCAA CATTGTTGAT TGAAGGAAAG TCTGTTGACG AAATACTTGA
 120
 AACATTAATG GAACCAAGAT GTAAGATGNA AATGATGTGA TTGACGATAA TGGATTGACA
 180
 ATAGTCTATG CTTGAACCAA GATCCAATTT CCAGTCGTTT CAAGATGCGC TTCGTNCACC
 240
 AGGTTGTTGG AAGAATTTAA AAGTTGCTTG AATTTGAAAT TGTTACCCTC CAAACAAGAT
 300
 ATTGAACTTT CTGAAGCGGA CCNAAGTAAC ATTTGAAAAA TTAATCGATG CATTAGAAGA
 360
 TTTAGAAGAT GTACAAAACG TATTCCATAA TGTGGATTG AAATAATGAA ATCAGCAGAA
 420
 CAATGGATTG ATGAATTGCA ACTTGAATCA CATCCTGAAG GTGGTTTCTA TAGAGAGACA
 480
 ATTCGAGAAG TATTGAAAGA TGGACGCAGA GCGCCGTTTA GNAGTATTTA TTTTTTACTT
 540
 ACAGATGACA ATATTTGCGA TTTTCATCGA ATTGATGCTG ATGAAGTATG GTACTATCAT
 600
 GCTGGTGATT CTCTAACAAAT TCATATGATA AATCCGGATG GGAATATAC GACTGCAACA
 660
 TTGGGTACTG ATATCCAAAA TGGAGATGTA TTGCAATATG TAGTGCCTAA AGGAACAATT
 720
 TTTGCTTCTT CAATCGAAAT TTCAAATACT TATAGTTTAG TAGGTTGTAT GTGTCAACCG
 780
 GCATNTGAGT TTAAGCAGTT TGAATTGTTT AAGCAATCTG AATTAATTAC ACAATATCCG
 840
 CATCTTAAAT CAGTGATTGA NAAATATGCT TTAAATAAAA AATGATCAAT GAAGTGGTTT

900
GAAGGTTGTT AATAAACCTT TGAGTCACTT CATTTTTATA TGTATTCTTG ATTGAATCAG
960
AATAGATTTG ATG
973

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1701 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GGCACGAGCT GGTTCATAT CTAAACTTTG GTAATCTACA CCTTCTTTAG ATTTACCGAA
60
TGCGATAGCT GGAGACTTAA CTGCGGCTAC TTTCGCATGT GGAATAGCAA TACCTCGCCG
120
ATACCAGTTG TACTTTGTGA TTCTCGATTG TGAATCGCTT CCTTAAATGA CGCGACATCA
180
CTTAATTTAC CTGCCTTGNC TAATTGGAAT TACCTAACTC ATCAATAACA CCATTTTTGT
240
CATTTGCCAN TAAATCCATT GCTATCGTAT CTTTTGTTAA TAACTCTGTT ACTCTCATTA
300
TTTTCACTCC CCATCAAGTA CGCTAATCGN AACTTGGTGA TTCTATTTTT TCTTATAGCG
360
GTCCCGTGTT TGCTAAGTCC TCAATCAAAA TGCCGGGGCA AGTACCGCAA TGCGACTGCT
420
TGGTTGGGAA TGCTTTTTCA ATCGTTAAAC CTGGAAGCAA TTCCAGCCAC CATGCCTGCA
480
ACTGTACTAT CACCAGAGCC AACTGTATTA ACCACTTTCC CTTGTGGATT AACTGCTTTA
540
ATACTGATTT CTTTATCAAT ATAAATAGCA CCATCACCGC CAAGCGAGAC AATAACAGAT
600
TGCGCACCTT TATCAACTAA CAAACGACCA TATTTAATAA CATCTGTGTC TGAGTTCACT
660
GTTGTATTAA ACATCACTTC TAATTCATCT TTATTAGGTT TAATAAATAG TGGNTGAAAT
720
GGTAAACGC TTTCAAGCCA ATTCTTTTTT AGCGTCGACC GACTAATTTA GCACCTGTCT
780
GTGCTGTAAT TTGTGCAAGT TTGCGCATAC GCATCGCTTG GAATACNACT TGGTACACTT
840
CCAGCAACAA TAACGATATC NTCGCTTGTT GTATTTTTTAA TGTGTTGTAA CAGTTGTTCA
900
AATTGTGTTG ACGTTATATG AGGACCCGGT GCATTGATTT CTGTTTCTTG TCCTGTTTTT
960
AATTTACAT TAATACGTGT ATCTTCATCN ACNNCAATAA AATTCGATTG AATTGCNCTG
1020
TTANTTAATG TATCTATAAT GAATTTCCCA GGAAATCCAC CTGCANATCC CAAGGCAGTT
1080
GACTCAACAT CTAATGTCTT TAAGACGGCG CGAGACGATT AATACCCTTT CCCCCCAGC
1140
GAAGTAATAT GTTGCTGTTG CTCTGTCCAA NNCCATCAAG GTTNAGAATC ATTCGTAAAA
1200
ATGACATAAG TCAATTGTAG GAGTGNGAGT CNCCTGTATA AATCATAAAG TCCCTCCTAT
1260
AAAGTGAGAC TTTTGTTGGT ATTCTTTTAN CGAGTCTTGA GTTAATGCTT TTTCAGATGT

1320
 GATGANTGTC GTACTTTCTA GCACAGGGAC ACGAGCACAA TATACTTTAT TAAACTTAGA
 1380
 NTGATCCTAT AAGNACANAT GANTGAGTGG CTAATGACAT TGCTGTTTGT GTAACATAATN
 1440
 CCTCTTGCTC ATCGGGAGTA GTTAATCCAA GTTCAATATC TAATCCATTC ATCCCGATAA
 1500
 AAGCTTTATC GNAACAATAT CGTCTTAATA TCTCCATAGC ACTAGANCCA ATCGTAGCNA
 1560
 GTGTATTTTC TTAACTTGA CCACCTAGCA TAATTGTTTT AATACCTTTT GGAAGTAAAG
 1620
 CTTCTACATG TGTTAAACCA TTGGTTACCA CAATGATATC TTTGCTTGA ATATATTTAA
 1680
 TTAGCGGCAC GAGCTCGTCC C
 1701

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 858 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

CCCGGTGTA ACCGTATGGA TGGATGCTAG CACCAANTTA ATAATCCTCC ACAATANCAT
 60
 TAAGGGTATT CATGTAGGTG NCACAACATG GTAAAGGCTC TACCAGTTGC TTACCTTAGA
 120
 ACAGCTTTAA GTTGNAATG GTTATGAAGT AGGTACATTT ACGTCGCCGT TTATTGAAAC
 180
 ATTTAATGAN CGAATTAGTC TAAATGGTGT GCCAATATCA AATGACGCTA TTGTAGAATT
 240
 AGTATCACGT ATTAAACCAG TAAGTGAAAT GATGGAACGT GAAACAGATT TAGGTGTTGC
 300
 AACTGAATTC GAAATAATCA CAGCGATGAT GTTTTTATAT TTTGGTGAAA TACATCCTGT
 360
 TGATTTTGTC ATTGTTGAGG CTGGATTGGG TATAAAGAAC GATTTCGACAA ATGTCTTTAC
 420
 ACCGGTTTTA TCAATCTTAA CTAGTATCGG TCTAGACCAT ACAGATATTT TAGGTGGTAC
 480
 TTATCTAGAT ATTGCTAGGG ATAAAGGCGC GATTATAAAG CCTAACGTTC CAGTGATATA
 540
 TGCTGTAA AATGAAGATG CATTAAAATA TGTTGCTGA ACGCGCAATT GAACAACATG
 600
 CAAAGCCAAT TGAATTAGAT AGAGAAATTG TTGTTGTATC GCAAAAATGA TGAATTTACT
 660
 TACCCGNTAT TAAAGATTAT GAATNAGAAA CAATCAATNT NAAGCATTGT TAGGGTNGAA
 720
 CATCAAGAAA CAANATGCTG CATTAGCCAT AACAANTCTT ATTGGANTCA AATTGAACAA
 780
 GGATTAATTG AATNCAGATT TNCAANAAGA TGATAGACGG GTTTGATCAA GTCCGTGGAC
 840
 NTGNCGTTTT GGGCAGGT
 858

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

```
GAATTCNAAG TCACTTTCTT TTTTAAGCTT TAAATTTCTC CCCATTTTTT TAGCCCCCTA
60
TAAGGATTGA ATATCAATGC CTTCTNTCAT TAAAATTTCT CTAATTTGCG AAACAAATAA
120
TAATGCATGT TCTCCATCAC CATGCACACA AATTGTATCT GCTTGTAACG TTACTTCCTT
180
ATTGTTTTGT GAAATAACTT TATTTTCCNN CACCATCTTT AAAACCTGCT TAAGTGCTTC
240
GTCAGTATCA GTAATCACAG CATCACTTTC TTTTCTGATT GATAAAATCA TATATGTTCC
300
TATAAACACT AAAAATCCTA TAACTAGGTA ATAATATTAA ATTCAAGGAT CGANCCTCCG
360
CTAAGCGACA ACAACAATGG TGACAATAAC AACAACAAC GAGAATTNAA ATACCTAATT
420
CAAAAAGGGG TNATNGGNCT TACAATGAAT GTGGCCNAAA ATTGGGGAGG NTCCAAGGNG
480
GGNTCAAATT RRDCTNS
497
```

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 969 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

```
CCCTGGTTGA TTGGAAAATG TAATTGAATG AAACGGGTAA AACCTTCCCC AAAGCACCAT
60
AATTGTTGCA AGTAGGTTGC CACCCCAATC CTGGTTTACC CTGATTTGAA AGGCTTTGGG
120
CAAGCCGAAA TATAGATATC TCTAACCGAC GAGATTTATA ATTTGATGAT TTATCAATTA
180
GGTGCATTAC AAGGGTTTTG TCGCATTATC CAACTTAAAA TTAATCATGT TAAACCCGCA
240
TGGTGCATTG TATCAGATGG GTGCAAAAGA CAGAGAAATA GCAAACCCCC GTNATANCAC
300
NACCTGTTNA TGNCNTTGAT CCATCACTAG TGTTAGTAGG ATTAGCAATC ATATCTAATT
360
TCAGAAGCAA AGAATGTCGG ATATAATCCA GCTTCTGAAG TGTTTGCTGA TAGACGATAC
420
GAAGATGATG GGCAGCTCGT TAGTAGAAAA GAAAGTGATG CTGTGATTAC TGATACTGAC
480
GAAGCACTTA AGCAGGTTTT AAAGATGGTG NAGGAAAATA AAGTTATTTT AAAAAACAAT
540
AAGGAAGTAA CGTTACAAGC AGATACAATT TGTGTGCATG GTGATGGAGA ACATGCATTA
600
```

TTATTTGTTT CGCAAATTAG AGAAATTTTA ATGAAAGAAG GCATTGATAT TCAATCCTTA
 660
 TAGGGGGCTA AAAAAATGGG GAGAAATTTA AAGCTTAAAA AAGAAAGTGA CTTTGAATTC
 720
 ACAAAAAATC ATAAAAGGTT ATTATTAGGT TCTGTATTTT ACGATGGCAA CTTCTGCAAT
 780
 TGGCCCAGCA TTTTAAACGC AAACAGNAGT ATCAACATCA CAATCGTTTG NAAGTCNCGN
 840
 ATCTGCCATA TNACTGTCTA TCATCATTGA CATTGGTGCA CAAATTAATA TATGGCGCAT
 900
 ATNAGTTGTA ACTGGTTTAA GAGGTCAAGA AATATCAAAT AAAGTTGTTC CTGGGCTTGG
 960
 TCTCGTGCC
 969

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 632 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GGNACGAGCG GCACGAGCGC ACTTATTTTA TCAGAACATT CTAAAAAGAA TATATTCAAT
 60
 ATAAAAAAGG CTGTGTAGGG GTGTCTTATG AATAATAGAA ATGTGTATGA TATCGAAGTA
 120
 AGTGATTATA AAGGCTTAAC TTATAAATTA GAAGCATTTA GAGGTAAAGT GATTTTAGTT
 180
 GTTAATACTG CAACAGAATG TATATATAGC GAACAATTGA AAAAAGTAGA GACTTTGTNT
 240
 CAAAAATATA AGGATCGTGG GTTTGTAGTG TTGAGTCCC CGAATAATAA TTGTGACAAT
 300
 CGACAACCAG GNTCTAATGA AGAAATCTTG AAAATTAGNC GGNGAGAAAT TTGGGTGTTA
 360
 CATTTCCAGT GCTAGCTTAA AATATCTTGT GAACGGGAAC GAATGAACAT CCCCNTATT
 420
 TACGCATTTN ANAGGAATGA ACAAACCAGG AATCTTNGGG CCCCCAATAA AATGGAATTT
 480
 CACAAAAATT TATAATCGAT CGACAAGGCA ATGTTGTAAA TCGATTCTTG CCAATGGAAG
 540
 ATCCAATGGA TATATCGACA AATATAGAAA TATTATTGGA AGAATCTTCA ATCTTAAATT
 600
 TAANATTGAG CGCTTAGTNT GCAAATACAC AA
 632

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

CCCCACNAAG TACNCGAAAC GCAAACAAAC ATCTTAAAAG GAGGAACGAA CAATGCAAGC
 60
 ATTACAAACA TTTAATTGGA AAGAGCTACC AGTAAGAACA GTGGAAATTG AAAACGAACC
 120
 TTATTTTGTG GGAAAAGATA TTGCTGAAAT TTTAGGATAT GCAAGGGCAG ACAATGCCAT
 180
 CAGAAATCAT GTTGATAGCG AGGACAAGCT GACGCACCAA TTTAGCGACA GCAGGTCAAA
 240
 ACAGAAATGT AACGATCAAT CAACGAATCA GGATTATACA GTTTAATCTT TTCTAGCAAA
 300
 TTAGAAAATG CGAAGCGGTT CAAACGTTGG GTAACCTCGG AAGTTTTACC AACATTAAGA
 360
 AAAACTGGTG CTTACCAAGT ACCTAGCGAC CCAATGCAAG CATTGAGATT AATGTTTGAA
 420
 GCTACAGAAG AAACAAAACA AGAAATTAAA AACGTAAAAG ATGATGTTGA TNGATTTGAA
 480
 AGAAAATCAA AAACCTGGATG CGGGAGACTA CAATTTCTTA ACTAGAACTA TCAATCAAAG
 540
 AGTAGCTCAC ATNCAAAGAC TACATGCGAT AACAAATCAA AAACAACGTA GCGAATTATT
 600
 CNGGGATATT AATTCAGAAG TGAAAAAGAT GACTGGTGCA AGTTCAAGAA CGAATGTTAG
 660
 AC
 662

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 960 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

TAATTCGCAA TAGGAGTGAT GAATATCATA AATTTTACCC TCCAAATGAA GCTAATGAAG
 60
 TCCTGGACCC GAGTAAGACG CATGTAGCCA AGCTAAAATA ATCCACTCTA CCTTATCTTT
 120
 AGTTAATAAT GTTACTAAAT GTTGTTTATA CGCTGCTTTT GAATCAAATT GTTTTGGTTC
 180
 ATTAATATAA ACAGGAATAT CGTGCTTGTT TGCTCTATCT ATACAAAACG CATTTTGATG
 240
 ATCCGTATAT AGCNCCGTAA CTTCAATATT TTCAAGTTTT CCTGATTCAA CATGCTCAAC
 300
 TATATTTTCA AAGTTACTTC CTGAACCTGA TGCAAAAATC GCAATTTTAA CCATTGTTAT
 360
 ACCCCCAACA ATTCAATTGC AGTTGACTCA TTTTTCACAA TATGACCAAT TTGATAAGCT
 420
 TCCACATTTT GTTCTGCTAA AATCTTCAAA GCGCGTCGAT GCATCTTTTT CATCAACGAT
 480
 AACCGTATAG CCAATACCCA TGTTAAAAAT GTTATACATT TCATTTGTGT CTATATTGCC
 540
 TTGTTGTTGT AACCAATCAA ATATTTTTGG CGTTGGAAAT GATGTAGTAT CAATTCTAGC
 600
 AGCATATCCG GCTGGCAATG CACGTGGAAT ATTTTCATAA AAACCTCCAC CAGTAATATG
 660
 ATTCATTGCC TTAATAGAAA CTTCTTTTTT TAAAGCAAGT ACAGGTNTGA CATATAATTT

720
 AGTTGGCTCT AAAAAGACAT CTATAAATGG ACGATTATCG NAGGGTGATG CCAAATCAAT
 780
 GNCTGATTCA NTAATTAATN TGCGCACTAA ACTGTNTCCA TTNGANTGAA TGNCACTTGG
 840
 ACGCAAGTCC TATAACAAC TGGCCCTCTT NCAATTCTTG AACCATCTTA CAATAGNCAA
 900
 CCTTTTTCAT CTGCTCCAAC AGCAAATCCG GCTACATCAT ATTACCTTC GTGATACATT
 960

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1013 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

TAATNAATTT GGCGANTCAC TTGTCGCTAA GTGGCTCCAC CTTGTCATCT ATTATTGCAT
 60
 CACTCATGGG NCGNACATCA TAGTGTGAT TTGATTCAGC CATATCNACG TTTTGATTTT
 120
 TCTAATAGAA GATCAGCAAC AACATCAACA TTTGAATGAT TCATATATGA TGCAGGTACG
 180
 TCTTTTAATG TTTTAATGTT ATCAATATAA AGATTGATGT AGTGTGCGG GATATTGTAG
 240
 TGATGTTCAA GTAACATATC AGTAACAAGT TGATTAAAGA CACTTTCATC TAATTCACCA
 300
 CGTGCCACAG CGCTTTCTAT TAATGCTTTA TTTGGGAAAA TAGGCACGAG CGAACGTCAC
 360
 GTAACCATTT NGCGACATCT TCAAACGTAT CCGCTTCTAA TCCTTCCCAG GGGTTACGTG
 420
 CTGCAAAAAT CGAAATCGGT GATAATGGTG TAATAACACG TTTCGCATTT TCAATGACTG
 480
 AATTGATATT TAACTGTGTT GTCATACCTT TCACCTCCTA TAAATACTTC TTCAAATAAT
 540
 TCGGATGACT TTCTATCGCT TTCGAGCGTG CTTACCTAG ATTAACAAAC CACACGTACA
 600
 ATACCGCAA ACCCTTAGAG TATCGATGAC GCGCCACCCA AATACTTAAT AAATGCCAA
 660
 AGATTAAAT GACAACACTA ATGATGACAC TCACTGTAGG CGGTGTTGTC GCATGTGTTG
 720
 TTATATTTTG GTAATACATC GTAAAAATAA TTGTGTGTGA TGACGTAGAT AAATGTCACA
 780
 ATTGCAATCA AAATCATGCC AACCAGACGT GCCATGCGCC CTTTACTAAA GGCTACCATC
 840
 TGATTCCAAG ATACAAGTTA ATGACCATGC TAGAATGAGT GCACTTAACA CTTCATATGC
 900
 ACTTCTGTCA CTACCATCCA AATAGAATGC ACGATAATAG CTAATACACG TCCATGACAT
 960
 CCAGCATAAG CTCTTACAAT GCTGTTTTGA ATATGATCGC TCCCAARRDC TNS
 1013

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1032 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

```
ATCCACCCAT NACGNTACTC ATANCATTGT CAACAGTAAG TAATGTCCAT ATGCATATCN
60
ATNCCGCTCG GCANTATANC ACCCAACCGG ATTTCATAAG TGGGCGGATA AAGTGATNAG
120
AGTGATCTCA ACACTATCGA NTAGNTACCA GCGTTCTTTA TCGGTNTTAT TTTATNATTT
180
ATTGTCACAN ATTTANTGAA TATAGATAGC GTTATACTAA GTCAGNTTAT ATTACCTGTA
240
ATCACGCTAT CTTTAGGTAT GTGTGCATAC ATCATTCGTT TAGTGCGTTC TAATTTATTG
300
ATGTTATTGC AAAGTAATAT CGTACAANCA GCAAGATTAC GCGGTATGAA TGANCGTTAT
360
ATTTTAATTC ATGATTTACT AAAACCAACA ATTTTGCCGA TTATCCCATT ACTAGGGATT
420
TCACTTGGCA GTCTAATAGG TGGTACTGTA GTGATTGAAA ATTTATTTGA TAATACCTGG
480
TATTGGTTAT CTATTAATGG GATAGTATTA AATCTCGAGA TTATCCTGTT ATTCANGGAT
540
GCGTGTTATT TATTGGCTTC TTCGTTGTTA TTATCAATAC GATTGCTGAT TTATTAACGT
600
TATTACTTGA TCCGAAGCAG CGTTTACAAT TAGGAAATCC CACAAAACAC AACCAATACA
660
CCATTGATAT CAGAAAGTAG TGNCCGTCAT GCATAAAATA TTTTCANAGA ATAACCTGAT
720
ATTTTTTTGTA TTCGTTGCAT TTATTTTTGT GGTAAATTGTA CTGCAATTCT TTGTCAGTAG
780
TGAAAATGCA ACCACAGTCA ATTTATCACA AACTTTTGAA CCGATTAGTT GGTTCGATTT
840
ATTAGGAACT GATGATTATG GGAGAGATTT ATTTACCCGA ATTATTATCG GTGCACGTTT
900
AACATTGTTT GTTACTGTTT TAACATTAAT AGCTATCGTT GTCATAGGTG TTACACTAGG
960
TCTATTTGCC GGATATAAAA AAGGGTGGAT TGAACGATTA GTGTTAAGGT TTATTGATGT
1020
TGGTCTAAGT AG
1032
```

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 646 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

```
GGCAGGAGAC TTTGGTGGTA GTTTTGAAAG ATTACAAGCA TTGACAACAA AAACAACATT
60
ACCCGTATTA TCCAAAGACT TTATAATAAG ACCCCCCCA ANTTGATGTT CCTAAACNA
120
```

GCTGGTGCAT CTATGATTTT ATTGATCGTT AACATCTTAT CGGATANACA ATTGAAAGAT
180
TNAATATACC CTACGCAATA TCCCAAATC NAGAAGTGTT AATTGAAGTA CATGATCCCC
240
ATGAATTAGA ACGTGCCNAT ANGGTTAATG CTAAATTGAT TGGTGTAAT AACAGGGACT
300
TAAAACGATT TGTCACAAAT GTGGAACATN CAAATACTAT TTTAGAAAAT AAAAAACCAA
360
ATCATCATTA TATTTCTGAA AGTGGTATTC ACGATGCATC TGATGTAAGA AAAATCTTGC
420
ATAGTGGTAT CGATGGCTTA CTAATAGGTG AGGCGCTTAT GCGTTGTGAC AATCTATCTG
480
AATTTTTACG ACAACTGAAA ATNCNAAAGG TGAAGTCATG ATGAAATTGA AATTTTGTGG
540
CTTTACATCA ATAAAGGATG TTACAGCGGC CAGTCAATTA CCTATTGATT CGATAGGTTT
600
CATCCATTAT GAAAAAGTA AAAGGCATCA AACAATACCC AAATAA
646

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GGCACGAGCG TCAGTCCAAA TCACGCCTTG TGGTTTCTCT GGAATTGTCA TCTATTACTC
60
ACCCCCAAAT ACATCATTA TGTTAATATT GTGAATTGCT TCAATTGGAT TTATTGTTTC
120
ATCTACAGNN CGATATCGCT TACTATCAAT CATGNCATCT ACATGACATA CCGATTGATA
180
ACTACAAAAA GCACATGGCA ATTTGTGTGT GTNCTTTAAT GGTGCAACTN CAGTATGTCC
240
ATCCATAATA TNTGAAGCTG TNTCTATAAA ATTCTCTNTG TTATGCTGAA TGAATTTATA
300
AATTGNTGGT TCATCTGACA CTTGGCTGGC TCGTTTACTC AAAGAGACAT CTTTTATTCA
360
ANCCAACTGG GTACAAATAT CTGAAGGTGA ANTTAGGGTT CTTNAACGAA TTTCCAATGC
420
ATCAAATAGC AGGGGGGTCT TGCATTCAAC TAAACCCTCA GGTTAANCTT NNNAATTAAT
480
CTTGNTCTTG GNTNTCTTTC ANCAATATCA AGACCATGAT TTAATTTACT CTTGGGCCAA
540
GTCATGGAGT TTTATATCCA CCGGG
565

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 919 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

```
CTTGAAGTAG TAGGGTTACA AGGCTCAACT TACCTTTTAA AAGGACCAAA CGGTGAAAAAC
60
GTAAAGTTAA ACCAATCAGA AATGAACGAT GATGATGAAT TAGAAGTAGG TGAAGAATAT
120
AGTTTCTTCA TTTATCCAAA CCGTTCAGGT GAATTATTTG GAACTCAAAA TATGCCTGAT
180
ATTACGAAAG ATAAATATGA TTTTGGTAAA GTACTTAAAA CGGATCGCGA TGGGGNACGT
240
ATAGATGTTG GGTTTACCCC GNGAAGTGTT AGTACCATGG GAAGATTTAC CAAAAGTGAA
300
ATCACTATGG CCACAACCTG GTGGATCATT TGNTAGTTAC ATTACGAATT GACCGTGAGA
360
ATCATATGTA TGGACGTTTA GCGAGTGAAT CTGTTGTAGA AAATATGTTT ACACCTGTAC
420
ACGATGATAA TTTAAAAAAC GAAGTCATTG AAGCCAAAACC TTGGCNCGAG CGTATTACGA
480
ATTGGTAGCT TCTTATTAAG CGAATCAGGT TACAAAATTT TCGTACATGA ATCAGAACGT
540
AAAGCTGAAC CAAGATTAGG TGAATCTGTT CAAGTTAGAA TTATCGGGCA TAATGATAAA
600
GGTGAGTTAA ATGGTTCATT TTTACCACTT GCACATGAAC GNTTTAGACG ATGACGGCCA
660
AGTCATCTGT GATTTACTAG GTGAATATGA TGGGGAATTA CCATTCTGGG ACAAATCAA
720
GCCCTGAAGC GATTAAAGAA GTATTCAAAT ATGAGTAAAG GTTCATTCAA AACGTGCAAA
780
TCGGNCACTT ATATTAAACA GAAGGATTAT TAATATTAGG AAACAGGGTA AAAATCACTT
840
TTAACTTAAA AAAGGGTTGG CGGGTCGNNT TTGGNCTCAA AAAGAATTAA TCATTNTNAC
900
AACGNNNTCG GNGGATGCG
919
```

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 955 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

```
CTGCATCTGG TGAAGGAAAT CAANTANNTN TTATNNCTGA AGTGATTGCA TGGTGCAACN
60
TCAATATCA CATATGGCTC AGTGGANTAT ATGGATAAAG GCTTAACAGG TCATATCATG
120
CGGCGTGGTA TTACTGAAGC GGATGCCTCA ATTAATTGGG CACTAGGTTT AATGAATGAG
180
GGTAGCCAAA TTATTGATAA TACAACAAAT TTATGTGGTG ATCGCACAAAC AAGNNCACTT
240
AAATCAGGAG GTGNAGGTAC AGGAGAACAA AAAATTAATC TAACATCTAA ANTCGCACAA
300
ATATGGTAAA GAAACAGATG GTTATNTCCT TAAACATGGT GTTATGAAAG AACATGCATC
360
ATCTTGTATT TTAATGGGTA TCCGGCTACA TTANGCATGG GGGGAACATA ATCAAGTGCT
```

420
AATCAGGAAT CACGTGTTAT TNATGTTATC TTGAACATGC TCGGGGGNGA CGCGAATCCT
480
ATTTTATTTA ATTGANGAAG ATGATGTACA AGCTGGTCAT GCTGCATCAG TAGGCCGTGT
540
TGGATCCCAG ATCAACTTTT ACTATTTAAT GAGTCGTGGT ATTTCTCAA GAGAAGCGGA
600
ACGTCTTGTT ATACAGGGTT TCTTAGATCC AGTAGTACGT GAATTACCTA TCGAAGACGT
660
TAAACGTCAA TTGAGAGAAG TAATTGAACG CAAAGTTTCT AAATAATATT TTGAAAATAA
720
AAGTTTGTA TAGATATAGA CTGTCGATAT TGGTATAAGA CTAATACAAC GTCAGTATTT
780
AAATGATTAG GATTTTTATT TAAGAAAGGT CGTGAATGAA GTGGCCGAAC ACTCATTTGA
840
CGTTNATGAA GTAATCAAGG ATTTTCCGAT ATTAGATCAA AAAGTCCATG GCAAACGTTT
900
AGCATATCTT GATTCAACAG CGACAAGTCC AACGCCTATG CCAGTGTTAA ATGTT
955

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

NAAATTCCT ATACGTTATA CTTTAATTGT TAATAAGCCA CATAAATAAG AGGGGGAAAT
60
GCTGTGTACA AGCAAGGTGA ACCAAATTTA TGGACTGGAA GGTTAGATAG TGAAACAGAC
120
CCGAAAAAAT TTAGACATTT TCAAACAGTA ACATTTGAAG ATTTGTCTAA GCTGGAAAAG
180
AGTAGTATGC CATCAGGGGT CGGTATATTA GGCTATGCTG TTGGACAAAG GTGTTGCTTT
240
ANACAAGGGG CGCATTGGTG CAAAAGAAGG ACCAGATGCG ATTAAACAAG CATTTGCAGG
300
TTTGGCGGAT TTGGATCACT GTGAACTNT AGTCGATTAC GGAAATGTTT NTCATGATCA
360
TGAGGAATTA NCTNGATACN CAACCANGAA TTTGGTACTG TNTTGGCAA TTGAGCTCTN
420
TCTTTAGAGC TTGGNNCATT GATAGGTTCT CTCGCAGGTG GT
462

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GGCACGAGCG TAAGATTAAC CATTGACCAT AATATATATT GTGTTTTTCC AAAATCGGCT
 60
 CTGCTAATTT TAAATAGGGG CGATATATTG TTATAAACT ATTGAAAAAT TCTTGTGATA
 120
 GCATAGTGAC ATCTCCTAAG ACAAATAGT TAGCTTAGCT AACCTTTTCA CAACAATAGT
 180
 AATTATAAAA CGGGAGCAAT TAGAAATCAA TATATAATTA TTAAGAGCAA AAATAATTAT
 240
 ACTTTGTAA AATAAGCGTA ATTACATGTA AATAGGGGGA TACTAATGAT ATTGAAATGT
 300
 GCATCACATC ACTCATTATA TAGATCAGTT AGATCGGTTT AGTTCTCCAG GAGATGTTAT
 360
 AAAATNACAT TCAGGTGGGT ATCATCATAA ATATGGAACA TTCAATAAAT TAGGTTATAT
 420
 CAATGAAAAT TATATTGAGC TACTGGATGT AGAAAATAAT GAAAAGTTGA AAAAGATGGC
 480
 AAANACGATA GAAGGTGGAG TCGCTTGCGC TACTCAAATT GCACAAGAGA AGTATGAGCA
 540
 AGGCTTTAAA AATATGTGTG TGCGNACAAA TGATATAGAG GCAGTTAAAA ATAATCTACA
 600
 ANGTGAGCAG GTTGANGTAG TAGCGCCGAC TCAAATGGAA AGAGATACAC ATAAAGATGG
 660
 TAAGGTAAAG TGGCAATTGC TTATATTATG AATCAGGATG ATGATGAAAT TACGCACCAT
 720
 TTTTATTCA ATGGGAGAAA GTGCCTCCAT GC
 752

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

CAAATGTTTA TCATGATATG ATGAATATAA TAATCGGGTA TATAACTGTA TGATTAATTA
 60
 CACAATAAAG AGAGGGAATA TAATATGNGN NAAGTGTCOA TTAAAGATGT TGCTAGAGAA
 120
 GCTGGTGTAT CAGTTNCANC TGTGTCACAT ATTTTAAATC ATAATGATAG TCGTTTTTCC
 180
 GCANCACCGA TAAAAACGT ACATGCTGTT CCAGAACGTT TAGGCTATGC CCCTAATAAA
 240
 CATGCAAAAC AAGCTCGTGC GCGGCAGTAA AATTCAAATC ATTGGCGTCA TTTTACCTAG
 300
 CTTAACAAAT CCGTTTTTCT CAGCACTGAT GCAAAGTATT CATGAACATA AACCATCTGA
 360
 TGTTGATTTA TGCTTTTTAA CATCTACAGC AACTGATNTG TATGACAATA TTAAACATTT
 420
 AATTGATCGA GGTATTGACG GATTAATTAT CGCACAATAC ATATCATCCC CGGACGCCCT
 480
 AAATAACTAT CTAAAGAAAC ATCATGTACC TTATGTCGTA CTGGATCAAA AATGACCATC
 540
 AAAGGCTATA CAGATTGTGN TCCGGACAAA ATTGAATATC AAGGGTGGGA CAACTTTGGC
 600
 AGCACAACAA TTTAATAGAA CTCGGGTCAC AAACCATATT GATAATTGGT TGCAACCATA
 660

TTGACAATGA TGGNGAATAT TGTCGACTCC TGTCGCTGGA TTTGTCGATA CTTTGC GCGC
720
GAATCAATTG CCAGAACCAC AAATCGTCCC TACTGAATTA TCTAAACGCC GTGGCTAACC
780
ATGTTGAATG A
791

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

TTTGCTTTTG GAATGGGCTC GTTTTTTTTA ACCTAATAAG AAATGATAGG GCATTTGAGA
60
TTGGAAGGNC ATTTTGGCTT TGTGCAAATA ATACAATAAG CTAAATGTCT NTTTTTGTTT
120
TTGTGAAAAT ATGATGGATG GCTTGTGTGG GCAAGTTTGC TAATTTAATA AGATATGCAT
180
TTTTCAATTT AGGAGTTGGC CATGCATCTA CACTTTATAA TGGTGAGAGC GTGGTGAGGT
240
ATTGTTAATC ACGCAATTGT AGCGAGGAGT TATTGCTACA TATGTCGTTA TGGCCTATTG
300
ATTTTCTAAA ATAGCTGTAT CAGATCATGT GACNAAATAA AAATAATTTG TTGAAAGCCT
360
TTACATAACT TGTCTAGACA AGTTATACTC GTTTTAAGAC ATTAAGGGAG TGAAATATAT
420
GGCTGTAAAA AGAGAAGATG TAAAAGCCAT CGTAAGNCGC TATTGGGGGA NAAGAAAATC
480
NTGAAGCTGC ANCGCATTGT GTAACNCGAT TACGTTTNGT GCTTAANGAT GAAANCANAG
540
TTGATAAAGA CGCATTAAAG AACACGCGT TGGTCAAGGG GCAGTTCAAA GCAGACCATC
600
AATATCAAAT TGTCATTGGT CCAGGANCAG TCGATGAAGT GTATAAGCAG TTTATTGATG
660
AAACAGGTGC TCAAGAAGCT TCGAAAGATG AAGCGAAACA AGCAGCTGCG AAAAAAGGGA
720
ATCCAGTACA ACGTTTGATC AAATTGTTAG GGGAGATTTT TATACCAATA TTACCTGCGA
780
TTGTGACAAC TGGTTTGTTA ATGGGGATTC AATAATTTAC TTACAATGAA AGGTTTATTT
840
GGTCCCAAAA GCACTTATTG AGATGTATCC CGCAAATTGC TGATATTTCA AACATCCATT
900
AATGTGATTG CGAGTTACCG CATTTATTTT CTTACCANCA TTAATTGGTT GGAGTAATAT
960
GCTGTGTATT TGGTGGTAGT CCGATCCTAG GCATAGTCTT AGGTTTGATT TTAATGCATC
1020
CGCAATTAGT ATCTCAGTAT GATTTGGCAA AAGGGAATAT TCCGACGTGG AACTTATTTG
1080
GCTTAGAGAT TAAGCAGTTG AATTACCAAG GTCAAGTGTT GCCTGTTTTA ATTGCAGCTT
1140
ATGTTCTAGC TAAAATTTGA AAAAGGATTA AATAAAGTCG TTCACGATTC GATAAAAATG
1200
TTGGTCGTTG GACCGTAACG CTTTTAGTTA CTGGATTTTT AGCATTTATT ATCATTGGAC
1260

CAGTTGCATT ATTGATTGGT ACAGGTATTA CTTCTGGTGT TACATTTATA TTCC
1314

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 972 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ATAATTATTG NTGGAAAATA ACATTGAGCC CAATTCCCAA CAGTGGCCGA CATTTTCCAT
60
CCATTTACCC CCCCCTGACT TTGTATCCGA ATTCNACCN TCCACCNAAG TTGNCATCAA
120
TATGTTAATA ACCCAAATCC CAAATTGGAA ATATTTTGCC AAGCCAAGTT TTGATGATGC
180
GCATTTGTCC TAATATTTTC CACTTAACAA GATCCGACCC CCAGCCAAGA AAATACATCA
240
ACTGAGAAAT ATAATGNCCA AGACTGGTTT CCAACACACA TTCGACATAA TGAGTTGTCT
300
AAATTGACTG AGCAACAAC TGTGATTCAG TTGCTTATGC ATATGATTCA TTATGGCACG
360
AGCGTACATA TCATTCGAAC CCAAAGTATC TTAAATGATG ATAAAGTGAA TCAAGTATGC
420
GACTATATCG AGTTACATTT TCATGAAGAT TTAAGCCTTT CAGAATTAAG CGAATACGTT
480
GGGTGGTCAG AGAGCCATCT GTCTAAAAG TTTACAGAAT CGCTAGGTGT AGGATTCCAA
540
CATTTCTTAA ATACGACGCG AATTGAGCAT GCGAACTCG ATTTAACATA CACAGATGAA
600
ACGATTACTG ATATTGCATT GCAAATGGC TTTTCAAGTG CAGCGAGCTT TGCGAGAACA
660
TTTAAACACT TTACGCATCA AACGCCTAAA CAATATCGAG GTGATCGTCC AGCAATCACT
720
GAAAATCAAC AATCGGCACA ACATAATTAT CACGACCGTG AATTGATATT ACTTTTAAAT
780
GACTACATTG AAGAAATGAA TCAATTCAAT TGAAGATATT GAAAAGNTGA ACTTATAAAG
840
AGATTGCCTT NAAACCAACT AATCAACAAC TAAATCCAAT TATAATCCAT ATTATTCAAG
900
TTGGGCTATT TGAGGAATTT GCTCCAATAC ACAGTATCAA TCCACAGTTG CTTACATGTT
960
CATCCCATGA TT
972

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

AAACCATTTT CCAAAAACCAA GCTGGGCATC CAAGTTTTCC TATTGTAATC TGCAGGTAAC
 60
 CAAGGGAATG CTTCCGTGAA TTTAGGTGGT AGCGTAACAT CTATTCAACC ATTACGTATT
 120
 AATTTAACAA GTAATGAGAA TTTTACAGAT AAAGATTGGC AAATTACAGG TATTCCGCGT
 180
 ACATTACACA TTGAAAACCTC GACAAATAGA ACTAATAATG CTAGAGAACG TAACATTGAA
 240
 CTTGTTGGTA ATTTATTACC AGGGGATTAC TTTGGTACGA TACGTTTTGG ACGTAAAGAA
 300
 CAATTATTTG AAATTCGTGT TANNCCACAT NCACCACAAT TACAACGACA GCTGAGCAAT
 360
 TANGAGGTCA GGAATTACAA AAGTGCCTGT TAATATTTTCG GGAATACCGT TGGATCCATC
 420
 GGCATTGGTT TATTTANTTG CACCAACTAA TCAACTACGA ATGGTGGTAG TGAGGCAGAT
 480
 CAAATACCAT CTGGTTATAC CAT
 503

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1118 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GGCACGAGAC TCAAANCACT GAAGCATTAA CAAAATAATA CTATATTACT GTCTAATCAT
 60
 AGACATGTTG TATTTAACTA ACAGTTCATT AAAGTAGAAT TTATTTCACT TTCAATGAAC
 120
 TGTTTTTTAT TTACGTTTGA CTAATTTACA ACCTTTTCAA TAGTAGTTTT CATGCCACGA
 180
 GCTATCCTAA CCCACAGATT AGTGATTTCT ATACAATTCC TCTTTTGTCT TTACATTTTC
 240
 TTAAATATT TGCGATGTTG AGTATAAATT TTTGTTTTCT TCCTACCTTT TTCGTTATGA
 300
 TTAAAGTTAT AAATATTATT ATGTACAACG ATTCAATCGC TCTATTTTTC AACTTTCAAC
 360
 ATATTATTAA TTCGGAAAGG ACCACTTTAA AATTTAACNG GCCACAACAA ATCAAATCAA
 420
 TTAATCACTT TTTCCAAAAT AATCATATAA GGAGGTTCTT TTCATTATGA ATATCATTGA
 480
 GCAAAAATTT TATGACAGTA AAGCTTTTTT CAATACACAA CAAACTAAAG TTATTAGTTT
 540
 TAGAAAAGAT CAATTAAAGA AGTTAAGCAA AGCTATTAAA TCATACGAGA GCGATATTTT
 600
 AGAAGCACTA TATACAGATT TAGGAAAAAA TAAAGGCACG AAGCTTATGC TACTGAAATT
 660
 GGCATAACTT TGAAAAGTAT CAAAATGCC CGNAAGGAAC TTAAAACTG GACTAAAACA
 720
 AAAAATGTAG ACACACCTTT ATATTTATTT CCAACAAAAA GCTATATCAA AAAAGAACCT
 780
 TATGGAACAG TTTTGATCAT TGCACCATTT AACTATCCTT TTCAACTAGT ATTGGAACCT
 840
 TTAATCGGTG CTATTGCAGC AGGTAATACA GCAATTATTA AACCATCTGA GTTGACACCA

900
AATGTTGCAC GAGTGATTAA ACGATTAATC AATGAAACAT TTGATGCAAA TTACATTGAA
960
GTTATTGAGG GAGGAATTGA AGAAACGCAA ACGTTAATTC ACTTACCTTT TGACTATGTC
1020
TCTTACAGGA GTGAAATTGT AGGCAAATCG TTTATCAAGC TGCAGCGAAA TTTAGTCCTG
1080
TGACATAGAA TGGTGGGGAA ATCTCCAGTC ATCGNGGG
1118

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

CCANTTGCCG TTTCTCCTA AACACCAGCG GNACGAGCTC ATGATGGCAT ACATTGTAAA
60
TCCGATAATT GACAGTCCAG TTGCTAATCC ATCTAAACCA TCTGTTAAAT TTACCGCATT
120
AGAAAAACCT ACTTGCCAAA AAACAATGAA AATAACATAT GCAAATGATA GTGGGATTGC
180
TACATTGCGTA AATGGAATAT GTATGCTCGT AGAAAAATTC ACCAAATGAA ACACATTACT
240
TAAAACAAAG AAAATAATCG CAATACCAAT TTGCGCCAAA AACTTCTGTT TACTTGTTAA
300
ACCTTGTTTA TTCTTTTAA CAACAATAAT ATAATCATCT ATAAAACCAA TTAACCCAAA
360
ACCAATCGGT CACAAATAAT AACAGGTATG ATTGGATTAG CTTGATCTTA CAAATATAAT
420
AGCCACCAA GACGGTTATC ACAAATACTT TAATAGAAAT GGTTAGGCCA CCCATCGTTG
480
GTGTACCAGT CTTCTTCATA TGGCTTTGTG GACCTTCTTC TCGAATACTT TGACCAAATT
540
TCATCCTTTT TAATGTAGGT ATTA AACAG GTACCAAAC AAATGTAATC ACTAGCGCTA
600
ATAACGCATA TACAAAAATC ATA ACTATCT CCTCTTCTTA ATCCAGACTT TTTTAACCAC
660
TAATATATTA TCAAG
675

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 746 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

CTTAGATACA ATTACTCAAT ATGATGTACT GGAAGCANTT ATAGATACTA AAAAACACAT
60

TGNCTGTNCG ATGANTNTCA TCTTCACATG ANNTANCGGG TTGATTAACN AAGATTGCAG
 120
 ACCGTGNTGT TGTGATGANA AATGGTCANC TGATAGAGCA TGGTACACGT GAATCAGTCT
 180
 TGCATCATCC AGAACATGTT TATACGAAGT ATTTATTATC ANCGNAGAAG AAGANTAATG
 240
 ATCATTTTAA ACATGTGATG AGGGGTGATG TACATGANTA AAGTTACAGA TGTTGAAAAA
 300
 TCATATCAAA GCNCACATGT TTTTAAGCGT CGTCGAACAC CTATCGTGAA AGGTGTGTCA
 360
 TTTGAGTGTC CAATCGGTGC GACGATTGCG ATTATCGGAG AAAGTGGTAG CGGTAAATCG
 420
 ACGTTGAGTC GTATGATATT AGGTATTGAG AAACCGGATA AAGGCTGTGT AACCTTAAAT
 480
 GATCTACCGA TGCATAAGAA GAAAGTCAGA CGTCATCAAA TTGGTGCTGT ATTTCAAGAT
 540
 TATACGTCAT CATTACACCC ATTTCAGACT GTTAGAGAAA TCTTATTTGA AGTGATGTGT
 600
 CAATGTGATG GACAACCTAA AGAAGTTATG GAAGTCCAAG CAATTACATT GTTGGAAGAA
 660
 GTCGGTCTAT CTAAGGCATA CATGGATAAA TATCCTAATA TGTTATCAGG TGGAGAAGCG
 720
 CAGCGTGTTG CGATTGCGCT CGTGCC
 746

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 692 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

AATGTCAGAC AGATACTGCC ACAAGATGCG TGCNTATGAG ATTTGCTGT GTATGAATAG
 60
 CGACACGAGC GGCACGAGCG CTCACNTCAT TTCCAATTAA AACTAATGCC TAAATCTGAT
 120
 GCAGTAAAT CTATCATGAT TCACTCTTAA CATCCGTATT TCGTGCTACT AATTGATGTC
 180
 TTGCATTGAA AAATTGACCA TAGCTTAAAT ATGTCGCAAT CAAAGCAGAC ATAATGNTCG
 240
 CAGTTGTATG AATAACACG ACTAACAATT GAAATTTAAT CGCTTGTAAG GGTGGTACGC
 300
 CACCAATAAT TAAGCCTGTC ATCATACCAG GAATCGACAC AAGCCCATAT GTTTTAACCG
 360
 AATCAATTGT TGGCACCTAT AGCTAAACGA ATACTTTCAC GTATTGCACC TTTAGAAGCC
 420
 AATTTAGGTG TAGCTGCAAG TGATAATTTA GATTCAATAT TAGTACCATC TTGTACGAAT
 480
 GCACGATCTA AATTCTGGTA AGCTAAATTA ATTGCAATCA AGCCATTATT TNCAAGCATN
 540
 CCGCCGATAG GTATAACTTC ATTGGCTGTA AAATGAATTG CCCCTGTAGC TACAGTACCT
 600
 GCAAGTGGTA ATGCTGTTCC AATGAAGATN GCTGGAAATG GTNTCCAAAA CACANGGGGC
 660
 ATCACTGTGA TGCTCGACTA ATGGTAAGAG TC
 692

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 857 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

```
AATATAGCGT TTTNACCCCT TTGTGTNACC CTCCCCAAGA GATATAACAT NCCGCCGTNT
60
AAAATCAATT AGAAATATCT TTTTATTCTG ATAATAGACA CAGTATAGAC ACATTTTAAT
120
GGGTGATACC ACTTGTAATA TCACGGGGTT GTNATGTNTT GNATATCANT NAAATACTTA
180
TATANAAATA TTGCTCGGAA TATAAAAAGN TAAATAGGNT TTTGAGTTTT AAATATGAAA
240
TACAAAGCGC CCANTCGAAC AAAGTATTTA TATTAAAATA TGGAAAATCC ATCANTATTA
300
AATTAAAATN GTTTTATTAT GATAAAGTGA AAGTAGGTAA GTCTATGGAA GGTCTTAATC
360
ATCGAAGAAA TACAGAAAAA GAAGAGACAA CACAAACGCA ATCAGTTGCA CCTAATACAG
420
GTGAAGAGGG GATGTCATCA GGCAAGTAAC ACAATCAANT AAGACGTCCG ACATACATAA
480
ATGAATCTAT CAATAAACAA ATGGAAGCCA AAGCGCATGA AACAGCGCAA AATGCAGATT
540
TAAAAACCGA AGCAAGAAGT TTATTTGATA ATGCAACCAA ATCAATCGGG AGACTAGCCG
600
GCAATGATGA AAGCATAAAT CTTAATTTAA AAGATATGTT TTCTGAAGTA TTTAAGCCGC
660
ATACTAAAAA CGAAGCAGAT GAAATATTTA TAGCGGGTAC TGCTAAAAC TACGCCAGCAA
720
TTTGTGACAT ATCAGAAGAA TGGGGGAAGC CATGGCTCTT TTCTCGAGTA TTCATCGCTT
780
TCACAGTAAC ATTTATTGGA TTATGGGTCA TGGCAGCGAT TTTTAATAAC AATGACGCTT
840
GTACCGGTGC TCGTGCC
857
```

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 907 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

```
CTCACTTTGT TTTCCAGTAT GGAACGCTTG CCCTAAGTCC TTAATTGCAT TATAAAATTC
60
AGGCGCTAAA ATAATCGCAA TTGCCGAGT TTTAAATCA ATATTATGAA ATACTACTAA
120
GCTTAGCGTT GCTTCCAATG CAACCAATCC AATACCTAAC ATACTTATAA ATTCGAGCAT
```

180
 TAATCCCGAT AAAAAAGCAC TCGTAAAAAT GCGCATTGTT AAAGTTCTAA ACTGAGTACT
 240
 ATCGTCGTAA ATATGCTTCT CTGTTTGCTC TGTACGATTA AATAGCTTTA ACGTCACTAA
 300
 ACCTNTAGCA ATATTTAAAA ACCGNCGACT AAATTGATTC ANATAAGTCA TTTGATCTTT
 360
 TTGACGCATC GAGCGTTTTT AAACCGAAAA TAATATAAAA CAAAGGAATA AATGGTGCAG
 420
 NTATTAACAT AATTAATGCG GNATTGAAAT GGATGAAAAA CAATGCAATG ATTATGATGA
 480
 GCNGAACCAT CAATCGATTT GAACAACCTG AGGCAAATAA CTCTTATAAA AAGGTGCTAA
 540
 ACCATCAATG TTTTCTGTGA GTATAGTCAT TTGTTACCG ATTGGATGAC CATTATTTTT
 600
 ATAAATAACC CGCTGTCTAA GCATATGCTT AACTTTAAAT GCTAATGTAT CACCTAACCA
 660
 TTGATTTAGA AATTGCACAG NTGCTCTTAA AAGTAAAACA CCTAATAAAA TAAATAATAC
 720
 AATCCATAAA CCTTGAAATT GATGTCTTAT AATTTTAGCT AAAAAATCTG CTATTAAAAT
 780
 ATTGTGCGTT ATAACGAGTA TGCCCGAGAC CAGTACTGAC CAAGAACATG AGTACCGGAA
 840
 AAATTTTATA TTGAAACAGT ATTGTTGTTA ATTTTTCACA ATTATATCAC CTAACCTATA
 900
 TAAAGTT
 907

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

AATTTTAAAG ACCCCNCGCA TAAATANCCA TCCCACCTAC TTATCCAAAA GTTANGTGGA
 60
 TGGTTTTTCA ATTAAAATTA ATATTAGTGT AANCCAATCA AAGATTTAAT CNAATATGCC
 120
 CCTGCTCAA ACATTTCTC ATTTAATTTG CTTTACTTTC AATTTAATAT CATTATCCAC
 180
 AACACTTGGC GTGTCATCGT TATTATTTTCG CATCTTTGAC ACGTTTATCA TCATTAGGAN
 240
 TCGGCACCGA ATAAAATTGC GATAAATGCC ATGATTCCCA TTAATACGTT AACCCAAAGT
 300
 GCAATCATCG CACCTGTATG AATGCTCGTT GCAGCAACTG CACCAACATA TACAGCACCA
 360
 CTAATTGCGA CACCGAATGC GCCACCAAGT GATGAAGCCA TTTTATAAAT ACCTGAAGCA
 420
 ACGCCAACTT TATCTAACGG TGCATTGCGA ATAGCTGTAT CTGTAGAAGG TGTTGCATAA
 480
 ATACCTAAGC CTAGTCCGAA ACATAAATAT CCTACGACAC AACTGATAAC ATAAAATATG
 540
 CCTGGTAAGA ATACTANTGA AATAAGTGCA ATNCCAATGA CCACAATGNA TGTACCTNAT
 600
 AACATTGGTC GCTTAGAACC CANTTNTGGT NATAATAATT TTTCACCAAC TCGAATCATC

660
AATAACAACA TGATTAAATA AGTAANTGAT NAGTATCCTG CCTGCCATNC TGTATAACCT
720
AAACCTTGTT GCACGCATGT ATTCGCTACA ATTNATGTAC CTACAACNCC GTTG
774

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CTCTGATTCA ACAAATGAT TATTCTTTAC GTAAACTACC TTTTTTTATT TGAGATGAAG
60
CATATGCTTT TAATAATATT GTCCCAATAA TACCAACTGA AATAATATTT AATACTGCAG
120
AGATAACACC TTGTGTATAA ACCTTGTTAG CCGGTTTCGTT ATAAATCAAA ATATCTAATG
180
TTGGTGCAAT AAGTGCCCAG CAAATAATAT TCGCAATAAT TTGACCGATA TTAAATAAAA
240
TCATCGATTT CCTAGAAAAT AGGCATGAAG AAAGATTTAA TTTTAGGGCC AATCCATCCA
300
TATTAAACAG GCGATAATTC CTGAACAAAT AACCCAACTC CACCAAGCAC TACCCGTATG
360
TCGGGGAAAT CTTTAATAGC GTGNCCAACT AATCCAGGCA TTAAACCAGC AAAAGGCCCA
420
AATATTGCAG ATATTAATGC TAAAAATGCA TAAGATGTTT CTATATTCGT ATTAGGAAAA
480
CCTGTTGGTA TTACAACAAA ACGCCCTAAA ATCACAATA CCGCNGCTCC TATACCAATC
540
GCAACAACAG TTTTAACTGA AATATCNTGT TTTTTCATCT TCATTACTCC TTACATAAAA
600
AATTCATTAA ATTGATGGTG CTTTAGATAA ATGAATCGTC CAATCATTTT CAGTACCAAT
660
ATGATATAAA TCTGAAAATG AGTCTCGATT GACTGCTACA CCAATATTTA CTAGCGAGTT
720
AACATACACA AGAGGTTTAC CCACATTAAC ATCTGCAAAC GATCGCTCGT GCC
773

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 676 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CATAAGACAT GTAAATTCTA AGATGATTTG TTGGATAGGG TAGCTCCATA TAATTCTTGA
60
ATCCNATCAT TATTACATTA ATAAAAAAA CACCCACAAT TGTGGGTGAT TGTAATGAAC
120

GTATTATCTT GGCACGAGTA CTCAACGATT AATTGTTTCGT TAATTTTCAGC AGGTAATTTCG
 180
 CTACGTTCTG GTAAACGTAC GAAAGTACCA GTTAAGCTGT CAGCATCAAA GTTTAAGTAC
 240
 TCAGGTACGA AATTGTTGAT TTCAACTGAT TCAACGATGA TGTTTAGTTT TTGAGATTTT
 300
 TCACGAACTG AAATTGTTTG ACCAGGTTTA ACAGAATAAG ATGGAATATC AACACGTTTA
 360
 CCATCTACTA AGATATGACC GTGGTTAACT AATTGACGTG CTTGACGACG AGTACGAGCT
 420
 AAACCTAATG AATAACAAC AGCGTCTAAA CGACTTGCTA ATAAAATCAT GAAGTTTTCA
 480
 CCCGCGTACA CCCNAATTTT TTACCAGCGA TGTCAAATGT GTTACGGAAT TGTCTTTCAG
 540
 TCAATCCATA TTANGTAACG TAATTTTTGT TTTTCACGTA ATTGTAAACC ATATTCTGAT
 600
 AATTTTTTAC GTTGGTTTGG ACCATGTTGT CCTGGTGCGT AAGGACGTTT TTCTAATTCT
 660
 TTACCAGTCT CGTGCC
 676

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GGCACGAGCG ATGATGGCTG TCGGAACAGG TGCATTTGGT GCGCATGGTT TACAAGGGAA
 60
 AAATAAGTGA TCACTATTTA TCAGTATGGG AAAAAGCAAC GACGTATCAA ATGTACCATG
 120
 GCTTAGCATT ATTAATTATA GGTGTAATTA GTGGTACAAC TTCAATCAAT GTTAACTGGG
 180
 CTGGCTGGTT AATATTTGCT GGTATTATTT TCTTTAGTGG ATCATTATAT ATTTTAGTAT
 240
 TAACTCAAAT TAAAGTTTTA GGTGCGATTA CGCCAATTGG TGGCGTATTG TTCATCATTG
 300
 GCTGGATAAT GTTAATCATT GCGACATTCA AATTTGCTGG TTAAATTTTA AACTTTTAGA
 360
 TTACCTATGT AACTAAACAT TAAATTTTAA ANAAAAA
 397

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 739 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

TATCTTTAAG AACAATTGAA GCCGCTAACC ATCGGAGAAA GCTGTAAAT CCAAGTGTG

60
 GCCTGCTAAA TACCCACAAT CATCACGGGT CGTTGCCTTG TACCACAATA GAAGGCAGCA
 120
 TTATCACCCA AATATTTGCA TAGCTAATTG TGATAAAACT GTCGTTTCCG TTTGTGGCAT
 180
 AATTCCATAA ACATATGCTA AACCACCGAT ACCAACTAAT AAAAACGCTA AAATTGAACC
 240
 CATAGCAATT AACGTTTTTA CAGCATTATT AGCACTTGGT TCTCTAAAAA TTGGTGACCG
 300
 CATTTGAAAT AGCTTCAACA CCTGTTAATG ATGAAGCCCC TGATGAAAAA GCTCTTAATA
 360
 GCAAGAATAA TGTTACTCCA GGANCCGCAG TTCCTACTGA TGCATGCATA TGTGGTTGAA
 420
 TATCTCCTGT CGCCACACGG AAAGTACCCT ATAAATATTA ATATCACTAA CCCATAATG
 480
 ANAAGATATA CTGGATAGGA TAATACGGTG NCAGATTCAG TTAAACCCAC GTAAATTTAA
 540
 TATTAAAATA AAAAGTACAA GTAAACATGC AATCAGTACT TTATGCCCAT ATAACTTGG
 600
 GAATGCAGCA ACANATGCAT CAGCACCAGA TGATATACTA ACAGCGACAG TCAGTATGTA
 660
 ATCGACTAAT AATGAGCCTC CTGCAAGCAA TCCCCATTTT TCTCCTAAAT TGGTCTTGGA
 720
 CACCATATAC GCTCGTGCC
 739

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GGCACGAGCG AGAACGATTG AAGCTACAAT ACCTGATGTT GCTGCGGGAA GTACGACTTT
 60
 AGTTGCTACT TCTAATTTAG TTGCTCCAAG TCCATAGGCA CCTTCTCGAA TTTTATTTGG
 120
 TACAGATGCC ATTGCATCCT CACTCAAACT TGTGATGAGA GGGACAATCA TAATACCGAC
 180
 AACTAAGCCG GGAATTATAG CATTAAACTC TCCAAGACCT GATATGAAAG ATCTTAATAC
 240
 TGGTGTAACA AAGGTTAATG CAAAGAAACC AAACACAATT GTTGGTATTC CTGCTAAAAAT
 300
 TTCTAATATC GGTTTAATTA TGCGTCGGGC ACGGGCACTT GCATATTCAC TTAAATAAAT
 360
 TGCTGCACCA AGCCCGACTG GAACTGCAAA TATAGTCGCA ATAACTGTGA TTTTAAAGT
 420
 CCCTATTATC AATGCCAGAT ACCAACTTA GGGTCTGAAC CGGTAGGATT CCAGTAGTAG
 480
 AAATAGAAAT CAGTATTGGA ATTCTGG
 507

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GAATAGTCTA CTCATTCATC GTCCTTCACC ATTGATGGAT CCAGAACAAG TTGCTGATGC
60
ATTAATAAAA CTTGTAAAC AAGGTAAGTT GAAGTCATTC GGGGTGTCGA ATTTTAATCA
120
TTCACAATAC CAATTGTAA ATCAATATAT TATGAAAGAA AGACTACATA TTAGCATCAA
180
TCAATTAGAA TTATCGCCAT ATCACGTTGA TAGTTTACAA GATGGAACAA TGGATTCAAT
240
GTATCAAAAC CATGTTCAAA TTATGGCTTG GAGTCCTTTT GCAGGCGGTA AAATTTTCGA
300
CAAGGAAGAT ATTAAAGCGC AACGTATTAT GAAAGTTGTC AATCAATAGC TGACAAATAT
360
GGTGTGAGTG ACACAGCTGT GATGATAGCA TGGTTAGTAA AAATACCGCA TAGTACCATG
420
CCGATACTGG GAACAAGTCA GTTAAAGCGT ATNGATCAAG CAATCGAAGG GCTACAACCT
480
AATTTAGATG ATCAAGTCGT GGGTTGACAT TTACAACGCT ATTATCGGAC AAGATATCCC
540
GTAAACTTAN NNACNENNA ATCATAAATG GAGCATACCA TGACAAACGA AGATAAACGT
600
TTCGAACAAT TAAGATTTGA ACGCAAATTT ATAGTTATCC CGTATTTAAT TTATGCAGTC
660
ATTGTATTAC TATTAAATAT TTTCTATTCT GATTTGAAAA TAACAATGAC ATTATTCGGA
720
CTTTTCTTTG CGTATAATGT AGTCATTTTG TTC
753

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 542 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

CCCATTATTA TTTNGAAAAT GAATTGGAAA ATACAGTAGA CGAAGTGTGG GTTGTATACA
60
CTTCTGAAAG TATACAAATG GATCGTTTAA TGCAACGTAA TAATCTGNCA TTAGAAGATG
120
CGAAAGCACG TGTCTACATA CATCAACGCG TACGTAAAGT AATGACTTAT TTATAGTGTA
180
ATATTAATCT TCTTCTCCGN AATTCGGNTT TNCAATATAA CCTTCTTCTT CTAACAANCT
240
CTCAAGGTTG TGNGTNAATN CAAGTTTATC CCCTAAATTA TCGATAACAT GATCGGCCAN
300
TCGGNTNNNN NNATCAATAG AAATTTGGNT TATAGACACG TGCTTTCGCA TCTTCTAATG
360
ACAGATCATN ACGTNGCATT AAACGATCCA TTTGTATACT TTCAGAAGTG TATACAACCC
420

ACACTTCGTC TACTGTATTT TCCAATTCAT TTTCAAATAA TAATGGAATA TCCACGAACC
480
ACATTATATC CTTGGTTTTA AATATTCTTG CTTTTCTTCT GCCATAATAT CTCGCACGAA
540
TA
542

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 731 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

TCAATCCANC CTCCAATTGC TGATGAAGAA CCTCCTTCAG CNCCCACCCA TTANNGGGGC
60
CANAGTCATA AGTAACAACT TTTGAACCAA TTGTATCTTC AATTGAATCT GTAATCTTAT
120
CTCCCGCTTC TTCCCATCCT AAATGTTCTA ACATTAATAC AGAACTTAAA ATTACTGAAG
180
NTGGATTAC TTTATTTAAA CCTGCATATT TTGGANCTGA GACCATGTGT TGCTTCAAAA
240
ATAGCATGAC CTGTTTCATA ATTAATGTTT GCACCTGGCG CAATACCAAT NCCACCAACT
300
TGTGCAGCTA AAGCATCTGA AATATAGTCA CCATTCAAGT TCATAGTTGC TACAACATCA
360
TGCTCAGCTG GACGAGTTAA AATTTGTTGT AAGAAAATGT CAGCAATAGA ATCTTTAATG
420
ATAATCTTGC CTTCTTTCAC AGCTTTTTCT TGAGCAGCAT TAGCAGCATC TCTGCCTTCA
480
TTTACAACAA TTTGCACATA TTGTTGCCAA GTGAATACTT GCATCACCAA ATTCAGATAA
540
TGCTAAATCG TAACCCCACT GCTTAAATGA GCCTTCTGTA AATTTCATAA TATTACCTTT
600
ATGAACTTAA AGTAACTTGA TTTACGGGTT ATTTATCGAT AGCATATTGG TATAGCTGCT
660
CTACTAATCG CTCAAGTCCT TCTTTTAGAA CTTGGTTTAA TACCAATACC TGAAGGTTCT
720
TGGAATCGAT T
731

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

TTTGACATCT CTCAAAAATT AAAGCATAAA GGTTCATCGG AAAGGCGCAA AATTCACAGT
60
TGTTTGTTGG TTTGTTATTT CCCTCNCAAT ATTCAGTATT AGACATTTAT AGTTTGAAA

120
 ATGCGTGATA ATTAGTTGTA TTCAGTTATT AAGTAATAAA TTTTGGAGG CAGAACATCA
 180
 TGAAATTAAC ATTAATGAAA TTTTGTGG GGGGATTGTC AGTATTATTA AGTTATATTG
 240
 TATCTGATAA CAATAACCTT GGGAAAGAAT TTGGCGGTAT ATTTGCAACG TTTCCGGGCA
 300
 GTATTTT TAG TGTCTATGTT TATTACAGGT ATGCAATATG GTGATAAAGT CGCTGTGCAT
 360
 GTAAGTCGTG GCGCAGTGTT TGGTATGACA GGGGTATTAG TTGTATTTTA GTAACATGGA
 420
 TGATGTTACA TATGACGCAC ATGTGGTTGA TTAGCATTAT TGTTGGTTTC CTAAGCTGGT
 480
 TCATCAGTGC AGTATGTATT TTTGAAGCGG TAGAATTTAT AGCACAAAAA AGATTAGAAA
 540
 AGCATAGTTG GAAAGCTGGA AAATCGAATA GTAAATAGTG TGAACGTAAT CTCTTAACTA
 600
 GGACTAACTT TGCAAGCATT GAATAGCATG GAAAAGTTGC ATCATTAAATA AGTGAAATTC
 660
 AAGTTGGCAT TGAGAAAATT ACAAGCGCTC GTGCC
 695

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 612 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

GGCACGAGCT CGGCTTGACG GTAGGAAATA TCAGCACGAG CTTGATTCAA CANCCGAATC
 60
 AGGGAGGAAA TGCAGGTATA ACTCAATCTA AGTTCGCTAA GAGACATCCA ACGTTTTACN
 120
 AGGCAAATCC AAGCNAAAAG GATTGCTTCN AATAATATCC CACCAAACAA TTTAAGACAT
 180
 TATGCTGTTA AGAGGTCACC AACNATATAT ATAGTGGTTA CGGATCAGTT ATTAGCGTTC
 240
 TTTAACAACA GATATTGGCG CTCACAGTTT AACCCAAGAG GTGGTTGGTC TCCAAGTGGT
 300
 CCAAGAAGAT ATGCGAATGG TGGTTTGATT ACAAAGCATC AACTTNCTGA AGTGGGTGAA
 360
 GGAGATAAAC AGGAGATGGT TATCCCTTTA ACTAGACGTA AACGAGCAAT TCAATTAACT
 420
 GAACAGGTTA TGCGCATCAT CGGTATGGAT GGCAANCCAA ATAACATCAC TGTAATAAAT
 480
 GATACTTCTA CAGTTGAAAA ATTGTTTGAA ACAAATTGTT ATGTTAAGTG ATAAAGGAAA
 540
 TAAATTAACC GATGCGTTGA TCAAAGTGT CTTCTCAGGA TAATACTTAG TTCTATGATG
 600
 CACTTAGAAG TT
 612

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

```
GGCACGAGCG ACTTTTTCTA GGCATAATCG AATTGACAAT GGTACTCAAG CTTAAAAATG
60
GCCCCACTTAA TTCAGGCAAT AACAGACTAG GCATAACATT ATTTTTCATC AATTTAAATG
120
TGTA AACAT CGATGACATT GTCTGTTGCT GTTGTCGATA AACATTCATA TCGTAGCGGT
180
CTGCAAATTC TTTAATGCGA TATGCCGGCG GCACGAGACA TGACAGGTAA TGAATCATGT
240
TTGAATTGTT CGTCTACGGC ATCTTTTGA ATAGGTAATC CAAAGAAACC TGCAATACCA
300
ATCGTTTCAA AGGGCCCTGC TGCTTCGATA TGTCTACGAA ATGGTTCTGA ACGAACATCT
360
ATACAAAATG CAATTTGCGC TTTCGTTGAT GTGCCACCT GATTTAGCTC GCTATTATTT
420
TCATCAACTG CTTGTGTGTC AATTAACAAT ACTGAATGTG GCTGATTAGC GTTATCATTT
480
TCTGAGACAT TTA CTGTT TACATCTAAT GCGCCCGCCA CACTTTCATG ACTGCTTTAA
540
TTTTTGT TTTT AACTGAGATC GTATGTCAAT TTCCAGGCA ATTAGCCATA AATTNTAAA
600
TACAT
605
```

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 508 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

```
GGCACGAGCT GATCAAGGGT GTAAGTTGGT AGTGGTCAAT AAAGAACAAT CATTACCAGC
60
TAACGTAACA CAAGTGGTTG TGCCGGACAC ATTAAGGAGT AGCTAGTATT TCTAGCAACA
120
ACAACATTAT ATGGATTATC CGGAGTCATC AGTTAGTGAC ATTTGGTGTA ACGGGTACAA
180
ATGGTAAAC TTCTATTGCG ACGGATGATT CATTTAATTC AANGAAAGTT ACAAAAAAAT
240
AGTGCATATT TAGGA ACTAA TGGTTTCCAA ATTAATGAAA CAAAGACAAA AGGTGCAAAT
300
ACGACACCAG AAAACAGTTT CTTTAACTAA GAAAATTAAA GAAGCAGTTG ATGCAGGCGC
360
TGAATCTATG ACATTAGAAG TATCAAGCCA TGGCTTAGTA TTAGGACGAC TGCGAGGCGT
420
TGAATTTGAC GTTGCAATAT TTTCAAATTT AACACAAGAC CATTTAGATT TTCATGGCAC
480
AATGGAAGCA TACGGACACG CTCGTGCC
508
```

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GGCNCGAGAC TGTCGAATAT TTAGTAGTAA CTTCAGATTA CAAGCGTATG ACTTATCGAC
60
CGAACGGTAC AAATAAAGTA TTTGTTAAAA GAAAAGAAGC GGGNTCATGG TCTGAGTGGT
120
CAGAATTAGC TATTAATGAT TACAATACAC CTTGTGAAAC TGNTCAAAGT GCCCANTCAA
180
AAGCTAATAT GGCCGAAAGT AACGCTAAAT TATACGCAGA TGACAAGTTT AATAAAAAGGC
240
ATTCGAGTTA TTTGTGGATG GAACAGCAAA TGGTGTGGGC TCTACATTGN ACTTAAATGA
300
GAGTTTAGAC CAATTTATTT TATTAATTTT TTATGGGACT TTTCCAGGTG GTGACTTTAC
360
AGAGTTTGGC AGTCCTTTTG GAGGAGGAAA GATTTCATTG AATCCCTCAA ATCTTCCAGA
420
TGGTGATGGA AATGGTGGAG GTGTTTATGA GTTTGGATTA ACTAAATCTA GTCGTACATC
480
TTTAACTATA TCAAACGATG TCTATTTCTGA CTTAGGAAGT CAAAGAGGCT CTGGTGCGAA
540
CGCAAATAGA GGGACAATTA ACAAATTAT AGGAGTGAGA AAATAATGCA AATATTAGTT
600
AACAAGCGTA ATGAGATAAT TTCATACGCT ATCATTGGTG GCTTTGAAGA AGTATGATAT
660
TGAAATTACA GAAATTCTCT CAAGTTTGTAG ACTAAGCTTT AAATATCAAT GGGGAATAGTT
720
TTACGAAGAT ATCCGAGAAA AGATGACTGC
750

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

AAATGCCGGG GGAGCTCAAG TATATGACTG AAATAACATT CAAAGGTGGA CCAATCCACT
60
AAAAAGGTCA ACAAATTAAT GAAGGTGATT TTGCACCTGA TTTTACAGTG TTAGATAATG
120
ACTTAAATCA AGTAACATTA GCAGATTATG CTGGTAAAAA GAAATTAATT AGTGTGGTAC
180
CATCAATTGA TACAGGTGTT TGTGATCAGC AGACTCGCAA ATTCAACTCT GAAGCTTCTA
240
AAGAAGAGGG GATTGTGCTT ACAATTTTCTAG CAGACTTACC ATTGCGACAA AAAAGATGGT

300
 GCGCTTCAGC AGGTTTAGAC AATGTCATTA CATTAAGTGA CCACCGTGAC TTATCATTTG
 360
 GTGAAACTA TGGCGTTGTT ATGGAACGAA CTTCGTGCCG AATTCGGCAC GAGCTCGTGC
 420
 AGTATTTGTA TTAGATGTAG ATAATAAAGT TGTTTATAAA GAAATCGTTA GTGAAGGTAC
 480
 TCGATGCCCC AGATTTTGAT GCTGCTTTAG CTGCATACAA AAATATTTAA TCATTAAAGA
 540
 GATAAATCTT AAAATGTATA CATCGTGTCC ATCGTTGTCA ACAGCATTAA AATAGAATTG
 600
 TTTTCTATGA TTGCTAAGAC CTATGGGCAC TTTTATTGG AGAGGGACGA ATATGGCAGA
 660
 ACAACAAACA ATTATGGAAC GCTTGTTTCA TACATTAGAT GAAAAAGCTA AAACATTAAA
 720
 TAATGAAAAT GGCCAAAGTT TTATTGAAAA TCTTGGGCTA GCAATGGAAC AAGTATATAC
 780
 CAATGAA
 787

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GGCACGAGCG CGTCATATAA TGAAAGTAAT GATAAAAAGA AAGGATAACT TAATGTGAGT
 60
 CAAGAACGTT ATTCAAGGCA AATTTTATTT AAACAAATAG GTGAAATAGG TCAAAGCAAA
 120
 ATAAATCAAA AATGTGCGTT GATTATTGGT ATGGGCGCAT TAGGTACACA TGTGGCCGAA
 180
 GGACTTGTTA GAGCAGGCAT TGCTAAACTA ATCATTGTTG ATAGAGATTA TATTGAATTT
 240
 AGTAATTTAC AAAGACAAAC ATTGTTTACT GAAGAAGATG CTTTGAAAAT GATGCCTAAA
 300
 GTGGTTGCAG CTAAAAGCA TTTGCTAGCG TTACGTAGTG ATGTTGATAT TGATGGTTGT
 360
 ATTGCCCATG TGGATTATTA TTTTTTGGGA AACACATGGA CAGGACGTTG GACGTTATTA
 420
 TTGATGCAAC CGATAACTTT GAAACACGAC AACTGATTAA TGATTTTGCA TATAAACATC
 480
 GTATTACCTG GATTTATGGC GGGCGTTGGT CAGAGTACAT ATTCAGGAAG CTGCATTTAT
 540
 ACCTGGNAAA CACCTGCTTT ACTGTTGG
 568

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

```
CTACNNTAAT AAGAAAATAT AACATACNAA TCAAAAACTA AAGGGATGTG ACGTTAATGA
60
AACTCGTATT TGTGGCACGA GCTGGTAATA TGGCACAAGC TATATTTACA GGAATTATTA
120
ACTCAAGCAA CTTAGATGCC AATGATATAT ATTTAACAAA TAAATCTAAT GAACAAGCTT
180
TAAAAGCATT CGCTGAAAAA CTAGGTGTTA ACTATAGTTA TGATGATGCG ACATTATTAA
240
AAGATGCAGA TTATGTTTTT TTAGGTACCA AACCGCATGA CTTTGATGCT CTAGCAACAC
300
GCATCAAACC ACATATCACA AAAGACANTT GCTTCATGTC AATTATGGCA GGTATTCCGA
360
CTGATTATAT TAANCAACAA TTAGAATGCC AAAATCCAGN TGCTAGAATT ATGCCANACA
420
CAANTGCGCA NGTTGGACAC TCAGTTACTG GCATTAGTTT TTCAAACAAC TTTGAACCCT
480
AAATCCTAAA GATTAAATTA ACGATTTAGT TAAAGCATTT GGTCTGTATT GAAGTATCCA
540
GAGATCATTT TACATCCAGT TACAGCTATC ACC
573
```

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

```
CTCTATTATA AACATATTAA AACGCATTTT TCATGCCTAA TTTATCTAAA TATGCATTTT
60
GTAATTTTTG AATATCACCT GCACCCATAA ATAAAAACAAC AGCATTATCA AATTGTTCTA
120
ATACATTAAT AAGAATCTTC ATTAATGAAC GATGCACCTC CAATTTTATC AATTAAATCT
180
TGTATCGTTA ATGCGCCAGA ATTTTCTCTA ATTGAGCCAA AAATTTTACA TAAGAATACA
240
CGATCTGCTT TACATAAACT TTCTGCAAAT TCATTTAAAA ATGCTTGTGT TCTAGAGAAA
300
GTGTGTGGTT GAAATACTGC AACAACTTCT TTATGTGGAT ATTTCTTTTCG TGCTGTGTCA
360
ATTGTAGCAC TAATTTCTCT TGGATGGTGT GCATAATCAT CTACAATAAC TTGATTTGCA
420
ATTGTAGTTT CATTGAAACG ACGTTTAACA CCACCAAACG TTTCTAATGC TTCTTTAATA
480
TTTGTAACAT CTAGCTTCTC TAAATAACTA ATCGCAATTA CAGCTAATGC ATTTAAAACT
540
GTATGGTCAC CATATTGTGG AGACAGGAAG TGATCATAAA ACTCACCATC CACATACACA
600
TCAAAAGCAG TCTCGTGCC
619
```

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

```
GGCACGAGCG TGTCAATATT TACATGATGA TTTCATTTAA TAGCCTTTTT TAGCATCAAC
60
TTCATTCTCA ATTAGACCAT TCTTATTGAG AAAATTAACT AGATTGTTTT TAAAAATATC
120
TAATAAGTCA TACTTTGCCT CATAATCATT ACCAGTTATA TGCGCTGTTA TAGTTACATT
180
TTCCAATTCA TATAATTCAT GATTAGGTTT CAAAGGTTCA TTTTCAAACA CATCTAAATA
240
TGCATGTCGA ATAACCTTAC TTTTAAATAC TTCTATTAAG AGCGCTTCCT TTAACATATGC
300
TACCTCGTCC TATATTTATA AAAAGTGCTT CCATCCTTTC ATTAATTCCA AAATGTTTTT
360
TTCCTTTAGT TAAATGAATC CGTTTCCTTG CGTTTCCTGG TAAAGCATTT ATAATAATGT
420
CAGCATTTGG TAATGTGCTT TCA
443
```

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

```
GGCACGAGCT ATGTGGTTTG AAGTCAATCG CCAAATGTTC CACCTACCAT TCTGATAAAA
60
GTATTTACTT GTTCTTTATT CCATAACACA TATACTTTAT GATCTCTATT TTCAAATTGT
120
CTATGCACAT ATTTTTGTAA AGGATGCAAC TTTCCTTTTT CTTGCTTCAT TTCTACAAAA
180
TATGTTTTTC CTTCTGGCAT AATAATAATT CTATCTGGCA CACCTCTTGT TCCAGGTGCG
240
ACCCATTTTA AACATAAACC GTTTAGCTTT GTTATCTCTT TCACTAAATA TTTTCTAAT
300
GTCGATTCCCT TTCATTTATT CACCTTGAT ACAAATTTA TATTTGTGTT CCGAATGTTT
360
GTTATCAATT CCTTGCCAAA CTTTTTAAAA ATAGCTGTTT AGAGGGTTTA CCCCTATACC
420
CCCTTTACTC CCCTAAACAC TACTTTTTTA AACTTTATAG TGAATTTGAA TGCAACATTG
480
GGAAACAAAC AGGTTTGAAC CCCTACAGCT AGAAAGAAGA GTGTTTGTA TCATTGTTGC
540
ATCATGTTGC ATCACC AAAA TGATACAAC
569
```

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

GGCACGAGCG CAAAATATTT CAAATAAAAA TGATTGTAAA AAGGCAAAAT ACAAATTTTC
60
ACTTAACAAC TAGTACATAA AGTAATACAA TTAAATTAAT TCTATCTGAA AGATGTGTGG
120
GGCATCGTTA TTTTAGGTGG ATATGAGCAA TTTATTAAAA GTCATTTACG GAAAATATAT
180
ATAGACGGGG TGAGTAATAT GCAAGAACAT GTGGTGGTTA CACTTGATGG AAAAGATTAT
240
CTTGTAGAAC CAGGTACGAA TTTACTTGAA TTTATTAAAT CACAAGATAC TTTTGTCCCT
300
TCAATTTGTT ATAACGAGTC GATGGGCCCA ATTCAAACAT GTGATACATG TACTGTTGAG
360
ATTGACGGTA AAATTGAACG CTCATGTAGT ACGGTGATTG ATCGCCCAAT GACTGTAAAT
420
ACTGTGAACA ATGATGTGAA AGATGCTCAA AAAGAGCCTT GATCCGAATT TTAGAAAAGC
480
ATATGCTGTA TTGGACAGTA TGTGATTATT A
511

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

ATCCTTTATT TNTAAGGCGT TTCATCAAGC TAACACTTCA TTATCTTTAG TCGCTTTAAT
60
GCCCTTCTAT TAAACTCGGA ACTAAAAATG GATTGNCTTT TCAACCACCC GANCACTAAA
120
ACATTGTCNT TTTTGATGGC CNATTAAGAC ACAATTTCCC GCTGTTTGCT TCAAAGTAGC
180
TTGCTTCTTG NATTNATTTT CAATATCTTT CTTGTTAAAA ACAAGANTGT TGCACAGTTT
240
GATTGGCATC TTTATTTAGA NCAATGGCAT CTGCTTGCCA CTTATCAATG CCTTCTTTAT
300
TCATATTGAT AAGACCATTG GCCAATCCAG ATAATAAAAA TAGCAAGTAA CTAATCATCG
360
TTAACACACC AATAATTAGT CCAAACCTCA ATTTGTTGCG CCGTATTTCA TTCCAAGCTA
420
AAAACATGCA TTTCTCTCCC TACTACTATG ATTTAAACAT TGTTTATATT CTTAGATGCA
480
CGTACGTCGT GTTGCGCTCT GTAATGTTAT ACATACACTT ATCCTTCATT ATACCCGANC
540

TTTTATATT AAAACCAAAT TTATGGAAAA TGCAANNANT TGTCTATTAT TTTTGTGCGG
 600
 TACATTTAAA ATTAAGGATC AATTTAAAAA CGCCTACATA TACCTTTAAG TACATGAAGA
 660
 CGTCCAATTC ATATATTATT TAACTTCGCC TGTTTTAGGA TCGGATTGCT TAATAGCATT
 720
 TTTACGTAAT TTATCTTTTG CTTTGTCACT TGCTTTATAG TTATTGTTGT AAATCGTAGC
 780
 TTCCCAACTA CCATACATTG GGTTAGGGAA AATGATATAT TTCTTACCGA AATCGTCTTT
 840
 ATGTTTTTCA ATTAATGCTT CACGAGATTC AGCTGTAGCT TCTTTTGGAT CTGTAAAGTC
 900
 TAATAAATTA TCTCCAAATA GCATGACAAG TTTATGATCC TTTTGAACCA TTTGTCTGCG
 960
 TGATTCTTTA CTCTTATCAT CTTTACCTTT TAGTAAAATA TGACTCTTCT TAGCTTGAGG
 1020
 GATACCTTGT TGTTTTAAGT TCTTTTGTGT TGCCTTTAAA TCTTTTCTT TATCTCTATC
 1080
 AGAAATATAG TAGATATCGA CACCTTTTTT GTCAGCATAT TTCAA
 1125

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

AGAAGCATAT AAACAAAACA TGTTTCGATT ATTAGGTAAA ACTGGTTTTG AAGACTTGAA
 60
 AAAAGAATTA GAAGAGCGTT TATAAAATAC ATTACTTCAA TGATTAGTGA AGTTTGAAAA
 120
 GATAGAACTA GACGTTAAC TTTTAAAGCA TATTTTCGAG GTTGTCATTA CAAATGTAAA
 180
 AATGTAATGA CAACCTCGTT TTTATTTATA TGCAAGAACT AGGTACTAG CTAATGTGAC
 240
 AAGATGTAA GAGAAAATTA AAGAAAAAAT AACATCTGTC ATACAATAAT ATTGTTATAC
 300
 TACTAGAGAC TGATTTATTA GCATGATTAC ATGTTAATGT TTCTTTACTT AGTAATTAAC
 360
 TTTATAATGT AAGAATAATT ATCTTCAACC AAAGAAAGGG ATTGATGATT TGTCGTTTCA
 420
 TCAAGTAGAA GAATGGTTTG AGATATTTTCG ACAGTTTGGT TATTTACCTG GATTTATATT
 480
 GTTATATATT AGAGCGATAA TTCCAGTATT TCCTTTAGCA CTCTATATTT TAATTAACAT
 540
 TCAAGCTTAT GGACCTATTT TAGGTATATT GATTAGTTGG CTTGGATTAA TTTCTGGAAC
 600
 ATTTACAGTC TATTTGATCT TGTAACGAT TGGTGAACAC TGAGAGGATG CAGCGAATTA
 660
 AACACGTAC TGCTGTTCAA ACGCTTGATT AGTTTTATTG ATCGCCAAGG ATTAATCCCA
 720
 TTGTTTATTT TACTTGGGNT TTCCTTTTAC GCCAAATACA TTAATAAATT TTGTAGCGAG
 780
 TCTATCTCAT ATTAGACCTA AATATTATTT CATTGTTTTG GCATCATCAA AGTTAGTTTC
 840

AACAAATTATT TTAGGTTATT TAGGTAAGGA AATTACTACA ATTTTAACGC ATCCTTTAAG
 900
 AGGGATATTA ATGTTAGTTG TGTGGTTGT ATTTTGGATT GTTGGAAAAA AGTTAGAACA
 960
 GCATTTTATG GGATCGAAAA AGGAGTGACA TCGTGAAAAA AGTTGTAAAA TATTTGATTT
 1020
 CATTGATACT TGCTATTATC ATTGTACTGT TCGTACAAAC TTTTGTAATA GTTGGTCATG
 1080
 TCATTCCGAA TAATGATATG TCGCCAACCC TTAACAAAGG GGATCGTGTT ATTGTAAATA
 1140
 AAATTAAAGT TACATTTAAT CAATTGAATA ATGGTGATAT CATTACATAT AGGCGTGTTA
 1200
 ACGAGATATA TACTAGTCGA ATTATTGCCA AACCTGGTCA ATCAATGGCG TTTTCGTCAGG
 1260
 GACAATTATA CCGTGATGAC CGACCGGTTG ACGCATCTTA TGCCAAGAAC AGAAAAATTA
 1320
 AAGATTTTAG TTTGCGCAAT TTTAAAGAAT TAGATGGAGA TATTATACCG CCTAACAATT
 1380
 TTGTTGTGCT AAATGATCAT GATAACAATC AGCATGATTC TAGACAATTT GGTTTAATTG
 1440
 ATAAAAAGGA TATTATTGGT AATATAAGTT TGAGATATTA TCCTTTTTCA AAATGGACGA
 1500
 TTCAGTTCAA ATCTTAAAAA GAGGTGTCAA AATTGAAAAA AGAATTATTG GAATGGATTA
 1560
 TTTCAATTGC AGTCGCTTTT GTCATTTTAT TTATAGTAGG TAAATTTATT GTTACACCAT
 1620
 ATACAATTAA AGGTGAATCA ATGGATCCAA CTTTGAAAGA TGGCGAGCGA GTAGCTGTAA
 1680
 ACATTATTGG ATATAAAACA GGTGGTTTGG AAAAAGGTAA TGTAGTTGTC TTCCATGCAA
 1740
 ACAAAAATGA TGACTATGTT AAACGTGTCA TCGGTGTTCC TGGTGATAAA GTAGAATATA
 1800
 AAAATGATAC ATTATATGTC AATGGTAAAA AACAAGATGA ACCATATTTA AACTATAATT
 1860
 TAAAACATAA ACAAGGTGAT TACATTACTG GGACTTTCCA AGTTAAAGAT TTACCCGAAT
 1920
 GCGAATCCCA AATCAAATGT CAATCCAAAA GGGTAAATAT TTAGCTCTTG GAGGATAATC
 1980
 GTGAAGTAAG TAAAGATAGC CGTGCGTTTG GCCTCATTGA TGAAGACCAA ATTGTTGGTA
 2040
 AAGTTTCATT TAGATTCTGG CCATTTAGTG AATTTAAACA TAATTTCAAT CCTGAAAATA
 2100
 CTAAAAATTA ATATGAAACA AATACAACAT CGTTTGTCGG TTTTAATACT GATAAACGAT
 2160
 GTTTTATTTG GTTAGTACCA CAATAAAAGC TAAGTTCGAA ATGAACCTAT AATAAATCAA
 2220
 TCACAATCAC TTTGTGTTAA AATATGTGTC AAAGGAAGTG AGGGTTTGTC ATGACATTAC
 2280
 ATGCTTATTT AGGTAGAGCG GGAACAGGTA AGTCTACGAA AATGTTGACC GAAATAAAAC
 2340
 AAAAAATGAA AGCAGATCCG CTTGGAGATC CAATCATTTT AATTGCGCCA ACTCAAAGTA
 2400
 CATTTCAATT AGAACAAGCC TTTGTCAATG ATCCGGAATT AAATGGTAGT TTAAGAACAG
 2460
 AAGTGTTGCA TTTTGAACGA TTAAGTCATC GTATTTTCCA AGAAGTTGGT AGTTATAGCG
 2520
 AACAAAAGTT ATCTAAAGCT GCAACGGAAA TGATGATTTA TAACATTGTT CAAGAACAAC
 2580
 AAAAGTATTT AAAACTTTAT CAATCACAAG CAAAATATTA TGGGTTTAGT GAAAAATTAA
 2640
 CAGAACAAAT TCAAGATTTT AAAAAATATG CAGTAACGCC TGAACATTTA GAACACTTTA

2700
 TTGCTGATAA AAATATGCAA ACTCGAACTA AAAATAAGTT AGAGGATATT GCTTTAATAT
 2760
 ACCGTGAGTT CGAACAACGC ATNCCANAAC GAGTTTATTA CTGNTGAGGA TTCATNACAA
 2820
 TATTTTATTG ATTGTATGCC GAAATCAGAG TGGCTAAAAC GTGCTGATAG ATATATTGAT
 2880
 GGTTCACACA ACTTTTCAAC GATTGAGTAT TTAATAATCA AAGGATTAAT TAAATATGCG
 2940
 AAGAGTGTCA CAATTATATT GACGACAGAT GGTAACCACG ATCAATTTAG TTTATTTAGA
 3000
 AAACCATCGG AAGTGTTACG ACATATTGAA GAAATAGCAA ATGAACTCAA TATTTCTATT
 3060
 GAACGTCAAT ATTTCAACCA ATTATATCGC TTCAATAATC
 3100

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GGTGGCGAGA AAATACCGCA AGGTCATAAA GATATCTTTG ATCCAAACTT ACCAACAGAT
 60
 CAAACGGAAA AAGTACCAGG TAAACCAGGA ATCAAGAATC CAGACACAGG AAAAGTGATC
 120
 GAAGAGCCAG TGGATGATGT GATTAAACAC GGACCAAAAA CGGGTACACC AGAAACAAAA
 180
 ACAGTAGAGA TACCGTNTGA AACAAAACGT GAGTTTAATC CAAAATTACA ACCTGGTGAA
 240
 GAGCGAGTGA AACAAGAAGG ACAACCAGGA AGTAAGACAA TCACAACACC AATCACAGTG
 300
 AACCCATTAA CAGGTGAAAA AGTTGGCGAG GGTCACCCAA CAGAAGAGAT CACAAAACAN
 360
 CCAAGTAGATA AGATTGTAGA GTTCGGGTGG AGAGAAACCA AAAGGTCCCA AANGGACCTG
 420
 AAAACCCAGA GAAGCCGAGC AGACCAACTC ATCCANGTGG GCCAGTAAAT CCTAACAAATC
 480
 CAGGATTATC GANAGACAGA GCAAAACCAA ATGGCCCAGG TCCATTCAAT TGGATAAAAA
 540
 TGATAAAGGT TAAAAAATCT AAAATTGCTA AAGAATCAGT AGCTAATCAA GAGAAAAAAC
 600
 GAGCAGAATT ACCAAAAACA GGTTTAGAAA GCACGCAAAA AGGTTTGATC TTTAGTAGTA
 660
 TAATTGGAAT TGCTGGATTA ATGTTATTGG CTCGTAGAAG AAAGAATTAA AATAATTCAT
 720
 AATTTAAATA ATAGTTGATT TGCATTCACT ATATTTAGTT TGTTAAAAAC AACCTAGAAT
 780
 ATGATGAGAA TGATATACAA CCCCAAAAGT TGGCTTG
 817

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1348 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

```
CCATCGACTA AGCAATGGTA TTTGTTTCATT AAATCCTCAT GTTGATCGTT TAACGTTAAG
60
CTGTGCGCATG GAAATCGATG CTAGTGGTCG CGTTGTTAAA CATGAAATTT NTGATAGTGT
120
TATACATTCTT GATTATCGAA TGACGTATGA TGCGGTAAAT CAGATTATTA CTGAAAAGGA
180
TCCTAACATT CGCGAACAAT ATAAAGAAAT TACGCCTATG TTAGATTTAG CACAAGATTT
240
ATCTAATCGN TTGATTCAAA TGAGAAAACG ACGTGGGGTG AAATCGATTT TGGATATTAG
300
NGAAGCAAAA GTATTAGTTA ACGAAGTCGG GTATACCAAC AGATGTTCAA TTAAGACAAC
360
GTGGCGAGGG TGAACGTCTA ATTGAATCAT TTATGTTAAT TGCAAATGAA ACAGTTGCTG
420
AACATTTTAG TAAGTTAAAT GTACCTTTTA TTTACCGAGT GCATGAGCAA CCTAAATCAG
480
ATCGCTTAAG ACAATTCTTT GATTTTATTA CAAACTTTGG CATCATGATT AAGGGCACTG
540
GCGAAGATAT TCATCCAACA ACACCTCAAA AGGTTCAAGA AGAAGTAGAA GGTGCGACCTG
600
AACAAATGGT CATTTCAACA ATGATGTTAC GTTCAATGCA ACAAGCGCAT TATGATGATG
660
TGAACCTGGG ACATTGTGGC TTATCAGCTG AATATTATAC GCATTTNACA TCACCAATTA
720
GACGTTATCC TGATTTAACA GNTCATCGTT TAATCCGTAA GTATTTAATT GAGAAATCAA
780
TGGATAACAA AGAAGTGAAG CGTTGGGAAG ACAAATTGCC TGAGTTAGCT GAACATACTT
840
CTAAACGTGA ACGTCGTGCT ATTGAGGCAG AACGTGATAC TGATGAATTG AAAAAAGCAG
900
AATATATGAT TCAACATATT GGTGATGAAT TTGAAGGTAT TGTCAGCTCA GTAGCTAACT
960
TCGGTATNTT CATTGAATTG NCAAAATACGA TAGAAGGTAT GGNTCATATT GCGAATATGA
1020
CTGATGATTA TTACCGCGTT GAAGAGCGTC AAATGGCATT AATTGGGTGA GCGTCAAGCT
1080
AAAGTATTTA GAATTGGTGA CACAGTTAAG GTTAAAGTGA CGCATGTTGA TGTAGATGAA
1140
CGATTAATTG ATTTTCAAAT TGTTGGAATG CCTTTACCTA AAAATGACCG CTCACAGCGA
1200
CCAGCAAGAG GTAAAACGAT TCAAGCTAAA ACGCGTGGCA AATCTTTAGA TAAATCGAAA
1260
TCTGATGATA AGGGTCGGTA AGAAAAAAGG TAAGCAACGT AAGGTAAAAA CCAACGTAAT
1320
AATGATAATC AGGTAATAGT AAGCATAG
1348
```

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 982 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

```
ATGAAAATTA TTTTAATTTT AGCATTAGCG CGTGTCGTTT CTAGACATAA TCAATTCACA
60
TTCAATAAAT CATTCCAAAG TGATTTGTTA TTATTTTTC AATTATTGG TGTCTCGTTA
120
GTACCAAGTA TTTTAATATT ACTGCAAAAT GACCTAGGAA CTACATTAGT ATTAGCTGCT
180
ATTATTGCAG GTGTGATGTT AGTAAGTGGT ATAACATGGC GTATCTTAGC ACCTATCTTT
240
ATTACAGGTA TTGTTGGTGC AATGACAGTC ATTTTAGGTA TTCTATATGC ACCCGCATT
300
ATTGAAAATT TATTAGGTGT CCAACTGTAT CAAATGGGAC GAATCAATTC AAGGCTTGAC
360
CCCTATACAT ATAGTAGGGG GGGGGATGGC TATCAATTAA CTGAATCACT TAAAGCTATC
420
GGGCTCTGGA CAAGGTACTA GGTAAAGGAT ACAATCACGG GGGAGGTTTA TATCCCTGA
480
AAATCATACT GACTTTTATC TTTNCAAGNG AATGGGAGAG GAACTTGGCT TTATCGGTTC
540
TGGCAAATTG AGNCTTAATA TTTTATTTT TAATCTTCCA TCTAATAAGA TTAGCTGCGA
600
AAATTGGAGA TCAATTTACC AAAATCTTTA TCGTTGGTTT CGTCACTTTA CTTGTGTTCC
660
ATATTTTACA AAATATTGGT ATGACAATTC AGTTGTTACC AATCACTGGT ATTCCATTAC
720
CATTTATTAG TTATGGTGGT AGTGCGCTAT GGAGTATGAT GACTGGAATA GGTATAGTCT
780
TATCAATTTA TTATCATGAA CAAAACGAT ATGTCGATTT ATACCATCCA AAAAGTAATT
840
AATTTAACT ATTTTGAGTT TCAAATATCA TAACTTTTCA AGATGACGTT ATATAGTCTA
900
TTTACGTCGT CGATTTAAAA TGTCATATAT AGATATTACT CGATAATAAC AATCCCTCTT
960
TGAAGTACAC ATTGTAAAAT GG
982
```

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1709 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

```
GGCACTAACT TCATTTGAGC ATCCTCCTAT CAATTGCTAT ATAAATTAGT ACCCTTTTGC
60
CACTTAATTA TAACAAATTC TCAAATTTTA AAAATTGAAA ATCTAGTTAA TGTATTAGCT
120
CGATTTTGAA ATCTAATAAT AATTGGCATA AAATGGAAGT AATATTATGT GAGGAGTGTT
180
ATGAAATGAC AAAAATATCA AAAATAATAG ACGAACTGAA CAATCAACAA GCTGATGCAG
240
```

CATGGATTAC AACACCGTTG AATGTATATT ATTTTACTGG ATACCGTAGC GAACCCATGA
 300
 AAGATTATTT GCATTATTGA TTAAGAAAGA TGGTAAACAA GGTACTATTT TGTCCAAANA
 360
 TTGGAAGTCG GAAGAAATCA AAGCATCACC CTTACACAGG TGAAATCGTT GGATATTTAA
 420
 GACACTTGAA ATCCTTTTTT ACTTTATCCA CAACNCAATC AATAAATTAC CTAATTGTAA
 480
 GCGGAGCACC TTAACAAGTA GCACCGCCAC AAACAATTAA TCTCTGTTTC NATGTCAATT
 540
 CATTCGGAGA TGTTGAGTTA ACAATCACAC AATTAAGAGA TATTAAATCC GAAGATGAAA
 600
 TTAGCACAAT ACGTAAAGCT GCTGAGTTAG CAGATAAGTG TATCGAAATA GGTGTTTCTT
 660
 ATTTAAAAGA AGGTGTGACT GNACGTGAAG TAGTCAACCA TATTGAGCAA ACTATCANAC
 720
 AATATGGCGT CAATGAAATG AGTTTTGATA CGATGGTTTT ATTTGGAGAT CATNCCGCAT
 780
 CACCTCATGG CACACCAGGA GATCGCAGAT TAAAAAGCAA TGAATATGTA CTATTTGATT
 840
 TAGGTGTAAT TTATGAGCAT TATTGTAGCG ATATGACACG TACCATTAAA TTTTGGTGAA
 900
 CCTAGCAAAG AAGCACNAGA AATTTATAAT ATTGTATTAG AAGCAGAAAC ATCTGCAATC
 960
 CAAGCAATTA AACCTGGAAT ACCTTTAAAA GATATCGATC ATATCGCTAG AAATATTATT
 1020
 TCAGANNAAG GTTATGGTGA ATATTTCCCT CATCGCTTAG GTCATGGTTT AGGATTACAA
 1080
 GAACATGAAT ATCAAGATGT TTCAAGTACT AATTCTAATT TGTTAGAAGC TGGCATGGTT
 1140
 ATTACAATCG AACCAGGTAT TTATGTACCA GGTGTTGCAG GTGTAAGAAT TGAAGATGAC
 1200
 ATACTTGTCA CTAATGAAGG ATATGAAGTA TTAACACATT ACGAAAAATA AGGAGTGGGA
 1260
 TAAAAATGAA AAGCTTGTTA CAAGCACATT CTCATTTCAGT CAAACACTGC CAATATAACA
 1320
 TTGTAGCGCC TAAGACATAA ATTTTATCC AAGTCTAAAT GCAATATGTA ACAAACAAGC
 1380
 TAGAAACACA TATGCAGGTA TGTTTCATCAG TAACATGTAA TGAATCAAAT CAATATCATT
 1440
 CATGTTTCGAT GATTTCTTCG CATTGTTTCT AGCTTTAATT TATCATTATT TAATTTTAAT
 1500
 AACCAAGGAG ATGATAACGT CAGTCTTTAG TACGCTGTAA TCCATTCCCT TTTCATCAAA
 1560
 TTCAAATTAT AATTGTAATG CTTCTTCTAC AGATTTATAT TCCATTTCAA ATGCCTCTGC
 1620
 AACGCCTTTA TTGGTTACGT GACCTTTGTA AGTATTTAAA CCTAATGATA ATGGTTGATT
 1680
 TGATTTAAAT GCTTCTCTAT ACCCTTTAG
 1709

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

AAAGAGGAAG ATGTGAACCA CCACTAGTAT TGAATCTAAA GATTGAGGAC GTTCCTTTAT
60
TAATTGGCTA NNNAAGNNAN ATCNNNAAGA TAGCCAATCC AAAGCCAAAA AGTCAGCATC
120
AAGAAATACT TCTANNAAGG TAGCAGCTNN NNAGAAGNGN NAGAAATCTA AGANAAATNN
180
NAAATAATTT GTTTCTTTGC TAAATAGAGG AGCACCGATT GACATCACAT CAGTCGGTGC
240
TCCTTTTATT TATTCTTTTT AATTAATTTA TACAAANCCN ATTCCCTGTT GAGCGTGTG
300
AATCGCCTTC CNTTGTTTTG TTCTCNCGGT ANCCCATTTA ACCAAATNAT AAACCNANAT
360
CTTTNTCCAA ATATTTCTAT TTGATCAAAA TAAGGTTTGA AATTTGCGTT TTTCACATAA
420
CCAGCTCGTG CCAATGCTAT CGTGCAATTA GCTTTGAGTC TGTATATAAT AGTGCGTTTT
480
GAACATTTAA TTCACGTGCA TGTTCTAGTG CATAAATACA TGCAGCCCAT TCTGCAGTGT
540
GGTTATCCAT TTCGCCTAAC TCATGTGTAT ATGTATNATG CTGCTTATCT TCTTTGATTA
600
CAATGGCACA NGTACTTATG CCTGGATTTT CTNTTCGTCG CAGCATCAAA ATTTATGTGC
660
GCCATAATAA ACCTACTTTC TATTCAATAC TTAGTTAAAG TTACTATTAC TGTAATACAA
720
AATATGTTGG GTAATCCATT AAAAAACACG CATCACTTAA ATAAGTAAAC ACGTTGTAA
780
AAATACTTCG CTTGATTCAA AAGATGATTT TCTAAATACG TAGTNCTTGT AAAATACTTC
840
CTAAANAAAT CATCTTCAGG CTGGGGACAT AAATCAATGT TCTATGCTCC TNCCGAAGTT
900
ATATTGGCAG TAGTTGACTG ANCGAAAATG CGCTTGTAAC AAGCTTTTTT CAATTCTAGT
960
CAGGGGCCCC AACACAGAAG CTGNCGAAAA GTCAGCTGAC AATAATGTGC AAGTTGGGGA
1020
TGGACCCCAN CAAAGAGAAA TTGTATTCCC AAATTCTACA GACNATNCAA GTTGGGGTGG
1080
GNCGACGAAA TAAATTTTGC GAAAATATCA TTTCTGTCCC ACTCCCTTAA AACTTATTCT
1140
TTTGTGTAGT AAGTGCGTTA ATAGCCTTGA TCTAACTTAT CAATCTTACC TTTACGATAA
1200
AATGATTTAG CAATATATCC ANNTGGTACA TTGAAACTG TTGAAGCTAA TTTTAATACG
1260
TAAGTTGTAA TAAATATTTT NAATNCAACT GTACCAGGTA AACTTCCGAT AAAAGCGATA
1320
GCTACAAATA AAGCTGTATC CAATTATTGA GCTTG
1355

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

CCAATTTTCC CTTCTACCTG CGTGGGTTAGT ATTCAAGCCC AAAGTTCAGC GGGAAAATAT
 60
 TGACAATTAA CCGGATCCAG CTAATCGGAG GTCGGATAAA GATGTTGAGT TGTAAGTTAT
 120
 TTGGAATATT ATTTTAATAG TGTCATCCCC CTTTGTAATA TAATTGTCTT ACTTTTAAAT
 180
 TAAAAGCCAA ATTAATATAA GAAANCTAAG ACTTAGTACN GTATCAATTT TGTGCGTTTC
 240
 AATTGAGTTC TAGTTTTTTT TAATATGTTA ATATTAACT TATAACTTTA TGGGAGTGGG
 300
 ACAAGAATGA TAAAGAGCCA CTAAATGATT TATTATGTAG TGGTTCTTAA TACATTAGCC
 360
 ACANCTAATG TGTACTTAAA AATAGGAATA CATGAGTAAA ACTCATGCAT AAGAAATACT
 420
 AATTTCTATA GAAAAAGTAT TACTTTATCG TTGTACCACA CCAACTTGCA CATTATCGTA
 480
 AGCTGACTTA TCGTAAGCTT CTGTGTTGGG GCCCACACCC CAACTCGCAT TGCCTGTAGA
 540
 ATTTCTTTTC GAAATTCTCT TTGTTGGGGC CCACACCCCA ACTTGCATTG TCTGAAGAAA
 600
 TTGGAAATCC AATTTNCTCT GTGTTGGGGC CCACACCCCA ACTCGCATTG CCTGGAAGCT
 660
 GAATTTCTTT TCGAAATTCA GCTTCTGTGT TGGGGCCAC ACCCCAATT GCATTGCCTG
 720
 TAGAAATTCT TTTCGAAATC CAATTTCTCT GTGTTGGGGC CCCTGACTAG GATTGAAAAA
 780
 AGCTTGTTAC AAGCGCATTT TCGTTCAGTC AACTACTGCC AATATAACTT CGTAGAGCAT
 840
 AGAACATTGA TTTATGTCCC AGCCTGATAT CACCATTAAA TACAATTCAT TTAGTNTTCA
 900
 ATTGGAAACA ATTNATCGAT ATATTGAATC TCATCATCTG ATAAAACGAT ATCTGCAGCT
 960
 TTAATATTTT CAATGACTTG TTCTGCACGT TTTGCACCAG GAATAATCAC ATCGATAGCT
 1020
 GGTCTCGTTA AATAAAATGC TAATACAATG TTCGCAATTG AAGTTTGATG TGCTGCAGNT
 1080
 AGNCTTTCCC AAAGCTTTTA CGCTCGTGAC GCACATTCTC TTCAAAAACA CCAGGTATAA
 1140
 AATCCCGACG TGTAGTACGA TGGTCACTAA ATTTAGTGTT CTCATCATAT TTTCCAGCTA
 1200
 AAATACCGGA TGCTAATGGG AAATAAGGAA TAAATGTGAT TAGGTGATCA ACACAATATT
 1260
 GCAATACTGC CTCATTTTCG CGGTGCAATA AATTATATTC TAACTGTACA ACATCAACGT
 1320
 AACCATCTTT ATTTGCTTCT TTAAGTTGAT CTAATGTGAA ATTTGATACA CCAATGGCTT
 1380
 TAATCTTCCC TTGTTCTTA AGCTCGTGCC
 1410

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GTGTTACGGT AGGTTGTTGA TCCTAATTTT CCCTGNCAGT TGGTCCCAGT ACCCACCACAT
 60
 TTCCCAACTT ACTAAAAAAG AAATCCAATT ANNCCGAAAG AAAATATTGA AGTCATTGAA
 120
 ATTAACCGAA GCGTTCCAGT GCACAGGTAG TTGCCTCCCC AACCAAGCTT TAAATATTTT
 180
 CAAATACGCA ATTAAATATA TGGGGTGGTG CATTAGCATC AGGTCATCCA TACGGTGCAA
 240
 GCGGTGCCCA ATTAGTGA CTGATTATTTT ATATGTTTGA CAAAGAGACT ATGATTGCAT
 300
 CTATGGGGAT AGGGGGAGGT CTAGGAAATG CAGCATTATT TACTCGATTG TAACCAGCGA
 360
 TTAAATGTGT CATTTTCTAA GGATAGTGTG GCTGCATATT ATCAGTGTTT TANCCAACCT
 420
 TATAGAAAAG AAGTCTCGTG CCCATTAATG TGTNCGTCAT TATGGCCACA ATTTGATTTA
 480
 TTTAAAAAAA TATCCAAATA GCGAGCTGAT TTTACCACAA ATCAGCAATT AATCAAATC
 540
 NCAAGATAGA AGTAGACACA ATATATGTAG GGCATTTAGA AGATATTGAA TGCCGACAGA
 600
 CTCGCAATAT CACACGTTAT ACAATGGCTT TAACATTAAC TAAAAATGAT CAACATGTCA
 660
 TANCGGTTAC ACAAACTTTT ATTAAGGCGA TGAAGTAGAG ATGAAGTTTA ATGAGATATG
 720
 GATAAATGAA TATTTGGCGC TCGTAAATGA TGATAATCCA ATACATAATG AGATTGTGCC
 780
 AGGACAATTA GTGAGTCAAA TGATGCTGAT GGCTATGTCA TTAGAGACAA ACCAGTGTCA
 840
 AATTAAC TAC GTTAAACCTA TTTTAATAAA TGAAAAATATC GAATTCATTG AACAAACACGA
 900
 ACACGAAATT ATAGCAATTA ATGACGATGG AGAGATTAAA ATAAAAATTT CTTTGAGCAC
 960
 AAAAAAATAA CCGATATTAG CTGCATGAAC GCATATTAAT TAGGAGATGA AAGGACAGCT
 1020
 AATATCAGTT ATGTATTGTT ATTATTATTG GGAACAGAGA TGAATATAGG TTACGTTTCT
 1080
 TTCTTTGCAC GGGGATGCAT TAATCTAAAA TAATAATAAC AACTATATCA ATGTTTAATA
 1140
 AATTCTGGAT TATTGGAACG ATTAGTCAAT TTAAC TAACT TNCATATGAT CTATATCGTC
 1200
 TTGTNATAAA GAGAGCAATT TGAATATTTT AGTATCACTA AATGAATCGN CACATTTAAT
 1260
 TGAAACATGC TGAAACGTTT GGGTTATAAT TTCATAAACT GGTGCGCCTT CATGGTGATA
 1320
 CTGTCGAATA AATAATCATA ACCATATTTA CCTCCTTNGG CTACTCTATG GGTATATTAT
 1380
 AAATAACATT TTTATGTGTG ACATCAACCT TAAGTATCAA CTTTTTATCA GACATAGAAC
 1440
 GTANGATTTA CTAAGACTAT TTATGTATAA AAGTTCTAAA TAAATATATA TTTATAGAGT
 1500
 CGCCTGGCAG NCATTTGGGA AATATAACAT ATATGATTAG AGAGGCATCT ATCGCAAAAG
 1560
 AATGATAATG ATAGAGGTAT TGAGCATATA GATGAGTTTA AGTTCATCTT GAAAATAAAG
 1620
 GGTTATTTAG TCATAGATGT AGATGTATAG GAAATATTTG TATGTATTGN TCGATATGTA
 1680
 TGAAATTTTC AATAAAAGCT AATAACGCTT ATATG TAACT TTCAAATTTA AATTATATAC
 1740
 AGAGCATGAT GATTATAAAA AAATANCCAC ATCACATAAA TTGAGTTCAT ACCCAATTTA
 1800
 AGTGGTGTGG CTAATAATGT TGATTTATAG ATGAACCGCC TAATCGTTAA ACCTCTGTTA

1860
 CTTCAACATC GATATGTTCA ATACGTTGT ATGCACCGTG ATCCACAGGA CCAACAAAAT
 1920
 CATTCAATTTT CCAACCGTTT TTAATAGCAG AAGCGACGAA AGCTTTCGCT CGTGCTAATC
 1980
 ACAGCTTCTT TCGGTGACTT ACCGTTAGCT AAATATGCAG GTGTTGCCGC AGCAAATGTA
 2040
 CAACCAGCAC CATGGTTATA ACTTTGTTGG AACATGTCTG TTGTTAGTTG ATAAAATGTG
 2100
 TGACCATCAT AGTATAAGTC ATACGATTTA TCTTGATCTA AAGCTNTGNC ACCTTTAATG
 2160
 ATGACATGCT GTGCGCCTTT ATCAAAGATA ATTGNTGCAG CCTTTNACAT ATCTTCAATT
 2220
 GAATTTAATT TACCTAATCC TGATAATTGA CCCGCTTCAA ATAAGTNTGG TGTCACTACC
 2280
 GGTGGTTTAG GTAGTAAATA TTTAATCATC GCCTCAGTAT TTCCAGGATT AAGCACTTCA
 2340
 TCTTCGGCCT TTACAANCCA TGACAGGATC TTACTACAAA ATATTGTGCA ATTAGATGCT
 2400
 CATATACTTC TCCAGNACGG GTGGATATCT CCTCAAG
 2437

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

TTTCCCCNA CTCCATAATC TTGGCCAAAA TCATGTTTAA ATTTGATCTT GATTGAGACC
 60
 CAAAGATAGC TTGCATATTG TTTCCCAACT TCTAANACAC CTGATGCGCC TAAAGCTTTA
 120
 AATACCTGCT ACATCTACTT TTGATTTATC CAACCCACTT CTACGCGCAG ACGTGTAATA
 180
 CATGCATCTA AATGTTTAAT GTTTTCTTTT CCACCCCAT TGNATCTAAGA CATCANATGG
 240
 TAATTTTGCG AACTAGAGT TACGAATTC AGTTTCTTCA TCTTCACGAC CTGGTGTGTTT
 300
 CAATTTAAAC TTACGAATTN CACAGTCGAA TGAGANGTAA NACACGATAG CAGACACGAC
 360
 AGCGTTCTNN GACTGGTAAT NGGGCATTNN GCCCAACCCA ATTTATGTGA GCTAACTCAG
 420
 GTTGAACNTT GACCATCTTT NNATTCTTCA ACCCANAACC TGCAGGCGTA TTCATAANT
 479

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2593 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

CCAAAGTGTT CTGGTCTAAG ATATTATCGC TAATCCGTGT TAAGCCACTC AGCTGTTTAA
60
TATCAATTAC CTTTTTNAAA TCCCTCCAAC CTAAAATCTT GATTCCCACC TTGCTTTAAT
120
AAAATCTTTC GTTTTAGTTG TATTATGTTT AAACCTCTTG CCAGTCTTTT CGGTAAGATA
180
ATCAATAATC TCTTTATATG GGATGCGTGT CGGGTTTCCC GACAATATAT CTA CTACTCTATT
240
TATATTGTTA TTA CTCTGTAT TATTAATACT TGTATTGTCT CTTTAACATT TGTGATAATA
300
GGGGTATTAA CAGAATTGTT AATAGGGGTA TTATCATTTG TGTTAATAGG TCTTATCATT
360
TCTGTTAAGG GGTATAGCTT TCTTTGTTTA ATTTCAATTAC CATTTCTAAT GATTTCAACA
420
TGTAATATC CACATTCTTT TAAGTTGGCT ATACGGCGTG ATACAGTAAC TTTTGTAAC T
480
TCATATAGTT TCGCAAAGTA ACCATTACTT GCTGTGCAGT ATCCGTA CTT GTTACTTAAA
540
GACGTTATTT CTGCAAAAAG TAAC TTTTCG CTGTCAGTAA GTCGGTTATC GTATCTGACA
600
TTTGCCGTTA TTATTGAGTA GTA ACTTGGT TGTT CAGTCA TTCTCAGCAC CTTCTTT CAG
660
TGCTTTGAAC TTGTCTGGTA TCTCCAGTT AGATATGAAT TCTTTCAATT CATCAGTCAT
720
AGGTA CTTCG TTTAGTATTG CGTCATCACC AAACAGATAT AAAACTATCT TGTTATATGC
780
TAATGCCGCT TTTTCTGTGC TATCAAAATA TTCCGTAGTA TATAGCTTGC CATCAATTTT
840
TTTCCTAACA GAAAATCGAT GCGGCATATC AGAGTGGTTT CCAATTCCTC TG TAGCCATA
900
TTTACTAGCG TTTCTTGTGT TGTTAATATT TTTATGAGGA AAATAATCTC TAACTTTACG
960
CATATCTCTT CCAATTATGT TTTTAAAACC TTCCACCACC CCAAACTCA TCTACAGCTT
1020
NGTTATACGC TTCAGCTGCT AATTCTTCTT GTTTNAAAAA TACCTAAACG TTTTNGGATT
1080
TCCTTCAACA TTTATATTGG CTGTCCATTT ATTGCAATCT TNACGCCAGT TAACACCTTT
1140
ANACTTAGAA GAACCATTAC TTTTAGGTNT CTCCCATCTT GANCNGTTNN NACCTTTTGT
1200
AGTTAAATTA GATTTAGTAA AATTATTATT TTTAATTTTT TGAAA ACTTC CTTCTTTTAT
1260
AAAGGTTGTT AATAGTACAA CCTTTCTCTC GTTGCCAATC CTAGTATGGA TATATCTTGT
1320
ATTACCTTTA TAGTATTTGA ACCATTTATA TCTGTTCCAC TCTTTCATAA TCTTCATCAT
1380
CAACAAAAAT TTCTTCTCCA TCTTGTA AAAA ATATCGATTT AACCATTATT CTCTTCCTTT
1440
CAGCATTTTG TTGAGCCTCT CATCAACTTT TATCCACGAG TCATGCAAGT GATATTTATC
1500
ATCAAACGAC TTAACACCAA TCGCATGTTG CTCGTTGTGA TGTT CGCGAC ATAACGCTAA
1560
TACATGTTTG TTGTAGTGAT TCATTTTGT TCTGTTCA TT CCTCTGCCGA CTGCTTCATA
1620
ATGCGCTAGG TCTGCGTGAG GCTTTCCACA AATTACACAG TTGCGGTTGA TTGTAGCCCA
1680
ATACAATAGT GCTTTATCCT CACTTAACAA CTTGCTCTCG TGCCTATGCT CATAGGTATT
1740
TGATGATGAA ACATAAACGC TATAATCAGT TCTATTA ACT CCCTTGCAAC TTTCATAGAA

1800
 CAGTCGCGCA GACTGATTTC TTCATAACCT TTCATAATTT CCAATTCTGT TTGTAATAAT
 1860
 TTNCTAATTG ATTCCACCGG TTCTCCCCAG TGAAGTTCTA TATCTCTACA CATNGCGAAT
 1920
 ATTTTTTTGC GTTGTCTAT AGATAGTTTT TTATTATCCG GAACCTCTAC TTCTGCTTTT
 1980
 AGTGGATATC CGTTTTCTAG TAAGTCAATG TGACTTTGTT CAAGTTCAAC ACCANTAGCA
 2040
 ACGACGGAAT AAGTNCCGTC ATTGTCNNTC TGGNATCTTG TAATGTATTG CANNTAAACC
 2100
 CACACCTTAA ACGCTAAATC TTGGTCGTCA TATCCAAATT GCCCCCTGCT TTCAAATGGA
 2160
 TTGCTTTGTT GAGACATTGA TGTTTGTTGT TGTGCCCCGT TATTTTCTTC AGCTTTTTGC
 2220
 TTATCTGTCT TCGGAATAGG TTTGTTAACA ACATCATCGC CCTTTTTGTA AGGTTTAATA
 2280
 AATGAAAAAT CCGTAAAATA CTTACCTTCA TCTTCATTGA ATTTCCATTT CAATACCAAG
 2340
 TGACANAAC TACCAATAAG ATCATTGGTA TCANAATCTA AGCTAGGAAG ATTTAACTTA
 2400
 ATACCTAATC GAGTAACTAA TTCAATCAAT TGTTTTTCTT GGAAATCATA TTTATACGGC
 2460
 GGTACAAATT GATTATGTTT ATATTGTTTG CCTTCATCAT TTTCAAATAC GATTGTGAAA
 2520
 TATCTATTTT CTCTATCATT AGAAGAAAAC CTGATCATCT TTTTtaggtt TCTTAGATTG
 2580
 GAATTGTTGA GGG
 2593

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

CCCCAGTCT CATATGAAGT AGTTGGATTA GTTCCGAAGT ATGAGGATGG GAATTTCTTG
 60
 ACATAGTAAA GTGCCGGATG ATAGTGCAAG AGGTATCGTT GCACAAAATA TGACAACTGC
 120
 TGAGATTGAA ACATTTGGTT CAGATCCAGT TATTATGCCA ACGGGGTGCC CCTGGTATTA
 180
 TTTTCGGTAA AACAACAAAC TCAATGATTA ATACAGGATC AGCGGCTTCC ATTGTTTACC
 240
 AACAAAGCGC TATTTATGCT AATGCTGAGT TCATTCAAAT TCATCCTACT GCAATCCCTG
 300
 GTGATGATAA ACTCCGACTA ATGAGTGATC AGCACCNNTG TTGAAGGTGG ACGAATTTGG
 360
 ACATATAAAG ATGGTAAGCC TTGGTACTTC TNAAGAAGAG AAATATCCTG ATTATGGTAA
 420
 CTTAGTACCT CGTGATATCG CAACCGCGTG ANATTTTCGA TGTATGTATT AACCAACAAA
 480
 TTAGGNATAA ATGNCGAAAA CATGGNATAT CTTGATTTGT CACATAAAGA TCCAACATGA
 540
 GTTAGATGTA AAAC TAGGTG GTATCATTGA AATTTATGAN AAATTCCTG GTGATGACCC

600
 ACGCAAAGTA CCAATGAAGA TTTTCCCAGC TGTTCACTAT TCAATGGGTG GTCTATATGT
 660
 AGATTATGAT CAAATGACAA ATATTAAAGG GTTATTTGCA GCTGGAGAAT GTGACTTCTC
 720
 TCAACATGGT GGTAACCGCT TAGGTGCCAA TTCATTGTTA TCAGCGATTT ATGGTGGTAC
 780
 AGTAGCAGGT CCAAACGCGA TTGATTAATA TTTCAAATAT TGATCCGATC CATATACTGA
 840
 TATGGACNGA AGTATTTTTG AAAAACGTAA AGCTGAAGAG CAAGGAACGT TTTGATAAAT
 900
 TATTAGCTAT GCGCGGTACA AGAAAATGCC TATAAATTAC ACCGTGAACT TGGTGAAATT
 960
 ATGACACCAA ATGTAACGTG TGTTTCGTGAA AATGAAAAAC TGTTAGAAAC AGATNAAAAG
 1020
 ATTGTTGAAT TGATGAAACG TTATGAAGAT ATTGATATGG AAGATACTCA AACTTGGAGT
 1080
 AACCAAGCGG TATTCTTTAC CCGTCAACTA TGGAACATGT TAGTACTTGC ACGTGTTATT
 1140
 ACGATTGGTG CATATAACCG TAACGAATCA CGCGGTGCCC ATTATAAACC AGAATTCCTG
 1200
 ATAAGTATTT TCGTCAGAAG TACATAATAT TTAAATCATT TAATTTTGAG AAGCATGGAA
 1260
 AATTTTGGAA CAAATGGTTT TACGTAAGAA AATGGAAACA TAAGATTTTA GATGGTCATC
 1320
 AGCTTAATCA AAATATATAT GATCAGCGTC ATTTAATGAC AATCAATACT GATGAAATTG
 1380
 AAAAAATGAT TATAGAGACA AAGAGGGCAG AGTTGATTCA TTGGATATCG ATACTTCCAG
 1440
 TCATCATATT CAATAAAGGC TCTCGTTTAG TAAAGTATAT AAATATTTTC TATGCAATGA
 1500
 TAGCTAATGT TCCAATCATT ATTGTGCAAC GCTATAATCG ACGAGATTAA CGCAGGTACT
 1560
 ACGCATTTTA AAACGAAGAG GTGAACGTCA TGAATAACA TATCATCCGN TATTGGGTGG
 1620
 GNGGCTTAGG TGGGATTTTCN TGCAGCAATT CGAATGGACA AAAGTGGCTA TTCGGNCTCA
 1680
 TTATATGAAC AAAATACTCA TATAGGAGGC AAAGTGAATC GNCATGAATC AGATGGCTTT
 1740
 GGCTTTGATT TAGGTCCATC TATTTTAACG ATGCCTTATA TTTGTGAAAA ATTATTCGAA
 1800
 TATAGCAAGA AGCAAATGTC AGACTACGTT ACAATCAAGC GTTTGNCACA TCAATGGCGT
 1860
 AGCTTTTTTC CAGATGGCAC GACTATCGAT TTGTATGAAG GTATTAAAGA AACAGGTCAG
 1920
 CATAATGCGA TATTGTCGAA ACAGGATATA GAGGAACTGC AAAATTATTT GAATTATACA
 1980
 AGACGAATCG ATCGTATTAC TGAAAAAGGG TATTTTAACT ATGGTTTAGA TACACTATCT
 2040
 CAAATTATTA AATTTTCATGG GCCATTAAAT GCTCTTATTA ATTATGATTA TGTACATACT
 2100
 ATGCAACAGG CCATAGACAA GCGTATCTCG AATCCATACT TGCGACAAAT GTTAGGCTAT
 2160
 TTTATCAAAT ATGTAGGTTT TTCATCATAC GATGCGNCAG CTGTATTATC TATGTTATTC
 2220
 CATATGCAAC AAGAGCAAGG CCNTTGNTAT GTAGAAGGTG GAATCCATCA TTTNGCCAAT
 2280
 GCCTTGGAAG AGCTAGCGCG TGAAGAAGGT GTCACAATTC ATACAGGTGC ACGTGTGGAC
 2340
 AATATTAAAA CATATCAAAG ACGTGTGACG GGTGTCAGAT TAGATACAGG TGAGTTTGTA
 2400

AAGGCAGATT ATATTATTTT AAATATGGAA GTCATACCTA CTTATAAATA TTTAATTCAC
 2460
 CTTGGATACT CAACGATTAA ACAAATTAGA GAGGGAATTT GAGCCGGCAA GCTCAGGATA
 2520
 TGTGATGCAT TTAGGTGTTG CTTGCCAATA CCCGCAATTA GCACATCATA ATTTCTTTTT
 2580
 TACGGAAAAT GCTTATCTCA ATTATCAACA AGTTTTTCAT GAAAAGGTAT TGCCAGATGA
 2640
 TCCGACCATT TATCTAGTAA ATACGAATAA AACTGATCAC ACACAAGCGC CAGTAGGGTT
 2700
 ATGAAAATAT CAAAGTCTTA CCACATATTC CATATATTCA AGATCAGCCT TTTACCACTG
 2760
 AAGATTATGC GAAGTTTAGG GATAAAATTT TGGATAAATT AGAAAAAATG GGACTTACTG
 2820
 ATTTAAGAAA ACACATTATT TATGAAGATG TTTGGACACC GGAGGATATT GAAAAAAATT
 2880
 ATCGNTCTAA TCGTGGTGCA ATATATGGTG TTGTCGCAGA TAAAAAGAAA AACAAAGGAT
 2940
 TTACCTTTCC TAAAGAAAGT CAGTATTTTG AAAACTTGTA CTTTGTAGGT GGATCAGNAA
 3000
 ATCCTGGTGG TGGCATGCCA ATGGTTACAT TAAGTGGGCA ACAANTCGCA GACAAANTNA
 3060
 ACGCGCGAAG AAGCGAANGA ATAGGANGGT GANATCTATT GAAATCGGTN NTCACGACTA
 3120
 TTTAANAGAC AATAGTGGNN ACCCATCNTC TTNTGGGGNC TTGGGAGCAT TTGGATNTTC
 3180
 NNCGGGGGNC A
 3191

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1189 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

CCTGGAATAA TTGGTGGTCC GTAATTGATG GGCCAAGTTG AAATTGGAAG CTAAAAAAGT
 60
 CTTAATCCGC CCAAATTGTT AACAACACAC CTATTGACTT TGTCAATCCA ACCCATCAAT
 120
 CCTTCATTAT TAACATGTCC CAGGTATCTT TAAGNTTGAT GAAACATTAG ATACCAGTTG
 180
 TTGGCGAAGG CTTAAAGCTT TGCCANCTTG AAAAATTAAG CCGGAATTAA GATGCATTGC
 240
 GTCGCCTATT TGAATCCAAA CCGATAGTGT TAAATATGAT AAATTAAAAG CACGTTATGA
 300
 GCGTTTCCAA AATCAATCAT TCAAAAACCTT AGATTATGAT TTCGAAAGCG TCGTACTTTC
 360
 AAGACAATCA CCATTGCGCG AACGTATTGA ACAACAACAA AAACGTTTGA ACTTACCGGA
 420
 TTTACCAACA ACAACTATTG GATCATTTCC ACAAGCCGA GAAGTTCGAA AATACCGTGC
 480
 AGATTGGAAG AACAAACGCA TTACAGACGA AGCATATGAA ACATTCTTAA AAAATGAAAT
 540
 TGCTCGATGG ATTAAAATTC AAGAAGACAT CGGCTTAGAT GTATTAGTTC ACGGTGAATT
 600

TGAACGTAAT GACATGGTTG AATTCTTCGG AGAAAAATTA CAAGGTTTCT TAGTAACTAA
 660
 ATTCGGTTGG GTGCAATCAT ATGGTTCACG CGCCGTAAAA CCACCAATCA TTTATGGTGA
 720
 TGTAAGATGG ACAGCGCCTT TAACTGTTGA TGAAACAGTT TATGCACAAA GCTTAACAGA
 780
 TAAACCAGTT AAAGGTATGT TAACTGGACC TGTAACAATT CTAAACTGGT CATTTGAACG
 840
 TGTGATTGTA CCACGTAAAG TCGCTCAAGA TCAAATTGCT TTAGCAATCA ACGAAGAAGT
 900
 ATTAGCACTT GAAGCTGCAG GAATCAAAGT TATCCAAGTT GACGAACCTG CATTACGTGA
 960
 AGGCTTACCA TTACGCTCTG AATATCACGA ACAATATCTT AAAGATGCTG GTTTTATCAT
 1020
 TTAANCTTGC AACGTCTTCA AGTTCGGTGA TGAANCTCAA ATCCATACAC ATATTGTGTT
 1080
 ATTCTCAANT CGGGCAAATC AATCAATGCT ATTCAAGATT TAGATTGCTT GATGTTATTC
 1140
 AATTGAACAC TCCGNGCCNT GGGGATTTAA TTAAGNTTGG AGGTTTTAT
 1189

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GGAGCATAAT AAAGAGCGTA TCTTAAACAT TAATTTTAAG TGTGATCCCA AAGTAATTTT
 60
 CGTGATTCAT TGAAAATTGT TCCGAAAGNA CCGTTGTTCA TCCAAGACAA TATTACCTT
 120
 AACAATATTG ATTTGGGGTT ACCTGGAACG ATGTTATTAA GTTTGGTTAG CTGACAAAAA
 180
 TAGTCGTTAC CGCCATCGCA GGACCCAATG CCGATTGTAA TGGTTAGCAT TATTAAATCA
 240
 ATGATGCATC CAAAAAATGG AATATATAGA TGCAAGTCAT ATTGTGATTG CGTTGTTAAT
 300
 CATCCTTGTTG ATAATCACAT TGTTTATCTT ATTATTCATT GAATTAGTAG AAGTGAGAAT
 360
 ACCATATATC GATTTAATGA ACGTTTCCGC AACAAATATG AAATCTTATT TATCTTGGAA
 420
 AGTTAACCCCT GCAGGCAGTA TTAAGTTAAT GATGAGTATT TCAGCATTTG TTTTCTTGAA
 480
 AAGTGGCATT CATTTTATTT TATCTATGTT TAATAAAAGC ATATCAGATG ACATGCCAAT
 540
 GCTGACATTT GATAGTCCAG TAGGTATTTT AGTATATTTA GTGATTCAAA TGTTATTGGG
 600
 TTATTTTSTA TCGAGATTTT TAATCAATAC TAAACAAAAA TCCAAAGATT TCTTAAAGAG
 660
 TGGCAATTAT TTTTCAGGAG TTAAACCTGG TAAGGATACA GAACGTTATT TAAATTATCA
 720
 AGCAAGACGC GTATGTTGGT TTGGATCGGC ATTAGTTACA GTCATTATTG GTATACCGCT
 780
 TTATTTTACA TTGTTTGTAC CGCATTTATC TACTGAAATT TATTTCTCAG TACAACGTAT
 840

TGTATTAGTT TACATCAGTA TTAATATTGC AGAAACAATT CGTACATATT TATATTTTGA
 900
 TAAATATAAG CCATTTTAA ACCAGTATTG GTAAGGAGGT AATTATGAAA TACTTTATTC
 960
 CAGCTTGGTA CGATGACCAA CGATGGTGGC AAGACACGAC TGTGCCGTAT TATCAACTAC
 1020
 AAAATAAGAC GGAATTTGAC GATATGATTA GTTTAATGGG AATGCACCTT GAAAATGACT
 1080
 TAGATTATCA ACTGATTGTT CTCAATCATG CACCAAATTT AAGAACATTT TTACATCGAT
 1140
 ATGACTTATA TGAAACAAAG TATTCGTCTG TGTTTGATGA AATTCAAGGA TTCAGTCACC
 1200
 ATGCGCCACA AGCGATTAAT TATCATCACT TAAAATGGNC GGATGATGTT GGAGTNTGGG
 1260
 TACACGCCCG NATTTATTAA AAATGTGTGA CGAGTGAACA GACCTATACA NATATTTATT
 1320
 TNAGNCAAGA AGGGTATTCA NTTGGGTTTG NAGANTGATT NGAAAGAGAT CAAGTNACAA
 1380
 CGGCGTTATA TTTTGGATGA CAGAGGTTAT TTATCAGCGA TACGTTATTT TGATGATCAG
 1440
 GGAGAGGCTT CTTACCAACA ATATTTAACG GATTAATGGA GATTGTGTAA CTTCATGGAA
 1500
 GATTGGANAA ATGGCAGGAG TCACTGTATC NANAAGGATA TTCAACATCA CTATCAACAA
 1560
 ACAGAAATATA ACAATATGGC TCAACTAATT GGAAGAAAAA TTTCAAGCAA TGATTGCACA
 1620
 ACAATACAT GAAGATGATC ATGTGATTGT GGCTTCAGAT GCTAGGCACA ATCGACAAAT
 1680
 AGCCAATCAT ATTCCAGCGA AATTGTAAAG TTATTCATTT TTTAAAAATA GAAATGAANC
 1740
 TGTGTCAGAT GAGGAATATC AATCTATCGT AAAGAATGCC CATTTAATTG TTGATAGTGT
 1800
 GCAACTAGAA CGTGATTTAA TTAGTCATCA AGAGAAGTAT CAGCGGGAGA ATACAATGAT
 1860
 TCGAATCACA CCATTTGAAA CGAGACAATC ACCTAATATA AGTAGTCAAT TGATGGAAAC
 1920
 ATTTATAGGT GTATGGATAG ATGGTATGAG TGACGCTGAT TTGCAACAAA TGATGCAACG
 1980
 ACTTGTGGAT TATATCGCAC AGGAAGATTA TTACCGTTTA ATTTTATTAT CGCGCCATCA
 2040
 AAATGACATA CCGATGTGGC TTCGTGAATG TATTACGTCG GTAAATGAGG AATACCAAGC
 2100
 TAAACAGAAT GCGGATGTTA ATGTTTCAGC ATTAATGACA CCTGAAGATC AAGATGACAT
 2160
 CATTGCTGTT AAGACGATAC ATGCTGAACA TGATGTTGTA GAAGCATTGC GGACGTTGCG
 2220
 ACTTGTGATA GATATGTCAA AAGAACCTGA TTTGTATTTA CAAATTAGTG CAATTAGCGC
 2280
 TGGGATTCCA CAAATTAATG GTCAACAAAC AGATTACGTC TCTGATTATG ACAATGGCCG
 2340
 TATTATAAAT ACAGCTGGAT GAATTAGATG ATGCGTTAAA TTATTATTTA TTTTATTTGA
 2400
 AAAATTGGAA TTATGCGTAC GCCTATTCTT TAAAATTAAT AGATGCATAT GCTTCTAAGA
 2460
 ATATTATTAA TCAGCTCGAT GAGTTAATAG AAGGTGAAAA TGATGCCACG TAAATTTAGA
 2520
 GTTTTGCAA TTGGAGGAGA CGATTTAGAA CCTATTTTTC AACACAAAAA AGGTGTGAGT
 2580
 TGGGATTACT TCGATATTGG ATTGTTTGAA TTTGATAGTG GTTATGTAGA GGCTATTGAA
 2640
 GCGATTGTTG AAGCAGAAGG GCGCTTTGAT TTTATCTATA TTCAAGCACC ATACTCGGAG

2700
 ACATTAACGA ATTTATTACA AATGATAAGC GAACCATACA ATACGTATGT TGATGAATCA
 2760
 TTTTGGTCAG TTGAATATGA ACAAGACGAA AATTGTCCAA AAATACGTTG TTCAACCAAT
 2820
 TACATTACCG GAATATTGGA AGGAACGTAA TAATNAATTA GAGGCAGGNT AGCTTCTCAA
 2880
 GGACAAGGAT TGGAGATAAA GTTTCCCCTA AGTTAGCACT TGTGCATCCG AATTTTAAAG
 2940
 GAGATGTCGA ATACCCAAGG TAATTCAAGA GCTCACGTTG AGTGGAGAAT TTGGAAAAGA
 3000
 ATTTAAACCT ATCGCATCTT GNCAAAATAA TCTCGTTTAC GATAAAGATA AAGTCATTCA
 3060
 NATATGGCCA GAATTTGATA TTGATGGTGC GGTGAGTTG CAATATACAT TTAGATTGAT
 3120
 TCAGACTGGC GCTGATGGTG CATTAAATTGA ACAAATCATA TTAAGTATG ATATGTTAGA
 3180
 CAGTCCTTTA GAGATACCTG CGAAACCATT TGATGCTTAT ATAAGTGTA CTGTTAAGGC
 3240
 GCGTGGGAAC GGGACGGTAC ATTTAGGACC TAAACACACA CGATGGTCCA GANTAGANAN
 3300
 GGNTCAATTT TTACNTGGTG GGAATCGTTT CGAAGATANN CNCCGNCNGG AATTTAATTA
 3360
 TTAATCCNC CCTGGTGATA TGANACCCCC ACTAAACGTA AATTTTAGTG GTTATCGANC
 3420
 ACCGGAAGGT TTCGAAGGAT ATTATATGAT GANACGTATG AATGCNCCGT TTTTACTTAT
 3480
 CGCCGATCCT CGTGTTGANG GTGGTAGCTT TTATATCGGT TCATCTGAAT ATGAACAACG
 3540
 TGATTATCAA TGTTATTGAC GAGACAATAT TCATGCTGTA AATCCAACAT CAGGTGCAGC
 3600
 TGGTAAGTAT CAATTCTTAC AATCAACTTG GGATTGAGTA GCACCTGCTA AATATNAAGG
 3660
 TGTATACCA GCAAATGCTC CTGGAAGTGT TCAAGATGCC GCAGCAGTAA AATTATATAA
 3720
 CACTGGTGGC GCTGGACATT GGGTTACTGC ATAAGCCATT TATGCATAGC TAATCAATAG
 3780
 TTATATAAGT AACTTTTAGA TCGGAATATA TCGGG
 3815

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2848 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

GGCNCGAGAC GCTTAATTAT GGAACNCCAA GATGCNATTG GACNCGGTTA TAACATTGGN
 60
 ACAGGCACTT TTAATAATTT ATTAGAGGTT TATCGTATTA TTGGTGAATT AAATATGGNA
 120
 AATCCAATCG AGCNTTGAAT TTAAAGGAAG CACGAAAAGG AGATATTAAC CATTCTTATT
 180
 GNAGATATCT CTAACCTAAA GGCATTAGGA TTTTGTGCTC CTAAAAAATA CAGTAGAAAC
 240
 AGGTTTAAAG GATTACTTTA ATTTTGAGGT AGATAATATT GAAGAAGTTA CAGCTAAAGA

300
 AGTGGAAATG TCGTGAAAAT GACATTGAAG CTGTCCATAA TAATAAGGGT TATGCCTATC
 360
 AAAGAAAATT AGATGCACTC GAAGAAGTGA GAAAAGGCTA TTACCCAATT AAACGTGCGA
 420
 TTGACTTAGT ATTAAGTATC GTTTTATTAT TTTTAACATT TCCGATTATG TTCATATTCTG
 480
 CCATTGCTAT CGTCATAGAT TCGCCAGGAA ACCCTATTTA TAGTCAGGTT AGAGTTGGGA
 540
 AGATGGGTAA ATTAATTAAA ATATACAAAT TACGTTTCGAT GTGTAAAAAC GCAGAGAAAA
 600
 ATGGTGCGCA ATGGGCTGAT AAAGATGATG ATCGTATAAC AAATGTCGGG AAGTTTATTC
 660
 GTAAAACACG CATTGATGAA TTACCACACC TAATTAATGT TGTTAAAGGG GAAATGAGTT
 720
 TTATTGGACC ACGCCCGGAA CGTCCGGAAT TTGTAGAATT ATTTAGTTCA GAAGTGATAG
 780
 GTTTCGAGCA AAGATGTCTT GTTACACCAG GGTAAACAGG ACTTGCGCAA ATTCAAGGTG
 840
 GATATGACTT AACACCGCAA CACAACTGA AATATGACAT GAAATATATA CATAAAGGTA
 900
 GTTTAATGAT GGAACATAT ATATCAATTA GAACATTGAT GGTTGTTATT ACAGGGGAAG
 960
 GCTCAAGGTA GTCTTAATTT ACTTAATAAG TTCAAATAAA AGTTATATTT TAAAGATTGT
 1020
 GACCAATNGT TACAGTNTAA CGAGGANTCC CTTGNGACNG TATCAAATGG CATTAAAGAA
 1080
 ATATGTNCCA TCNTTTGATT TGCNTGGCCA ATAAATACTA TTCATCTTGA TGAGATAAGC
 1140
 CATGTTAAGA AATTGAAAGT ATAGCATTAA NGGGGTTTGT AACAGTTGAA AATTATATAT
 1200
 TGTATTACTA AAGCAGACAA TGGTGGTGCA CAAAACACAT CTCATTCAAC TCGCCAACCA
 1260
 TTTTTCGTA CACCATGATG TTTATGTCAT TGTAGGCAAT CATGGACCAA TGATTGAACA
 1320
 NCTAGATGCA AGAGTTAATG TAATTATTCT CGAACATTTA GTAGGTCCAA TTGACTTTAA
 1380
 ACAAGATATT TTAGCTGTCA AAGTGTTAGC ACAGTTATTC TCGAAAATTA AGCCTGATGT
 1440
 TATCCATTTA CATTCTTCCA AAGCTGGAAC GGTCGGACGA ATTGCGAAGT TCATTTTCGA
 1500
 ATCGAAAGAC ACACGTGTAG TTTTACTGTC GCATGGATGG GCTTTTACAG AGGGTGTTAA
 1560
 ACCAGCTAAA AAATTTCTAT ATCTAGTTAT CGAAAAATTA ATGTCATGTA TTACAGATAG
 1620
 CATTATTTGT GTTTCAGATT TCGATAAACA GTTAGCGTTA AAATATCGAT TTAATCGATT
 1680
 GAAATTAACC ACAATACATA ATGGTATTGC AGATGTTCCC GCTGTTAANC AAACGCTAAA
 1740
 AAGCCAATCA CATAACAATA TTGGCGAAGT AGTTGGANTG TTGCCTAATA AACAAGATTT
 1800
 ACAGATTAAT GCCCCGACAA AGCATCAATT TGTTATGATT GCAAGATTTG CTTATCCAAA
 1860
 ATTGCCNCAA AATCTAATCG CGGCAATAGA GATATTGAAA TTACATAACA GTAATCATGC
 1920
 GCATTTTACA TTTATAGGCG ATGGACCTAC ATTAAATGAT TGTCAGCCAC CAAGTTGTAC
 1980
 AAGCTGGGTT AAGAAAATGA TGTCACATTT TTGGGCAATG TCATTAATGC GAGTCATTTA
 2040
 TTATCACAAT ACGATACGTT TATTTTAATA AGTAAGCATG AAGGTTTGCC AATTAGCATT
 2100

ATAGAAGCTA TGCCTACAGG TTTGCCTGTT ATAGCCAGTC ATGTTGGCGG TATTTTCAGAA
 2160
 TTAGTAGCTG ATAATGGTAT ATGTATGATG AACACCCAAC CCGAAACTAT TGCTAAAGTC
 2220
 CTGGAAAAAT ATTTAATAGA CAGTGATTAC ATCAAAATGA GTAATCAATC TAGAAAACGT
 2280
 TATTTAGAAT GTTTTACTGA GGAGAAAAATG ATTAAAGAAG TGAAGACGT TTATAATGGA
 2340
 AAATCAACAC AATAGTAAAT TACTAACATT GTTACTTATC GGTTTAGCGG TTTTATTCA
 2400
 GCAATCTTCG GTTATTGCCG GTGTGAATGT TTCTATAGCT GACTTTATCA CATTACTAAT
 2460
 ATTAGTTTAT TTAGTGT TCGCTAACCA TTTATTAAAG GCAATCATT TTTTACAGTT
 2520
 TTTCATTATT TTGTATACAT ATCGTATGAT TATTACGCTT TGTTTGCTAT TTTTGTATGA
 2580
 TTTGATATTT ATTACGGTTA AGGAAGTTCT TGCATCTACA GNTAAATATG CATTTGTAGT
 2640
 CATTTATTTT TATTTAGGGA TGATCATCTT TAAGTTAGGT AATAGCAAAA AAGTGATCGT
 2700
 TACCTCTTAT ATTATAAGCA GTGTGACTAT AGGTCTATTT TGTATTATAG CTGGTTTGAA
 2760
 CAAGTCCCCT TTACTAATGA AATCGTTATA TTTTGATGAA ATACGTTCAA AAGGATTAAG
 2820
 GAATGACCCT AACTATTTTCG CTCGTGCC
 2848

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

CCCCAGAGAA ATACANTTGT TGGTAGAAGA ACCCCCAACC CACAAGNTGG GGACCCTTCA
 60
 TTTCCAACCN TATGGCGGAG GGTAAAGTA AATTCTTGAA GCTTTGGTTG CCCNCAAATA
 120
 ATATGATATT TCCGAAATGG GCCGGAGCCG TATCCAACAA TTAAAAATCT GCCGGAGGTA
 180
 TTAAAGCATT ACTTAACCGC TCCGATTAAG ATGNNATTGA AGGAGAGATT AATATGGTAG
 240
 AATCAATGCT AACTTTTATG CTTGGGCCAT TAAGACAAAT CNCTGATTTT TATATGGAAC
 300
 ATTTACTCGT AAGTAATTCC ATCGTCATTG CAGGTATTTT TGCGACAGGT ATTTTAAAAA
 360
 AGAAAAAAGT TGTGAATTAA ATCANATTTG AGGTGATTTA CAAGTGAAAG CATTGAAATT
 420
 ATATGGCGTA GAAGATTTAC GGTATGAGGA TAATGAAAAG CCAGTCATTG AAAGTGCGAA
 480
 TGACGTTATT GTTAAAGTAC GAGCGACTGG CATATGTGGT TCAGACACGT CACGAAACAN
 540
 AAANATGGGG CCATACATTA AAGGTATGCC ATTTGGTCAT GAATTTTCAG GTGTAGTAGA
 600
 TGCCATTGGA AGTGATGTTA CGCATGTTAA TGTGGGCGAC AAAGTGACAG GTTGCCAGC
 660

AATACCTTGT TATCAATGCG AGTAGTGTTT GAAAGGTGAA TATGCACGAT GTGAAAAAGT
 720
 TATTCGTCAT TTGNCTCAAT ATGAACCTTG GATCGTTCNG CGGAATATGT CAAATTCCCA
 780
 CCCCCAAAATG TTTTNAAGGG TTCCAAGCCA ATGTTGATTA CCATTGAANC AACCAATGGT
 840
 TTGAGCCATC AGCCCGTTGT TGC GCATGGG TTTTATAAAT CCGAATANAC AACCTGGTAT
 900
 GACTGTTGCA GTAATGGGGT GTGGCAGTAT AGGTTTGTTA GCTATTCAAT GGGCACGAAT
 960
 ATTTGGTGCT GCACATATCA TCGCTATAGA TATAGATGCG CATAAACTAG ATATTGCAAC
 1020
 ATCATTGGGC GCACATCAAA CAATCAATTC AAAAGAAGAA AATCTTGAGA AATTCATCGA
 1080
 AAATCATTAC GCCAATCAAA TCGATTTAGC TATAGAATCA TCAGGTGCTA AAGTTACGAT
 1140
 TGGTCAAATA TTGACGCTAC CTAAAAAAGG TGGCGAGGTG GTATTACTCG GAATACCATA
 1200
 TGATGATATT GAGATTGATC GCGTTCATTT TGAAAAAATT CTGCGTAACG AGTTGACAGT
 1260
 ATGTGGCTCT TGGAACTGTT TGTCCAGTAA TTTTCCGGGC AAAGAGTGGA CGGCAACCTT
 1320
 ACATTATATG AAGACGAAAG ATATTAATGT AAAGCCTATT ATTTCTCATT TTTTACCGTT
 1380
 AAGAAAAAGG CCCGGAGACA TTTTGATAAA TTAGTTAATA AGAAAGACCG ATTTGATAAA
 1440
 GTCATGTTTA CGATTTATTA GTATGCACCT TTGAGGACGA AAACGCTGGT ATAGTTATAG
 1500
 CTATGAAAGT GCGAATGCCG TCTGGTCTAC AGATACTATC GAAATAATTC ATCTTCGAAT
 1560
 ATACGTTGAT AAATAGCCGG TTTACTTGTG TGAAATATGC TTGTGAATCG GTTGT TTTGTC
 1620
 ATTTTGTATA CTTAAAATGA GATGGCAATA TTTGATAATT TTTAAAGTGA AAATCAAGTA
 1680
 CAGCCACTTA ATAAGATAAA TTTATTATAA TATATGGTAA AATGATGGCA GTAATAATGA
 1740
 ATTTGAAAAA GAGTAAACAT TAATACCTTT AACAATTTAA TATCGTCAGA GTTAATGATT
 1800
 AACTGCATGG CAAAACAACT TAGAATGGTC AGTTACNNAA ATACATTTTT ATAAAAAATT
 1860
 ATCACACTAT TGTGACAACT ATCTTTGGAT TAATAAAAGA GGCAAGTGAG CAATAGGTTA
 1920
 GGCTTATGTG CGGGCATAGG TCAGTAATGT AGAAATGGAA ATGATGTAAT ACGTTAATTC
 1980
 GTTTGAATCT TTAAAAGTAT TGGATAAATC AGATAATCGC CTGTTATACG CATCAATCAA
 2040
 TGTTTTATAC ATAAATATGT CTGATATTTT TAAGTCGTTA TTTTGAATG GAATAAATGG
 2100
 AATCTTACCC CACGACCCTG TACTAAAATG CGTTTTTTRD CTNS
 2144

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2178 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

CAAATAACGG ACCCTTTNGT TAATATCCCA TTTTTTTGGC GGAGTATGGG ACCTTAGCAG
60
AGAAAATAGC CATAAGATAA GATTTCGCCC CANNCGTTGG AGCCCAACTT ACATTGTTTG
120
TAGAATTTCT TTTCGAAATT CTTTGTGTTG GGCCCCCACC CCAACTTGCA TCGTCTGNAG
180
AAATTGGGGG TCCAATTTCA CTGTGTTGGG NCCCCCTGAA CTAAATAGTA TGGAAATATA
240
TATATCTAAA TAATTAAAC GGNCAAATAG TTTAATATGG CAGTAACAAT TTTTATAATT
300
TAGATATTTT GATATAGACT AATGCTTAAA TTAAGCAACT TTTCTANNNA GGGAGTATGA
360
AAATGATTAG TACTTTGAAT GAAATTATGA AATGTATCGG AAGACCNCGA TACAATTATT
420
AATACACAAG ACATGTTAGA CCAGATCCAG ATGCATATGG TTCACAACTT GGTTTAAAAT
480
ACTATATTCA GCAGAAATTT CCGCAAAAGC AAGTATTTGC AGTGGGTGAA GCGGAATCAT
540
CATTAAGTTT TATTGGAGAG TTGGATAACA TTGATGATAA AACATATCAA GATGCGCTTG
600
TAATTGTATG TGATACTGCC AATGCTCCAC GAATTGACGA TGAACGATAT AGTACAGGTA
660
GTAAACTTAT TAAAATAGAT CATCATCCTG CAGTTGATCA GTATGGTGAT ATTAATTTAG
720
TTAATACGAA CGCGTCATCT ACAAGTGAAA TCATTTATGA TTTAATCTCA CATTTTAATG
780
ATGAAGCAAT TGTTAATAAA GGCACGAGCG AGTGTTTTAT ACCTTGGTAT CGTCGGTGAT
840
ACTGGGCGAT TCCTTTTTTAA CAATACCTCA GAACATACTA TGGAAATTGC TGGAAAGTTA
900
ATTGGGCATG ATATTGATCA TAATGCGCTA TTAAATAAAA TGATGGAGAA GGACCCAAAA
960
ATGTTGCCGT TTCAAGGTTA TGTTTTACAA CATTTCGAAC TTATGGATGA TGGATTCTGC
1020
CAAGTTAAAA TAACTGAAGA TGTATTGGAG CAATTCCGTA TTCAGCCAAA TGAAGCATCT
1080
CAGTTTGTTA ATACAATTGC TGACATCAAA GGTTTGAAAA TATGGGTGTT TCCAAGTTGT
1140
TGAGGGTAGT GAAATAAGAT GTCGCTTACG CTCTAAAGGG CAATTGATTA TTAATGATAT
1200
TGCGCAAGAT TTTGGTGGCG GTGCCCATCC GGAATGCGTC AGGAGTTTCA GTGAACAGCT
1260
GGGATGAATT TGAGCAACTT GCTACAGCTT TACGCACAAA ACTTAACTAA TAGAAAGGAG
1320
CCATTCAATC ATGGTGGCAT ATTTAAATAT TCATACGGCT TATGATTTGT TAAATTCAAG
1380
CTTAAAAATA GAAGATGCCG TAAGACTTGC TGTGTCTGAA AATGTTGATG CACTTGCCAT
1440
AACTGACACC AATGTATTGT ATGGTTTTCC TAAATTTTAT GATGCATGTA TAGCAAATAA
1500
CATTAACCG ATTTTTGGTA TGACAATATA TGTGACAAAT GGATTAAATA CAGTCGAAAC
1560
AGTTGTTCTA GCTAAAAATA ATGATGGATT AAAAGATTTG TATCAACTAT CATCGGAAAT
1620
AAAAATGAAA ACAATGGAAA ATGTTTCATT TGAAGTATTG CAACAATTTT CATCGAATTT
1680
GATTATCATT TTTAAAAATG TTGCAGACGA ACATCGTGAC ATTGTTCAAG TTTGTGATTC
1740
GCATGAAGAT ACGTATTTAG ATCATCAAAG TGTTTTAGTT CAGGGTATAA AGCACGTATG

1800
 GATTCAAAAT GTTTGTTACC AAACACGTCA AGATGCCGAT ACGATTTCTG CATTAGCAGC
 1860
 TATTAGAGAC AATGCAAAAT TAGACTTAAT TCATGATCAA GAAGATTTTG GTGCACATTT
 1920
 TTTAACTGAA AAGGAAATTA AACAAATTAGA TATTAACCAA GAATATTTAA CGCAGGTTGA
 1980
 TGTTATAGCT CAAAAGTGTA ATGCAGAATT AAAATATCAT CAATCTCTAC TTCCTCAATA
 2040
 TCAGACAACT AACGATGAAT CAGCTAAAAA ATATTTGGTG GCGTGTCTTA GTTACACAAA
 2100
 TTGAAAAAAT TAGAACTTAA TTATGACGTC TATTTAGAGC GATGGAATAT GAGTATTAAG
 2160
 TTATTACTAA TATGGGTT
 2178

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

TCATTTTTTTT GATTGAGCCA AAAGGAGTCC CCCCTGTGAG CGGAATATTT AATTTATTGA
 60
 GCTATTTAAT ATTAAACGTA CGCTTAACCC CCCTANAGTG ATATCGTTTC TAGCGTTGTC
 120
 ATTATCATTA AGCGAAACAT TTTAAAGACA AATACACACT GTACGATCAC CAAACTGCAT
 180
 GTCGAACAAT GTAACATTTG GATTTCGATAT TTAAAATTGC TTGTGATGAT AAACTTTCTC
 240
 ATTTAGAAAA CGCTTCCACG TACATTCAAA AAAATAACTT TGTTAACCAT ATTGTAACAT
 300
 TATTTTCATAT ATTTTGGGGC ATGAGAATGA TTCTCACGCC CAGTAATTTA TTTATGCAAT
 360
 TGTTTCATGTA GGTTCCTTTC GACGTTTTCA GGAATACCTA TATTTTTAAA ATCTTCAAGT
 420
 GTAGCTCGTG CCTTCATTTT CTTGATTGAA CCGAATGAAC GCAATAATAA TGTTTTAACG
 480
 TTTGTTACCG ATACCATCTA TATCATCAAG TATTGATTTT AAGCCTGTCT TTTGACGTGT
 540
 TTGTCTATGA AATGTGATTG CGAATCTGTG AACCTCATCT TGGATACGGA TGCAACAAAT
 600
 AAAATGCCTG CCTATTTTTC TTCAGTGGAC AATTTCTCTG ACTAGCGCCA TAATAATAAT
 660
 TCAGATGTTT GGTGTTTATC ATTTTCTCTG AAACCTGCAA CAGGGATATC AAGACCTAAT
 720
 TCGTTTTGTA GCACATCAAT AACCCCGTTC ATATGTCCTT TACCACCATC GACTATTATT
 780
 AAATCAGGTA ATGGTAATCC TTCGTTTAAA ACGCGAGAAT ATCGTCGTCT TACTACTTCT
 840
 CTCATTGATT TGTAATCATC TGGACCTTTA ACCGTTTTGA TTTTATACTT TCTATAATTT
 900
 TTCTTATCTG GTTTACCGTC GACAAATGTA ACCATTGCTG AACTGGATC CACACCTTGA
 960
 ATATTAGAAT TATCGAATGC TTCAATTCTA ATTGGTGTTT GAATTCCCAT TTGTGTTCCA

1020
 AGTTCTTCAA TAGCTTTAAT CGTTCTTGAC TCATCACGTG ATATTAATTC AAATTTATTA
 1080
 TTTAAGGATA CTTTAGCGTT ATGTGCAGCT AGGTCAACCA TATCTTTTTT GGGACCTCGC
 1140
 GCGGGTTGAA CGATTTTAGT GTCCACAACA GATTGAATCA TTTCTTTATC CAAATTACGT
 1200
 GGTACATGAA CTTCCTTAGG TAAAATATGT TGGTTTAAGC TATAAAATTG TCCAATAAAT
 1260
 GTATAAAATT CTTCTTCTTC TGTTTGGTGT AATGGAATCA TCGNGTATC TCGCTTTATC
 1320
 ATATTACCTT GTCGGATTAA AGAAACTTG GATACACATC CATCCTTTAT CAACACAATA
 1380
 ACCAAAGACA TCACGAATCG GNTTATCTGA TGACATAATT TNGGGTGGGT GGGCAAGATT
 1440
 TGGATATTGT TGGATTAAAT CTCTATATTC TTNAGCCGCN CAAAATCAAG TGATTCACTT
 1500
 GGAGGNCACA TNCGCTCTTC TAANCTTT
 1528

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2933 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

AGGTTGATAC ATATGTCTTG TAAATACATG TGTCATTGCT TGACCAATTG CAGCAATCTG
 60
 GACCCAGGAT NGGTGCCTAC CCAGTTATCT CCAAATTTCA CATTTCTGCG TAATCTGGTG
 120
 CTACTTGAAA TGACTTTTGT ACCTTAATAG CGGACTTCTG TCATAAAATG TGCATCCGGA
 180
 GTACGTGTTA AAGGTACATT AGAGCCCCAC ATAATAATGT ATGATGCGTT ATACCAGTCA
 240
 CTTGATTCAG GCACATCTGT TTGCTCTCCC CAAATTTGTG GAGAGGCAGG TGGTAAATCT
 300
 GCATACCAGT CATAAAACT AAGCATTTCA CCACCAAGCA AATTGATGAA TCGAGCACCT
 360
 GCTGCATAAC TAATCATTGA CATCGCTGGA ATAGGTGTAA ATCCTGCGAT TCGATCTGGA
 420
 CCATATTTTT TTATTGTATA CAGTAATTGT GCTGCGATTA TCTCTGTAAC GTCTTTCCAA
 480
 TTTGAACGCA CGTGCCCTCC CATACTCGG GCTTGCTTAT ATTGTTTGGC TTTGTCTTCA
 540
 TTTTCAACAA TAGACGCCCA TGCAGCAACG CGATTACCAT AGTTTTCTTC TAATGCTTCA
 600
 GTCCATAAAT CCCAGAGTTT TCCACGAATA TATGGATATT TGATTGGAAG CGGACTGTAT
 660
 TCATACCAAG AGAATGACGC ACCTCGTGGA CATCCTCTCG GTTCATATTC AGGCATATCC
 720
 GGACCACAAC TTGGATAGTC AGTTTGTGTA TTTTCCCAGG TAATCACACC ATTTTTCACA
 780
 AATACTTTCC AAGAACATGA GCCTGTACAG TTAACACCAT GTGTTGTTCT TACTTCTTTA
 840
 TCGTGGCTCC AACGTTCTCT GTACATTTTT TCCCATTCTC TACTTTTACT TTCTAGGATC

900
 GACCAATTCC CATTAAATTT TCTGTTGGCT TAAAGAATTC AATCCAAATT TTCCCATATT
 960
 TATATCCTCC TACGTATAAA AAATACGATG TGTAGATGTC GTGTTNTTAA ATACTTTAAA
 1020
 ATGCCCAAGA CTATTGCTTT AATTAGATTG TACATTTTTT CACAAATATA AAATATTAGG
 1080
 GAATCACCTA ATTACTTAAG GAATTTCCCT ATCAATAACG GGATTTTCATT GAAATAATAC
 1140
 ACAATCATGT ATGGTCGTGC TTATTGCCAA TCTAAATCGT TCAAATTTGC CACAACGACA
 1200
 AATAAGGCTT CAACACGAAT ATATTCTCTC GGTTGAAACC TTACTTATTC ATTTATTTTT
 1260
 TATAAATTAG TGACATAACA CTGTATTAGC ATCTGCACGA TCGGTTGAAA TATATGTTAC
 1320
 ATTTTCTTGC TGCTTAATAA ATGCATCATA GTAATCATAT TGCCGACCGG AATGATATGT
 1380
 CCCATTGAT GTATCATTTG GGTTTAGCAA ACAGCCATAA CCTTCGTCAT ATAAATGTTC
 1440
 ACAGAGCATA AGGGCGTCAT GTCTAGAACC ACTTACTACA TAAATTGCT GAGTCGGATT
 1500
 AGAAGTTGTT GAGACATTTT CAGTATAACC CACTACTTCG CCTATAATAC ATATACCTGG
 1560
 TTTGCGCTCA ATTGCGTAAT GCTCCAGTTT CCCAACAATA TTACTTAAAC GCCCCTTAAC
 1620
 AACAACTCG TTAAACACG ATGCTTGAAA GACAATCGCT ATCGGATAAT CAATATCTGT
 1680
 GTACTGTTGT ATCTGGGCGA TAATTTTCCC TAAACGTTTA ACTCCCATAT ATATCGCCAA
 1740
 CGTACCACCA TTTACTAAAG NGTTGACATC TACGTCATTT TCTTCTGAAT CTNTNAAGTG
 1800
 ACCTGTAGAA AATGTCNCAC TCTTAGCAAC AGCACGCNTC GNTAATCCTG TTTGCATCGT
 1860
 AGCAGCTGCA GCACTCGCAA GATGTCACAC CAGGTACAAT GTCANACGCA ATAGTAAAAG
 1920
 TTGTTTAGTG TGTCAACTTC TTCTTGAAC CGNCCAAATA TTGCTGGGTC GCCACCTTTA
 1980
 ACCCTCACCA ACCTTGTTAT ATCGACGTGC TGCTTCCACG ATACATTCAT TTATTTTTTC
 2040
 TTGCTGAATG TGTTTTGCAT ACGGCTTTTT ACCAACATCG ATAATTTAG TAGTCAAATT
 2100
 CGCATATTGT AAAATTAACG GATTCATAA TCGATCATAT AGTATAACAT CCGCTTCACG
 2160
 TATTAAACGC TCAGCCTTTT TAGTCAAATA ATTCCGATTA CCTGGTCCCG CACCTATCAA
 2220
 GTAAACCTTG CCATATTTAT CTACAGACAT ATATATACGT TCCCGTCTGT AACTTCTACC
 2280
 TCATAAACAT CTACACAACC TTCATCAGGT TCTTGTACAA TCCCAGTATT TAAATCAATC
 2340
 TTTTGATCAT GAAGTGGACA GAATACATAT TCACCACTCA CTGTTCCCTC TGACAATGGT
 2400
 CCTTGTTTAT GCGGACAAAT ATTGTGGAAT CGCGTGANTT GTACCACTTT CAGATAAAAA
 2460
 CCAATCCTAC CTCTTTGCCT TTGNCAATAA CCTTTTTTCC AATTAGGGGT GTTAATTCAT
 2520
 CTATAGTTGT CACTTTAATT TTTTCTTTTG TTTCCATGTA TTACACCTTC TCCACTTCAA
 2580
 AAATTTTACG TGCTTGCGCA TTGCTAGNTA TTGCTTCCCA AGGTTGAGCT TCGACTGCTT
 2640
 TTTTAGCATC CATAATGCGT TCAAATAGTT CATTTTGTCT TTCTGGGTCA AGTAAGACTT
 2700

CTTTTACATT TTCAAATCCA AGTCTTCTTA ACCATGGCGC TGTTCTTTCA GCATATATAC
2760
CTGTTTCGCG ATATAGTGCA TCAAAGCACC ACATAATGTG NTTACTTCAT CTTCTGTTTC
2820
TACAGTTGTT AAAAATTCAG CTTTTTCGAC TTCTGTACCA CCATTACCAC CGATATAGAT
2880
TTGGAATCCA TTTTCAACTG AGATAATACC AAAATCTTTA ACACCTGATT CAG
2933

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1866 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

TAAAGTTCNT TCCCCTGCTN AATGTCCAAN TTTCCCCCAT AGCAACTTTC AAATATTTTT
60
CATGACTTGC TTTAGCCCCA TCAAGTTCTT TACCTGAAGG TATATTAAAT TGATTTGTTG
120
AAAAGTTCCA AAAATTCTGC GCTTGGGTAA GTCCTTGTGG GACAATTTTT TGAAATCCTC
180
CAACTTCTTA AATATTTCTG GTGATTTTTG ATTAAAACTC ACGTAATTTA CGTAGTTTCT
240
CTTCTAATTC ATGTTTTTTG TTGACCTAAT GTTTGTATTA TTTGTTGGTT CGATGAAATG
300
GCTTGCTGAT TATCGGAAGC ATGCTTTTTT AAATTGTTAG TTAAATTTTC ATATCGCGTA
360
ATTTGTTGAC TTAATGATCT GATATCTTCT TCAAGCTCTG ATTCTTTTAA AGATATGCTA
420
TCAACCTCAC TCGTATAACG TGACACAAAA TTATCGCAAG CTTGCTTCGT TAAATCACTC
480
AATGTTTTCA TACTTGTTGA TAATGGAATT AACACCGTAC TAAAAAATTG CTTAGCTGAC
540
GTATACGCTT TCCCTTTAAG CGCATCATCA TTGATAAATT GAGTAATTGC TTTTCCAAC
600
GCATCATAAT TTGAATTCAT TGTTTGACTC AAATTCCCCA CACTTGAAGC TTGGTTTCGA
660
GATCTGTCTA AATACATGTC AATACTCATC GGCATGCTCC TTTTCAAAA ATATATGATT
720
TTCAAACAT TTAATAATCAA ATGCTTTTTA CATCTACAAA GTTGTAATAA TTTAAACTC
780
GGCGATGATT ATTTCTTATG TAAAGGAGTC TAGATGCAGG TAAATTGAGA TAACATGTCG
840
CCTTTTTTCT TATTTTAGCA TATGGATATA ATGGTGTCTT TGTATATTCG CAATTAATCA
900
ATAAAAAATTA TCTTTCAATA TTTTAATTTT ATTGCGACAA CATCCTTAAC ATTAAATATA
960
TTAATATCTC AAAATATATT CACTATTAAA ATATGTCATC AGTTGTAAA AGTATTTCT
1020
CATCATGCGA AATATCAAAA CGTATCTAAA ATACGAATAG TTTATCAATC ACACAACATC
1080
ATCATCCAAA ATTTNATTGC TCTCATNTNC AATATTCATT TCATATCTAT CAGTTCATAC
1140
ATAATTAAAA TTTCAATTGT GCAATCTCAC CGTTAATGCA TCAACTTTCA AACAATAAAT
1200

CATCACAATA ACCACACCTA ATTCAACACT TTTCAAACAT AAGTATTGAC ACATTGAGCA
 1260
 AAATGATTTT TAATTGTAAC TAATACAGTT ACAATTATGA GGTGAGAAAC ATTGAATTTA
 1320
 GAATTTAACA TTGCCGTGCA TGTATTAGCT TTTTAACTA AGCATCATTC AGAAAAATTC
 1380
 AATAGTAGTT CATTAGCAGA ATTAACCTGT TTANATCCTG TTCAATTACG ACGCGTGACG
 1440
 ACTCAACTTG TCGATTTAAN AATGATTGAC ACAATACGAG GTAAAGATGG CGGTTATTTA
 1500
 GCAATGATC AAAGTGCTGA TGTCTCTCTA GCAACATTAT ATAAACATTT TGTCTTAGAG
 1560
 AAAGAACAAC ACACACGTCT ATTTACTTGG CGACGAAGGC AGTCACTGTC AAATTGCTCG
 1620
 TAATATTGCA ACTACCATGT CACATTATCA GCAAGACGAA CAGAATATCA TTATTAATTT
 1680
 TTATAATGAA AAAACAATCA AAGATGTCAT TGAAGACATT CAAAAGGAGG ATTTATGTCA
 1740
 TGAAAACATA TGATTTAATT GTAATAGGAT TTGGGNAAGC TGGTAAAACT TTAGCGAAAT
 1800
 ATGCTGCATC AACAGGTCAA CACGTTTCGA GGTATCGAAC AATCTTCCAA AATGTATGGN
 1860
 GGCAC
 1866

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

ACAATGCCTC CAAGAGGTAC ANCCGATAAC TGTCTCACAA AACTAAATAA ATTTAACTCT
 60
 GTGTCCTCTT CCCATCCGTT CACTTTAATA TCTTCTCCAT AAGCATCAAC GGAAAGATAA
 120
 AANCCGGACC TGGAAATGTA TGTGCCATCT CTTTAACCCA ATCAGTATCT TGAATGCCTT
 180
 TCGNTCCCAA CCTATGCAAT AATTAATCCC TGCGGCAAAG TAGTCCATGA TTTGGTGACT
 240
 TCGTACGAAT GCCACCACCT ACTTCAATAT CTTTGGTTGT TAATCTCCTC AATGACTTAA
 300
 TATAATCAAA CTCTCGGGCA TACTGTGCCT TAGCACCTAT CAAGTCGACG ATATGAATAC
 360
 GATTACACA TTCAAATTGA CTATAGTAAG CAATACTTCC TTCAGCCGAA CGCGACATTT
 420
 TTTCTTCAC TATCATATTTA CCCTCTGTTA ACCTCACACT TGTTGACCCA ATCAAATCAA
 480
 TCGCTGGCCA TAATTCAATC ATTTATAAAT CCCCTTGTA TTGCCTGACG CAAAATTTGT
 540
 AACCCATATG TACCGCTTTT TTCAGGATGG AATTGAATAC CAATATAATT GTTAAATTGA
 600
 ACAATTGCCG GAATATCAGC CCCATACTGC GCATATGCAA TGACATTTTC TGACATCGGC
 660
 GCTTGTAAG AATGTACGAA GTAAACATCT TGATTTAACA TAGGATGCTT ACTCACTAAA
 720

TTATTCCAAC CTAAGTGCGG CACTGGGTAT TCTGTTGGGA TACGCGAAAT ATTCCTGGG
 780
 ATAAACCCTA ATCCAGATGC ATCGCCTTCA TCACTATGCT CATACTTAA TTGCATGCCT
 840
 AAACAAATAC CAATCATCTT CTTATCAGTA TTCTTAGCCA ATATTGCATT GAGATTTAAT
 900
 CGTTTTATCT CTGACATCGC ATCTTTAAAA TGGCCGACAC CGGGCAATAT GATTGTTTCT
 960
 GCTTGATCGA TTATTTTTGA GGTATTTGAG ACAACCACCT CATACCCTAA ATGTTCAATA
 1020
 GCGCGTTTTA CATTACTAAT ATTCCCTAAT CCATAATCAA CGATGACAAT CATTCAATCA
 1080
 CACCTTTTCA TGACGGCACA CGCTGATCAT CAGTTGCAGT TAGCGCTATG CCTAATGCAC
 1140
 GGGAAAACGC TTTGAATATA GCTTCAATTT CATGGTGTGT ATTACCTCCA CGAATTAAAT
 1200
 CAATATGCGT TGTTAATCTT GCATTGATTA CGACCGCTCT AAAAAATTCT TCTACTAACT
 1260
 CCGTATCAA CGTACCAACT TTTTCTTTAC TTAATGATGC ATTGAATGAT AGGTATGGGC
 1320
 GCCCACTTAT ATCCACAACG ACACGTGCTA ATGTTTCATC CATTGGAATG TACATCGTTC
 1380
 CATAACGAAC GAAATGCTTT TTATCTTTAA TCATTTCAAG TAACAATTGG CCAATGACAA
 1440
 TGCCGATATC TTCAGTTACA TGGTGATCAT CTACGTCAAT ATCACCTTGT GCCTCAATGT
 1500
 TTAATGACAG ACCGCTATGA AATGTAAACA ATGTTAACAT ATGATTTAAA AAGCCCACAC
 1560
 CTGTATTAAT ATGCGATGGT GACTGGTCAT CTGATATTGA AATATTTAGT TGGGGTTTCA
 1620
 GCTGTGTTTC GGTGGTTGTG AATAAATCAT ATTGTGCGCT CCANTCTTTA ACAATNTCTT
 1680
 CCTAATTGCT TTAAGTGC GAATGCTTGA ATTGAGTATC TTACATAGCC CTTTCATCAAC
 1740
 CGGCTCAACA TAAAAGCGAG GTTTAAATCC TTGTTCAAAT ACGTATTGTC CTAATTGGTG
 1800
 CGCTGCTGAA CCTTTAGTAA GTACAAAATT GGCATTTGAT GGAATACTG ACATTTTATC
 1860
 TGCAACATGT GTATCAAATA TTTGTTTTAA CTGCTCAGCT AACTGTCGTT GCATCGTTAA
 1920
 AAATACTCTT GTCTCTTCTC TATGTCTAAA AATATAAGTC GCAATATTTA GCGTAAATAC
 1980
 ATTTAATGGA TATGGATGTT CTATTTTTTG AATATGCTTT ATCGTTCCAG CAGTACTAAT
 2040
 TAAGACACCT AATCTTAAGC CGGCAATTCC AAACGCCTTT GATAATGTAC GCATTCTTAA
 2100
 GATGTGTGGT GCCAGTTCCA CGTCATATGC CGTACCATAA TCTAAATATG CTTTCATCAAT
 2160
 GACAAAGTAT CCGTTTAAATG CTTTCATCTT ATCTGCAATA GCTGTTAAAA ATGCCGNATC
 2220
 AAATTGCTTG CCTGAAGGGT TATGTGGATT ACTCATAATA AAAAATGATG GNTGTNCTTC
 2280
 ATCGATTTTC GTTAAAATGG TTTCCAAATC AAACGTNAAA TCTGATCCNG CATCTTACAA
 2340
 ATGCAATTTT ACGATTTACT TGTGCCGCAT ATGCTTGATA CATAAAAAAA TCAGGATTTA
 2400
 GCGTTAATGC CGGACCTTCT GGCATGATCA GCATTAACCT TTGANTCANT TCATCAGATC
 2460
 CATTTCCTGC AATAANTTGT TCAGGCGATA ACCCGTAAAA CTTAGCATNA GCTTCCGTGA
 2520
 ATTGTTTATA TGCTGCATCA GGATATAAAT TATATGGCGT TGCATAATA ATAGACGTCA

2580
 TTGTTTTTTC ATCCAACGGC GTAACGGAC TTTCATTTTT ATCAATATAA ATCATTTCAA
 2640
 TTACACTCCC CTAAGACTGA CGTATTAAAA TAGACTGCTG GTGATTGTAT AATGCTTCAA
 2700
 CATGAGCAAT ATGTTGTGCT GAATCAGCAA TTTGTTCAAA CGTATCTTTT GATAAATGGA
 2760
 TGACCGTGTT CCGTGTTAAG AAATCATTGA CCGATAACCC ATTGGTAAAT CTAGCTGTTC
 2820
 TATTTGTAGG TAATACATGA CTTGGACCTG CAACGTAATC TCCTATGACC TCTGGCGAAT
 2880
 AATGTCCAAT AAACAATGCA CCCACATATT TCACTTNCNC AATATATGGN TGAGGATTTA
 2940
 CTGTGTGAAT CGACGCATGT TCAGGCGCGA TCGTGCCTTT CATGACATGG
 2990

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

GCATCGGTTA AATGGCGTCA TTCCAATTAC GGGCATCTTN AGGCATTTTG CTTTTCAAGT
 60
 GGCTAATTTA GCTTCACCGT TTAAGGCTAT TTTTAGCATC AGTCACTTGA GTTAATGCAC
 120
 GGAGTAATGT CATCTGGGTT AAGCGTTGGA TTTGTCGTTT GATTGATAAT ACCTTCCGCT
 180
 TGAGACACTG CATTTGTATA TGCTGTTTGC TTATCGACAT CAGCATCGTG GTAGTTCTCA
 240
 CTTGCTTTCA CAGTATCTTT ATTTGCAATA CTTGTTTCA AGTTACCCAT TGCTGTATTC
 300
 ACATTTTGTG CATTTTGTGTT TAGTTTGTCC AACCTGTAGC TAAAGCTTGT GCTTGATTGA
 360
 NTTGGTTTCG TAATGCATCA CGTTGTGGTG ATTTAAGTCA CGTNACGTAT CAAGATTTGC
 420
 TAAAGCATCT TGTTTCGCTT GCGCTAATTT TTCATCACCG TTTAATGCAT CTTTCGCTTG
 480
 ATTCATAGTT GTAACGTCTT TTGTTACTGT ATCAGGCGCC AATACAGGTG TTGGTGTGCC
 540
 ATTTGCGATT TGTTGCGCTT GGTTAGCTGC ATTGTTATAA GCTTGTTGTT TGTCTTGATC
 600
 CGCTTGTGTA AAGTCAACTG ATTGTGGTAC TTGACTATTC GCTTGAATTT GTTGTGTCAA
 660
 CGTACCCATT GCATTATTTA ACGCATCAGC ATTTTGCTTA ATAGCATTA CACCTGTAAC
 720
 AAGTTCTGCA TGCGACACTT GGGTCTTTTA ATGCTGTTTT TTGTGGTTGA TTTAAGTTTG
 780
 GTAACGATC AATGGCTGTA TTTGNATTGT CTTTAGCAAC TTGTAAGTTA TGGTTACCGT
 840
 TTAAATCACC CTTAGCTCGA GCCACTTGTT GTAACGCTTG AGCCACTTGT TGTGGACCCA
 900
 CGCTTGCAAT TGGGTGNACC ACTAATGATT TGGTCCAGCA TGCGCTACCG CATTTGAAAA
 960
 ATGCATTTTT GCTTATCAGT ATCAGCATTT GCCAAAGTTA CCATTTGCTT NAGGTGGTCT

1020
 TAATCTGCAA TACCTTGTNT CAATTGTGTC ATTGCTTTGA NNTAAATCTT TGTGCTGTTT
 1080
 GCTTAATCGT GTTNACATTT GCAACAGTTT GCGCAGCATC GACTTGTTGT TTAAAGGCAT
 1140
 CTTTGTGCGC TGGATTTAAA TCATTTGCAT TTGTAATAAC TTGTTTCGCT GCATCTTTTG
 1200
 CACGTTGTAA CATTGTCATT ACCATTCAAT GCTTGTTTCG GCTTCGTTCA CACGTTGCAT
 1260
 CGCTTGTTTC CAACTTCAGT TTGAACTTGC ATTGCTGCCA TTTGCTTTAG ATAAAATACC
 1320
 TTCTGCATGT GAAACCGCAT TAGTATAATC ATCTTTCTTA GCTNGATCTG CATCAGTAAA
 1380
 GTTAATGCTA TCTAATGTCT CAGTTTTATC TTGTAATGCA TTGTTTAAGT TAGTCATAGC
 1440
 ATTATTCAGA TTTTGAGCAT TTTGCTTAAC ATTATTAAC TTTGCAATAT CTGGTGCTTG
 1500
 TTCAACTTGA GTTGTTAGCG CTTGTTTTTG AGCATCATTT AAATGATCTA GTGTACCAAG
 1560
 TGTTGTCTTA GCATCTTGTT TGGCATCAGC TAATTTGTGA TTACCGTTAA GTGCTTGATT
 1620
 TGTGTCATTC ACTTTAGTTA ATGCTTGTTG AATTGTATTT GGATCCATTG TTGGATTTGT
 1680
 TGTTTGTTTT AACAATTCTT CTGCTTGNGT TACTGCATTA TCATATGCTG TTTGCTTGTC
 1740
 AGTATCAGCA TCGTGATAGN TCTCGCTACC TTTAATTTGT GCTTTATTCT CAATACCTTG
 1800
 TTTCAATTGT GTCATCGCGT CATTAAGCGT TGTTGCCGCT TGTTGAATAG CATTGACGTT
 1860
 TGGTACAAGT GTTGCTTGCG TGATTTGTTT GCTGTATTCA TCACGTTGCG CTTGGTTTTAA
 1920
 GTTTGGCAAT TGATCAATAG CATGTTGAAC ATTTTGTTTC GCCGTTGCTA AGTTTGTATT
 1980
 ACCATTTAAA TCATTTTTAG CTTGCGTAAC TNNATCTAAC GCTGCAGGAA TTTGCTAGG
 2040
 TGTAACGACA ACATCAGGCG TACCACTAAT TAATGCTTCA GCTTTGCTA CTGCTTGATT
 2100
 ATATGCATTT TTCTTGTCAG AATCTGCATT GACAAAGTTA CCATCAGCTT TTGTTTGTTT
 2160
 TTTATCTGCA ATGCCTTGTT TTAATTGTGT CATCGCATTG TNTAACTCTT GCGCCGTTTG
 2220
 TTTAACATTG TTTACACCAG CTACAGTAGT TGCATTTCTG ACTTGTTGTT TTAATGCATC
 2280
 TTTCTGTGCT TGGTTAAGAT CATTAGAGTT ATTAATTAAT GCTGTTGCTT CGTCTTNTGC
 2340
 ATGTTGAACG TTGGCATTAC CATTTAATGC TTGTTNTGCT GCATTTACTT GTTGGATTGC
 2400
 TTGNNCAACT TCAGTTTGTG TTGCATTACC ACCATTAGCT TGTGGAAATG ATATTTNCAG
 2460
 CATTTGTAAC TGCAGTGTTA TATGCTTGTT GTTNGGCTTG ATCTNNATCA GNGAAGTTAC
 2520
 CTGNTGCTNG CGTAGCATCT ATATCACCTA TCGCTTGTC CAAGTTACCC ATCGCAGTAT
 2580
 TTAAGTTTTG CGCATTTTGC TTAATTTGAT TTGCTTCATC ACCAGTATGC GCGCCATTAA
 2640
 TTTGATTAGT AACAGCTTGT TTTTGCGCAT TATTTAAGNT GTCTAATGAA CCTAAAGATT
 2700
 GCGTTGCTAG TTGCTTCGCT GCCTCTAAGT TTTTATTACC ATTTAAAGCA TTTTATAGCG
 2760
 TGCTTACTTG TCCAGCAGCT TGATTGATAA CAGTCGGATC TAATGAAGGG TTTGTAGTTT
 2820

GATCAATAAT ACCTTGTGCA GTTGTGACAG CATTATTGTA CGCATCCTTT TTATTCGGAC
 2880
 TTGCATCAGT ATAATTTTGG TTTTGTTTTG TTGTCGCATT ATCTGCAATA CTTTGACGTA
 2940
 ATTTGTCCAT TGCTGCATCA ACATTGTTTG CTTTTTGTTT ATTACCTTGT GCTTCTGCAA
 3000
 CAGTAGTCGA TTGTTGTACC AATTGTTTTA ATGCCTCTTT TTGTGCATTT GTTAAATGGC
 3060
 TTAAACCGTC AATTGCTGTA TTTGCGTGTT GTTTCGCTTT TTCAAGGTTT TGAGTACCAT
 3120
 TAAGCGCTGC TTTTGTAGTA TTCACTTGAT TCATAGCTGC TTCAACTTGA TCTTTAGGCA
 3180
 CGTTCGTACC TGTAGATTTA TTTAAAATAT TTTCAGCATT ACGAACCGCT TCATTGTATG
 3240
 CATTTTNCCT CTCTGGATCT TGCATCTTGC AAAGTNNNGG ACTGGCAAGT GTAGTGTCTT
 3300
 TATCATTCAA GCTATTTTTC AAGTTANCCA TCGCTGTTTC AAAATCCTGA GNGGGNTTGA
 3360
 TTGGTTGGNG TTNACTTCAN CTACAG
 3386

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 761 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

AAAATACAAG CGTCTAAATA TTAACAATCT NCCTGTGACG CTATATGGCA TATCTTGCTT
 60
 TTTAAGCATC TGTTGTATCT CTGCCATCGA GCGCATTGGC CAGCTTCACA ATAATTATAA
 120
 TGAATTGTTT TTATCGATGG AGACACTAAT TGTGTCATTG GGTCACCACC ANAACCATAT
 180
 ATTTGATGTG GTTTCATAAC ATCATTTTTTA TCAGAATAAT ATTTATAGGC AGCTAATGCA
 240
 ATCGTATCAG TTGCTCCAAC ANCCGCATCT ACTTGCTCCA CATTTTCCAA AACATTTGCA
 300
 ACATCTTTTT GTGCTTCCAC ATAAGTAAAA TTTGTTTCAT GTATATTAGG TTTAATTTGG
 360
 TATTTAGCTA ACTGGTCCAA GTAAACCCAC GTTTTCTATG AATACCACCT GCAATATCTT
 420
 TTTCACTTAC ACTAAACACT TCAACTTGTT GATATCCCTG TTGACCAATC CATTCGCCTA
 480
 TAATTTGACC TGCTTTATAA TCATCATGCA CAATACTATG AAGTTGTTCA TGTTGTTGAC
 540
 CAACAATAAC GATTGGTACA TTCATTTTAT TAATGACTTC AATATGTCTC TCTGTTATGT
 600
 CTGTAGCCAT TAAACAATA CCATCTACTT TACTGCGTGC TAATGTTTCA AGCGCTTGTA
 660
 TTTCTGCTTC GATATTTAAA CCTGTGTAAT TTAAATTTAA TTGTGATTCA TATTTTGGC
 720
 ATTGTTTTGC CAATCCTTTG ATTGTTTCAT CTAATGCATA T
 761

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2334 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

```
CCACCCANCT GATTATAATG TTTTAGCANG AGCTAGACTT GGTTGGTTAC CATCATATCC
60
ACAATTTAAT AAAAATAGTT TGTTGTTTGC AGAAGAAGCT AAAGATGAAG GCATTGAGTC
120
GAATGAGGCA ATTTTAAAAC GAGCGATAAA TGGAAGTTAA GTCAAAACAA ACGCAATTTG
180
CGATAGAAGA TCCGGATTTG AAAAAGAATC ATCCGGAAAT CACTGTTTAT ATGGCGCTCA
240
AATCTAATCT CAAGTTCTGC AAAAGGTCAA GAATACTTTA TGAAGCATTT ACTTGGCACA
300
AAATCAGGGT TATTAGCTAC ACCAAATGAA GATGAAAAGC CAGAAGAAAT TACGTGGCGT
360
GAGGAAACAA CAGGGAAATT AGATTTAGTC GTTCTTTAG ATTTCAGAAT GACAGCAACA
420
CCTTTATATT CTGACATTGT TTTGCCAGCA GCGACTTGGT ATGAGAAGCA TGATTTGTCA
480
TCTACAGATA TGCATCCATA TGTACATCCT TTTAATCCAG CTATTGATCC ATTATGGGAA
540
TCGCGTTCAG ACTGGGATAT TTATAAAACG TTGGCAAAAG CATTTTCAGA AATGGCAAAA
600
GACTATTTAC CTGGAACGTT TAAAGATGTT GTGACAACTC CACTTAGTCA TGATACAAAG
660
CAAGAAATTT CAACACCATA CGGCGTAGTG AAAGATTGGT CGAAGGGTGA AATTGAAGCG
720
GTACCTGGAC GTACAATGCC TAACTTTGCA ATTGTAGAAC GCGACTACAC TAAAATTTAC
780
GACAAATATG TCACGCTTGG TCCTGTACTT GAAAAAGGGA AAGTTGGAGC ACATGGTGTA
840
AGTTTCGGTG TCAGTGAACA ATATGAAGAA TTAAAAAGTA TGTTAGGTAC GTGGAGTGAT
900
ACAAATGATG ATTCTGTGAG AGCGAATCGT CCGCGTATTG ATACAGCACG TAATGTAGCA
960
GATGCAATAC TAAGTATTTT ATCTGCTACG AATGGTAAAT TATCACAAAA ATCATATGAA
1020
GATCTTGAAG AACAACTGG AATGCCGTTA AAAGATATTT CTAGCGAACG TGCTGCTGAG
1080
AAAATTCGTT TTTAAATATA ACTTCACAAC CACGAGAAGT AATACCGACA GCAGTATTCC
1140
CAGGTTCAAA TAAACAAGGT CGACGATATT CACCATTTAC AACGAATATA GAACGTCTAG
1200
TACCTTTTAG AACATTAAAC GGACGTCAAA GTTATTATGT GGATCACGAA GTTTTCCAAC
1260
AATTTGGGGA GAGCTTACCA GTATATAAAC CGACATTGCC GCCAATGGTA TTTGGGAATA
1320
GAGATAAGAA AATTAANGGT GGTACAGATG CTTTGGTACT GCGTTATTTA ACGCCTCATG
1380
GANAATGGAA TATACACTCA ATGTATCAAG ATAATAAGCA TATGTTGACA CTATTTAGAG
1440
GTGTCCACCG GTTTGGATAT CANATGAAGA TGCTGNAAAA CACGATATCC AAGATAATGA
1500
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TTGGCTAGAA GTGTATANCC GTAATGGTGT TGTAACGGCA AGAGCAGTTA TTTCGCATCG
 1560
 TATGCCTAAA GGTACAATGT TTATGTATCA TGCACAAGAT AAACATATTC AAACGCCTGG
 1620
 GTCAGAAATT ACAGATACAC GTGGTGGTTC ACACAACGCG CCGACTAGAA TCCATTTGAA
 1680
 ACCAACACAA CTAGTCGGAG GATACGCACA AATTAGTTAT CACTTTAATT ATTATGGACC
 1740
 AATTGGGAAC CAAAGGGATT TATATGTAGC AGTTAGAAAG ATGAAGGAGG TTAATTGGCT
 1800
 TGAAGATTAA AGCGCAAGTT GCGATGGTAT TAAATTTAGA TAAATGCATA GGATGCCATA
 1860
 CGTGTAGTGT GACATGTAAA AACACTTGGA CAAATCGTCC AGGTGCTGAG TAACATGTGG
 1920
 TTCAATAACG TAGAAACGAA GCCAGGTGTA GGGTATCCGA AACGTTGGGA AGACCAAGAA
 1980
 CACTACAAAG GTGGTTGGGT ACTAAANTCG TAAAGGGAAA CTTGAATTAA AATCTGGAAG
 2040
 TAGAATTTCA CAAATTGCTT TAGGTAAAAT TTTTATAAC CCAGATATNC CATTAATAAA
 2100
 AGATTATTAT GANCCATGGA NCTATAATTA TGAACATTTA ACAACTGCGA AATCAGGGAA
 2160
 GCATTCGCCA GTTGCTAGAG CGTATTCAGA AATTACAGGG GATAACATTG AAATTGAATG
 2220
 GGGACCTAAC TGGGAAGATG ACTTAGCAGG TGGTCATGTT ACAGGCCCAA AAGATCCTAA
 2280
 CATAACAAA ATAGAAGAAG AGATTAAATT CCAATTTGAC GAAACTTTTA TGAG
 2334

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2698 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

GGCACGAGAC TAATACCTGA AATTAATCCA CCACCACCAA TAGCGGCAAA TAAATAATCA
 60
 AAGTTAACGG AATTGTCAGT CTTTGATTGT TCTAGCATTT CTTTAGCAAG CGTACCTTGT
 120
 CCAGAAATTG TATGAACATT ATTGAATGGA TCTATAAAGT TCATTTGATG TTCACTTGTA
 180
 TAAGTTAAAG CTTCAGCTAA ACAGNGATCA AATGTATCAC CAGTGAGTAC AACTTCAACG
 240
 TTACTATTTT CAAAGAACTT TACTTGATTT ACCTTTTGTN AAGGTGTAGT GACTGGCATA
 300
 AAGATAACAG CGTTTANATT AAGTTTTTTA GCTGTATAGG CAACACCTTG AGCATGATTA
 360
 CCTGCACTCG CACATGTAAT ACCTTTACTT TTAGCTTCAT CTGATAAAAC AGAAATAGCG
 420
 TTGTAAGCAC CTCTTAATTT AAAAGAACGT ACCCATTGTA AATCTTCTCG TTTTAAATAA
 480
 ACTTTACAAT CATACTTTTG AGATAAGTAA TGGTCTAATT GTAAAGGTGT TTCTTTGACA
 540
 ATATCTTTAA GTCTTAAAAA TGCTTCATCG ATATCTTNCG TAGAACTGN TGTTTTGACT
 600

GGCATAATAT TCAACTCCCT TAAAGTGATT TNNCATATTN NTCTATTAAT GATTCATATT
660
GTAGGGTGAT TGCAATTGTC ATCTAAGCCA TTTACCAAGT TTATTTTTCC AAAGTTTCAT
720
CAATTTCAAA ATGGAAACGC TTGTCTGGTG ATGACACAGT TTGATTGGT AAATCTATTT
780
CAATTTCCCTC ATATTGTGCA AGATGTTTAC GAGCACTTTT TTCTAAANCG ATAGGCAACA
840
TCGCATTTTT AGTGCAATTC ATATAAAATA TGTCCTGAA ACTTCCTGCA ATAATAATAT
900
GNAAACCATA GTCCTTAAGA GCCCAAGCAG CATGTTTACG ACTTGAACCA CATCCAAAAT
960
TATCTCCAGT AATTAATAA GAAGCCCCTT TATATTGTGG TTTGTTAGGA TTGAAATCAG
1020
GATTATCTGA ACCATCAGGT AAGTACCGCC ATTCATCAAA AGCAAATGGA CCAAAGCCAC
1080
TTTTTGAAAT ACGCTTTAAG TGTACCTTAG GAATGATTTG GTCTGTATCG ATATTGTCTG
1140
TGAAGAGAGG GACTATTTTA CCTTTATATG TTGTAATAGG TTTGATTGCT GCCATTTAAA
1200
CAACCACCTT TCTTACGTCC ACAAATTTAC CATGAATAGC TGCTGCTGCT GCCATAGCAG
1260
GGGATACTAA ATGTGTTCTT GCACCTTTGC CTTGTCTGCC TTCAAAGTTT CGATTACTTG
1320
TAGATGCACA ATGTACGCCC TCAGGTACTT GGTCAGGATT CATGCCTAAA CACATTGAAC
1380
ATCCTGGTTC ACGCCATTCA AATCCTGCAT TTTTAAAGAT AGTATCTAGA CCTAATTTTT
1440
CTGCTTCTTT TTTTACTGTA CGAGAACCTG GTACGACAAT AGCTGTAATA TTTGGATGAA
1500
CTTTATTTCC TTTAACAATA TGACTAGCTT CAATCAAATC TGATAGTCTA GCATTTGTAC
1560
ATGAACCGAG AAAAACATAC CCTAAGTCGA TGTCTTCAGC TTTTGGACCT GGTTCCTAACC
1620
CCATATAATC ATACGCACGT TGATCGTTGA TATCATTGAT TTCAGGGAAT GGTTCCTGA
1680
AATTAACACC CATTTTCAAG TTAGTTCCCC ATGTCACCTG TGGTTCCTAAT GTTGAAACAT
1740
CAAGTTCAAT TACACGATCA AATATCGCGT CGTGCCATCA GAATATAGCT CACGCCACTT
1800
ATCAACTGAT TTAGCGAAGT TATCGGCAAA TGGTCTCCCT TTAACATATT CAAATGTTAT
1860
ATCATCAGGT TGGATTATGC CGTATTTGGC ACCACCTTCG ATAGCCATGT TACAAATAGT
1920
CATTGACCG TCCATTGAAA GGTTTTTAAT TGTTTCGCCA GTAAATTCCA AAGCATAGCC
1980
TGTACCAAAA TCAACACCAT ACGTTTTAAT TAAATGCAGA ATAATGTCCT TAGCATAGAC
2040
GCCTGTTGGT AAGGTACCAT TAATATCGAT TTTTAAGTTT TTGGGTTTTG TTTGCCATAG
2100
CGTTTGAGTT GCGAAAACAT GTTCAACTTC ACTTGTTCCA ATTCCAAATG CAATAGCACC
2160
AAATGCTCCA TGTGTTGCTG TGTGAGAGTC ACCACAAACG ATTGTTTTGC CGGGCTGTGT
2220
AAGTCCTGTC TCAGGTCCTA CCATGTGAAC AATACCTTGT TCATCAGAGC CCATATCAAA
2280
AATATGCACC CCAAATCTA TGGCGTTTTT TTGTAATGTT GTGATTTGTT TGTGCAAT
2340
TTCATCTTTA ATATTGAAAA TATCAATAGT AGGAACATTG TGATCGAGTG TTGCAAATGT
2400
TAAATCTGGG CGTCTTAATT TTCTGTTTTG AAGCCTAAGT CCTTCAAATG CTTGAGGAGA

2460
AGTAACTTCA TGTATAAGGT GTAAATCAAT GTATAATAGT TGCGGGTCGC CCNATTTCCC
2520
GNATAACACA TGTCTGTTCC ACACCTTGTC AAATAATGTT TGACCCAGTT ACATCTCCCC
2580
CTNAGTGATT CAATTTTGA GATAGCATTT CGAAAATATC AGTAGTATTC AATTTGCCGC
2640
CTAAATCTGC TGTCGTTTGC CCATGTTCAA TCATGTTATA AATATGTTGT TCTAATTC
2698

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 706 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

CTAAGANGAT ANTTTAAGCT TGTAACCCAA CAGTTCGCAG GTTAAATCCA ATCCAGTTTG
60
ACCAAAGAAA TACCGACCCA AACCGCCTTT GNACCGTAGT TGGATAATTA ATGGGGACCG
120
CCCAAAGATA ATAAGCAGTT AGCCGNNNAG GTTCCGGGAA TAGGNCCGTT TAAATTNAAA
180
ACCCAGCTGC CTTTGTCTTC TTGAAATACA TTGGGGAATC TGGATTAGAT GGTCCGAAAC
240
TACCGTCGAC ACCATCACGT CAAGCAGTTG CAATNCCAGC ATCAGATGTG ATTATAAACA
300
AAGTGATGAC GAGTGATACA CCTGTAACAA TTGTAGCGAC AGGTCCTCTT ACGAATGTAG
360
CAACGGCATT GATTCGTGAT CCAAGAATCG CTGAGCATAT TGAATCTATT ACTTTGATGG
420
GTGGTGGTAC ATTTGGAAAT TGGACCGCCT ACAGCAGAAT TCTATCAATA CCTACTTCTT
480
TCTTGACTAA ATCANACTGT GGCTTCGTTA ACATGCCACT TGGTGTGATA TAAAACTAT
540
TTTTAAAGTA ATAGCTTACA GAGTGGTTCA AATGTTTCAGC GAATAAAGCT TCATCCATAC
600
GTTCTAAGAA GAATGGGATA AACTCACCCC AATGTCCAAT AATCATATTT AACTTTGGAT
660
AACGATCAAN AATGCCAGAT AATACTAGAT GTATTGCATR RDCTNS
706

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 634 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

CTTGTTGGAT CAGATCCAAC ACTACCTGAT GGATCNCTAT CNAGATTGAG CACGCCACCA
60

TATCAGATGG AATATCAACC TTGTCATGGG ACAGACTGAC ACCTGAATGA NGGGGTGTCT
 120
 GGNCANNCAC ATCATCACCA TTAATGGGAC AGCGAGTGGC ACATNTCCAT GTAGTAAATG
 180
 GCACTTATTA CTTACACGGN CATATCGTGN CAGGTTGGCA AGGTGTGAAA AAGACATGTG
 240
 ATACAGCGGA AGAGCTTGAC ACATATATAA AGCANAGTGA TGTGGTATAT GAGGAACAGA
 300
 AGCATCTANC TTTATTTTAA GNNGGCGGAA ACAATGAAAC TCAANGTTAA AAGAGANATG
 360
 AGATTAGATG AATTAATTAA NTGGGCGAGA GAAAATCCGG ATCTATCACA NGGAAAAATA
 420
 TTTTTCNCAA CAAGGATTTA GTGATGGATT CCGTCCGNTT TCATCCANAT ACAAATAAGT
 480
 GTCTCGACGN CAAGTTTTAT TCCAATTGAT ATCCCCTTCA TAGTTGATAT TGAAAAAGAA
 540
 GTAACGGAAG AGACTAAGGT TGATAGGTTG ATTGAATTAT TCGAGATTCA AGAAGGAGAC
 600
 TATAACTCTA CACTATATGA GAACACGRRD CTNS
 634

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GGCACGAGCG CCCATTTAAT TAATTCATCT AATCTCATTT CTTTTTTAAC TTTGATTTTC
 60
 ATTGTTATAT CTCCTCTTGA ACAGTAAATT TATCGTTAAT TGATACGTAT CCAGTCACAT
 120
 TACATAAGAT GCTATCAACA TCAAAAGTCA CACAACAGTT GCGTTCAACA TCATTTGAAT
 180
 AGAATCTTTT ATTACCTGAT AACTTGGCGG TTATCACCAA GCCCATTGAA TAAATTCAGC
 240
 TAAATCTCAT TTCTTTTTCA ACTTTGATTT TCATTGTTTC CGCCCTTTTA AAATAAAGTT
 300
 AGTTGCTTCT GTTCCTCATA TTCCAGAATC ACTTTGCTTT ATATATGTTT CAAGCTCTTC
 360
 CGCTGTATCA AATGTCTTTT TCACACCTTG CCAACCTGGC ACGATATGAC CGTGAAAGTA
 420
 ATAAGTGCCA TTTACTACAT GGATATGTGC CACTCGTTCTG TTATCCTGAT ACAGATATCT
 480
 CTTAGAGCCG AAAAAATGTT TTAAGTATTC TTTACGTCCG CTATCTGTCA TGGTCATCAC
 540
 TCCCGCAAGT CAAATACTCT ATCGACGTAA AACTTCGCCT TTGCTAAATC CTCATGACCA
 600
 TTCTTTAACG GTGCTCTAGA CAAGTATTTA ATTGCATTAC CTATTGCGAA TGCTAATTGT
 660
 GGTGGGTACT GTGCCGTAAC TTGTTCAATA AAATCTATAA TTTCAATGTT CGCCGTATGT
 720
 TGTTAATGCG CAGGTTGCTT AACGTTGTCT TGC GTTTTGT TCATATCTAC TTTTCTGTTA
 780
 CTGATTATGC TCATTATGTT TCACTCCATT TCTTGAACAT TTGGTTATAG TTGACATCGA
 840

ACCAGTACGA TCACGTTGAA TGTTTTTGAG TACATCAAAT AATGTTGCTC CTTCTCTAGC
 900
 TCAGCTTCTT TACGTCGTAG CCTAGCCATT TCACGCTCTC GCTCCAAAGC TTTTGTTATT
 960
 TGTATTTCTC TATAGTCGTT TAGCTTCATG CCGAAAGGTG CATCAATTGC TTCCGACATC
 1020
 TCCCAACCCT TCGCAACTCT GTTTCTAACT ATTTCTGGGCG TGAGTCCTTT CTTTTTCATC
 1080
 TGCTCATTTT CATATTCAGT GTATTTAGAA GGGGGTTTTT CTTGTGGTGG CGCAATAAGC
 1140
 GCATCGCCCG TTAGCCC
 1157

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

GGCACGAGCT CGTGCCGATT CGGCACGAGC TTCGGCTGTA TTGGTACCTA TCAATACAGA
 60
 CATTGCCGCT TTTTCTAAAT CTTCAATACT ACCTTGAGTC ACCCGCCGTG TCCAACCGTT
 120
 CTAAATAAGC CTTTTGTTGC AGGTGCTTGN CAATATCTTT GNACAAGCTA TCAACGTTAT
 180
 TTGTGCCAAT AACTTGCTT GCTAATTTTT GCANTAAANA CGATTCTTCA TTCGTCGCTT
 240
 TAGAAGAAGA AATGAATGAT AGTGCATCTG GGCCATACTT TTCTTTAATA GATGTAAAAT
 300
 TATCTGCAAT GACATTTAAA GCTTCATCCC ATTCTACTTC ATGGAAGTCA CCATTTTCC
 360
 TTACTAGTGG TTTAGTTAAG CGTTGATCTG AATTAATATG TCCCCATGAA AACTTACCTT
 420
 TAACACAAGT CGCAATTTTA TTTGCTGGAG AATCATGTGA TGGTTGTACT TTTAAAATTT
 480
 CTCTATCTTT AGTCCAACT TCAAATGAAC AACCCACACC ACAATAAGTA CACACTGTTT
 540
 TAGTTTTCTT AATACGCTCT TAACGCAGTT CTGCTTCTGA ATCTGAGATT GCAAATAGTG
 600
 GACCATAACC AGGTTCTGCT TTTTGTAGTTA AATCAATCAT TGCTGCTAAT GAACCAGGTT
 660
 CCGTATCAGT CATATAACCC GCATTACCTT CCAGATTCAC TTCCATCATG GCATTACATG
 720
 GACAG
 725

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1676 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

AAAATCCAAG GCACAAAGTT CTAAATACGG AGTCAAAAGA ATATTGAACA AGCACATTTT
60
CAACAATACT TTGAAAATTT ATTATTTTCAT AAGTTCATCA TTGATCCAAA GTAATATTGC
120
CCTTGCCGAT GTTCATCTTA TTGACTATTT ATTTACAGCC ATTAGTTAGA TATATTTTTG
180
AGCGAATTGT CATGGCTGTG ATTGTCATCA TTGGTGTTAT TGTCAGTGTG TTTACCATTC
240
TGTATTTTTTC ACCGCTTGAT GCGGCTTATA GCATACTGGG ACACAATGCA ACANAGGCAC
300
AGATACATCA ATTCAATGTA TTACATCATC TTAACGAACC TTATTTTATT CAATTGTGGG
360
ATACCATCAA GGGTGTTTTT ACCTTTGACT TAGGTACGAC TTACAAAGGG AATGAGGTTG
420
TGAATAAGC AGTTGGCGAA AGAATTCCAA TTACAATAAT TGTCGCAGTA TTAGCGCTAA
480
TTGTGGCATT AATTATTGCA ATACCAATTG GTATTATCAG TGCGATGAAG CGAAATAGTT
540
GGCTTGATAT CACGTTAATG ATAATTGCAT TAATTGGTTT ATCTATTCCA AGTTTCTGGC
600
AAGGGCTATT ATTCATTTTA GCGNTCTCAT TGAAATTGGA TATTTTGCCA CCATCTTATA
660
TGCCAGAACA TCCAATATCG GTGGATTTTA CCTGTACTTG TCATTGGAAC AAGTATTGCT
720
GCTTCTATCA CGCGTATTGA CAAGGTCTTC TTGTACTTGA AGGTAATGCG CAGCGATTAT
780
GTTTTNACTG CTTATGCAAA AGGATTATCG ACGACACAAG TTGGTTATTA AACATATTGT
840
GGAAAAATGC CATTATTCCA ATTGTACGGT AAGTGGGTCT TCCTNGGTGG CAGAGTTACT
900
AGGCGGTTCA GCAGTGACGG AACAAGTATT TAACATTAAT GGTATCGGTC GTTATATCGT
960
CCAAAAACAA CTAATACCTG ATATCCCAGC AGTCATGGGT GGGGTCGTAT ATATATATCA
1020
ATTGTAATAT CTTTAGCAAA CTTAATTATT GATATATTTT ATGCTTTAAT CGATCCAAAA
1080
TTACGTAGTG AAATTAACGA AAGGAAGTGA GGCATATGGT AAAACTTACA ACAAAGATAG
1140
CTTCCTTAAA ACTATTCGCA AGTTATGCTA TAGCAACTTA TATTTTAGTT ATGTTAACGA
1200
GTGCATTAAA TCTTTTTTAAA GGTTATGTGG CCGATACGTT CTATATTGCT GAAACATTGC
1260
TAATCATTTT AACCATCATT TTAATTATCA TTTTAACAAC GGAACAAACA TGGAAGCATC
1320
ATGACCTATG GCGACGTATC GTCGAAGTGT TGTTATTGTT GATGGCATT A ACAGGCAACG
1380
TATTTACATT ATTAATGTGT GTAAGTATTA GACGTTACCA ACGTACATCG CAAATACATA
1440
GTTATAACGG GGTGGGAATC CGNTTATACG AAAAATACT' AGACATCCGT ATTTGCGATT
1500
ATCGGGGTTA CTTATTTTAG TCTACATGCT GACATTATCA ATNGTGTCAC AATTTAAATT
1560
TGATACGACA ATGGCTTACT AAAAATCCAG TCCAATGAAC TNGTACAATG GACCGAGTCT
1620
AGCCTATCCG TTTGGTACTG ATGATTTCCG TAGAGACTTA TTTACACGCT CGTGCC
1676

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1978 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

```
CTAATCGTAT GAACGAGTAC CCAGAGGTTT GAAATTTAAT ATTGATTCTA TNAATGATTC
60
CTTAGTGTCTG CATAACGGTG CAAGAGCACG ATACTTAGGA TCAATAAAAC CTTCGTCAAT
120
CATATGGTCA ATCATTGNTT GTAGTGGNTT GAAAANGCCA TTAATATTAT AAATGGCAAT
180
AGGCTTGTCA TGGATACCTA TTTGAGCCCA ACTAATACAT TTCGAAAAAT TCTTCTAGTG
240
AACCTGCGC CACCAGGAGC CATGACAAAT GCATCTGCAA GTTCTGCCAT TTTATTTTTA
300
CGTTCATGCA TAGAATCCAA CTAAAATTAA TTCAGTTAAA CGTTGGCTTG TGATTTTCATG
360
TTCATCTAAC ATTTTAGGCA TGACGCCAAT AGCTTTGCCG CCATGATTTA ATACACCATC
420
TTGAATGGCA CCCATAATGC CAATTGACCC TGCACCAAAT ACTAATTCAT AACCTTGTTT
480
AGCAAAATAT TTACCTAAAT CGTATGCTTT TTGTACATAT GAAGGGTCAT GACCTTTGCT
540
TGCACCACAA TAACTGCGA TTCGTTTCAT GTTAATCCAG CTCCTTAATT CGATGAATGA
600
CTTTTAATAG TGATTGTTCA AACACTTTTT GATCTTGCTT TGTAAGAGGT GGGGGACCTT
660
TGTGGCGACC ACCTTGTTTT CTAATTTGTG CATTATATA TCGTTTATCT AATAGTTGTT
720
GAATATTTTT GGAATTGTAT ATCTTCCCAT TATGATGCAT GACAATTAAG ACTTTGTCGA
780
CTAATAAACT TGCGAGTCCA TAATCTTGAG TGACTACGAT ATCATCCTTC GTTGATAATT
840
GAACAATTTT GTAATCAACT GCATCTGGTC CATCATCAAC ATATAATGTT GATACATGTG
900
GAGGATATAA TTGGTTCGAA AAATGGCTGA AGCTCCGAAT AATTGTCACA AAAATGCCTG
960
TCTCAGTTGT TAAATCTATA ATAGAATCNA CAACAGGACA AGCATCTCCA TCAATAATAA
1020
TATGTGTCAC AATTATGCCT CTGTATTGTT TTCTTTATTT TGTTGAGAGG CGCTTTTGGC
1080
AACATAATCT TTATATTTTT TAAATGACTT GATGCGTGCT TTATCAGCTT CTTGTTGGCG
1140
TTTGTTCTTC TTTGTGTCGT TTTTCAATAT TTTTTGTAA CTTTTTATTC ATTTTAGCGA
1200
TTTCTTTGCG ATTTTTTTCA GCTAGTTTAT CGCCTTTTCT CTCAGTTTTT TCATCTAATT
1260
TATTAGGTGT TAAGCCTGCT TTTTCTTCGT ATTTTGTGA TTTTTCATA TCTTTAATAC
1320
GTTGTATTTT ATTCTTTTCG CGGGCTTTTT GCTCTTCTTT ATGACGCTTT TCGATATTTT
1380
TTTGAAGTAT TTTATTCATT TTATCAGCGT CTTTACGATT TTGTTTAGCT AATTTTTCGC
1440
CTTTTTTCTC AATATAGGCA GGATCATGTT CTCTAGCAAA CTTTTTAAGT TCACGTTTAT
1500
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TTTCAAATC TTGTTTTTTA TCGCCGACAT ATTCTTTAAC ATCACTCGCT GTGTTACTGA
 1560
 TTGCTGCAGA TGTTTTTGAA GCAACTTTAC TTGGTAGCAT CTGTAACTTT TGGGACGTCC
 1620
 GGATGTTGTT TGATACGTTT ACGTTCAACA ATTAACGGTA CCAATACAAT TGGTAATACA
 1680
 TTAATCATAA ATTTGATGAC TTTTTTCTTA TCCATAGATC TTGCCTCCAT AATTACTTTA
 1740
 TTAATTTTAC ATACCCTATG ATACATCAAT ATAAACGATG ATAGTAGTGA NTCACTATTA
 1800
 AGTATTTTCAAG ATGTTTTTTA NAAGAAGACA ATAAAACTG CCAATCACGT GGTTCCTTAA
 1860
 TTGACAGTCT ATATTTTANA CAGGAAATTA AATACCTTTA CCAATGCCAA TCCGAAGTAA
 1920
 AGTATAGCAA TANAGATTAC TAATACANTT CTGCTAAATG GCANATGGAA TTAGTCTG
 1978

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

GGCACGAGCG ATGTGCCAG CTTTTTCAA TTGCAATACC ATCGGTCCTT GATATTGTTC
 60
 TTCTGGTACG TCTTTAAGTC CTAATGTAA TTCCACTTCT TTTGCATCAT CTGACCATAA
 120
 TTTTCTGAAA TCTGTTTCTA CTAAATCTTC TTGATATACA TTTTCTGGTA ATGGTGGTAA
 180
 CCATGGACGC TTAACTTCTT CAATTTCTAA TCGTGTTGTA ATAGATTCGA TATGATCGAT
 240
 AACCGCTTCT AACTCGGTTT GGTTTTCTTT CGTTTCTTCA TCTTCAAGTC CACTCAAGTC
 300
 TTTGTTGATT GCTTGAAGTT GACCATAGTC ATTAATCATG TAAATCGTCT TATCTTCAAC
 360
 TTCTAATTTA TCGCCTTCGA TGTCATATGT TGCACCACTC CATGCAGATT GGAATAATTC
 420
 ATAAATTTCA TTATTACCAA CTTTGTAAT ACGCACGACC TGGTAATGTA ATGTCTGCTG
 480
 CATCTGGTGT TTTTAAAATT TCATTACTGT CTTGTCTATC TGGNACGAGT TNTAATGCCA
 540
 ATTTAAATTN AGAGTTAGAC CAAATTTGGT CATCAACAAC ACCCGATGGT TTNTGTGTCG
 600
 CAAGTATTAA ATGAATACCT AACGAACGTC CAATACGTGN CGGNGATACA AGTTCTNTNC
 660
 ACATAAAATC AGGTTGNTCT GATTTTAAAT CGGCAAACCTC ATCGGAAATA ATGAATAAAT
 720
 GTGGCATTGG CTCTGNTGCA ACACCTTCTT TAAATAACTT ATGGTATTGA TTAATATGGT
 780
 TAACATCATG CTCTCCGAAT AAACGTTGAC GTTTCTCAAT TCGGCTTTGA TTGATGTTAA
 840
 GGCACGCATC GCTTCATCGC CATCTAAGTT TGTAATCCGT ACCAACTAAA TGGACTAAAT
 900
 CTTTAAATAA GTTCGCCATA CCCCCACCTT TATAGTCAAT CAATAGGAAC GCAACTTCAT
 960

GTGGATGAAA ATTAATAGCT AAAGATAAAA TGTATGATTG GATAATCTCA AGATTTCCT
 1020
 GAACCAAGTGG TACCAGCAAC TAAACCATGT GGCCCGTGTG CTTTTTCATG TAAGTTCAAT
 1080
 GATAAAATAT CATCTTTACC TCTTACACCT AAAGGTACTG CCATCGTTTT GTATGTTTCG
 1140
 TTTTGTCTCC ATCGATTAA CACATCAAGC TGATCTACTT CTTTCACGTT ATACATCTCT
 1200
 AAAAATGTAA TACTATCAGG AATTGCATTT TTCAAATGTT CGACGTGTAT CAAATTCGCC
 1260
 AAACGTCTCG CGATGATATT CTTTATCAAC GTTATCAATA TTTTCAGGTG TAAATTTCAA
 1320
 TTGAACTAAT TCTTTTTCTT TCGTAATCAG TTCGCCTTCA GTACGAGACT TGATATCAAT
 1380
 AATGGTATCT ACATGCTCTG GCAAACCTTC AATCACATCT TCAACAAAGA TTAATGAAAT
 1440
 ACCATATTCT GATNAATCTT GGNTNACATA GTCTAAAATG ACATGATCAA TAATTAATGA
 1500
 CATATCTGTA ATGACAAACA CTAATTGCGG TGTGAAAATA ATTTGCTCAT TACTTCTGCT
 1560
 GCGTTCACGC ACAGCTTGGA TACGTTCTTT AATCATGCTA TAAATTGACG TTAAATTTG
 1620
 GTCACGTGTT CGGTGATTGT AAACAAACCC TCTAATGTTT TGACCTCTCA ATGTCATATG
 1680
 TGGCAACCAA CGTGCCCAT TCAATGTTTC AACTTCATCT TCACGTGTCA CAAATAGAAA
 1740
 CTCTAAATCA TGATAACTAT GGAACGTTGA CAATTGGATT AGCATTTTCT CCAATTCTTC
 1800
 TAAATGAGA TGTGCGGCAC CAATATATGC AATTGGTCCA TGATTTAAAT CATTGATTAA
 1860
 TGGGTGCTTT GTCCNACANC TNTGANAAAT TCATACAATT CTTTAGCATC GTCGAATAGT
 1920
 TCATCACGAC GTTGGTTAAA TTCTCNTCT TGGTAATCTA ATTTGAATGA CTTTTCTACA
 1980
 TTCGCAATAC CTAACCTATA ATGTAAGAAA TCGTGATGAT GCGATGTTTT TTCATATATT
 2040
 CTTGGTGCTT TCGTTTCAAC GATATCTTTA ATTTCANCA CCGTTGGATA ATGGTAATTC
 2100
 AAATAAAAC GTTGTGCTTT AATCGCTTTA TTAATTTCTT TAGATTTATT ATCCAAATAA
 2160
 GCTTTGTAAT CTTTCTCTCG TTTTCAACA TCTTTGTTAT ACTTTTTCTT TTCAGAGAAA
 2220
 TACGTTGTAA TACCAAATAC TATCGTTACT GTACTCATAC CAATCATCAT TAAATATAA
 2280
 ATACCAATTG GTCTCACTAA AAAGATGACA ACAGTTAAAG CAATCATTAC TAATGGCGGT
 2340
 ATAATGGAAC GCCATATCAC TGTATTCCGG AATTCCGGAA TTCCGTATTG GCTGTGGCGG
 2400
 TCTTTCAATC TTAATATCAT CGGTCGGGTC NCGGTGNATA ATCCTTGGCG AGCGATGGTA
 2460
 CGTATTGTAA TCATCTGCCT GTGCATGTGG CATCTCTTGT GTTAAGCGAA TTAATGACGA
 2520
 TGCCACTGTA TTCTGACTCA ATACANTTAA ACCATCAG
 2558

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 668 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

```
CCGGCTGATT ATTAGCGAAG CGAGATTTTG AAGAGATGCA ACCATTATAT GAATGGTTAG
60
GTTTAACTGC TTCATTAGGT TTTGTTGATA TTGTGGATTA TGAGTATCAA AAAGGGAAAA
120
ACGTAATATA TATGAACATG ATATTATAAA TACAATAAT GGACGTCTCG GTTTTGATTA
180
TTTAATTGAT AATTTGGCTG ATAGTGC GGA AGGGAAATTT TTACCACAAT TAAATTACGG
240
TATTATTGAT GAAGTGGATT CAATCATTTT AGATGCTGCT CAAACACCAT TAGTTATTTT
300
GGGTGCACCA AGATTACAAT CAAATCTATT TCATATTGTG AAAGAGTTTG TAGATACATT
360
GATTGAAGAC GTGCATTTTA AAATGAAGAA GACCAAAAAA GAAATATGGC TGTAAATCA
420
AGGTATTGAA GCGGCACAAT CATACTTTAA TGTTGNAGAT TTATATAGCG AACAAGCGAT
480
GGTCCTAGTG CGTAATATTA ATTTAGCACT GCGCTCGTGC CGAATGTTCC TTGGTTCATA
540
TAAGTCATAT CGATGTAAAA ATGTTCTTAA ATTTGGGTGC ATGATTGGAG AACAACCAGG
600
TGGATAATCT TAGTCATTTT CAAGGGTGCA TTCCCATTA ACTTATCATA TCGGCAAATT
660
CCCGCTTT
668
```

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

```
CCCAAATCCT TTGAAATAAA ACTTAATTAA GTTCAAGAAN TCGNGGTGAT TTTCCCCGGA
60
AGTTTGTTTG AATATTATTA TGGATTGATT TGATAGAGCT TATGGACCCC ACATTAATAT
120
TGAAGTCCTG GGGCCAAGTT CACNCCCCCG TGGGTGGAAT TTCCTATTTG ATCCCTAAAC
180
CCAAACTATG GACGTCCCAA ATTCTAAATA TGAAAAAATG GCTGAGCATC GTTTGATGAA
240
TCATGATTTA TATCCCGAAA AAATAGATAA TCGTTAAATG TATCATTTTAA TAAACACACC
300
AATAAGTTGA TTTTCCTAAC TTATTGGTGT GTGTTTTTCA TTTAGCATAC ATAATAGGTT
360
ACATTAAAT AACATTTTAT ACCCAAAGTA CACCAAAAGA ATATTAGTAC ACGAATTANA
420
CAACATTTTT ATAGAAACCT ATTGCACTTT AACGTCAATA AGTATATTTT TATATTATCT
480
CTAATTAATT GTGCGCGCTT AATAACAGAA TATTCTCAAT ATTTTATTTT TTTTGTGATT
540
```

TGTGTGAATA TTTAGTTGAT AAGGCACAAT CAAATTTACT TAAACTATTG TATTAGGGGA
 600
 AGAAAAGGATG GGATGTATAC ATGACACAAC AAAACTCCCA TGGAAATCAA ATTCAAGACA
 660
 TACCTCAAAC AGGATTTTTTC GGGCATCCTC GAGGACTAGG CGTACTCTTC TTTGTAGAGT
 720
 TCTGGGAAAG GTTTAGTTAT TATGGCATGC GTGCCCTACT CATTTTCTAC ATGTACTTTG
 780
 CCGTAACAGA TAATGGCCTT GGAATTGATA AAACAACAGC TATGTCAATT ATGTCAGTTT
 840
 ATGGTTCATT AATCTATATG ACATCCAATA CCAGGCGGAA TGGATTGCTG ACAGAATTAC
 900
 AGGCACTAGA AGCGCTACTT TATTAGGTGC AGTCTTTATT ATTATCCGAC ATATTTGTTT
 960
 AAGCTTACCA TTTGCATTAA TCCGCTTATT CACATCAATG TTCTNCATCA TTATTGGCTC
 1020
 AGGTTTAATG AAGCCAAACA TTCCAAATAT CGGTGGCCGT TTATATCCTG AAAATGATAG
 1080
 ACGTATGGAT GCAGGTTGTG TTATTTTCTA TATGTCAGTT AATATGGGTG CATTATTATC
 1140
 ACCTATTATT GTGCAACACT GTGTTAATGT TAAAACTTC CACGGCGGAT TCTTGATTGC
 1200
 AGCAGTTGGT ATGGCATTAG GTTTAGTATG GTATGTACTT NACANCCGCA AAAACTTAGG
 1260
 TAGCGGTGGT ATTGAAACCN ACTAACCCAT TGACNACCAG CTTGNAAAGA AAAAGTATGG
 1320
 TCTTTATTAT CGGAAGTGGT GTCTTTAGCA ANTGTATTAA TTATCGGTAT TGGGGCATT
 1380
 ACTAACTCAA TATCAANTAA CTTAGGTAGG AATACTGTTT TAGTATTAGG TATTGCATTA
 1440
 CCANTCATTT ACTTCACTTT AATTATTAGA AGTANAGATG TCANNGATAC TGNACGTTCT
 1500
 CGTGTTAAAG CATTTATTCC ATTATTTATT CTTGGAATGG TGTCTGGGC TATTCAAGAA
 1560
 CAAGGGTCTA ATGTATTAAA CATATATGGA ANTGNACATT CAGATATGAA ATTAAACTTA
 1620
 TTTGGTTGGA AAACANACTT TGGTGAAGCG ATCTTCCAAT CAATTAACCC ATTATTTATT
 1680
 TTATTATTAG CTCCAATTAT TTCACTTTTA TGGCAAAAGC NTGGAATAA ACAACCTAGC
 1740
 CTGCCAGTAA AATTTGCAAT TGGTACGTTT TTAGCAGGTG CGTCATACAT ACTAATTGGT
 1800
 ATTGTAGGTT ATGCATCAGG TTCATCAAAC TTCTCAGTTA ACTGGGTTAT TTTATCGTAC
 1860
 ATTATTTGTG TTATCGGTGA GCTATGCTTA TCACCAACGG GTAATAGTGC TGCTGTTAAG
 1920
 TTAGCACCTA AAGCATTTAA TGCCCAAATG ATGAGTATTT GGTACTTAAC TAACGCTTCT
 1980
 GCACAAGCAA TCAATGGTAC TTTAGTTAAG TTAATAGAAC CACTAGGTCA AACAAATTAC
 2040
 TTTATTTTCC TAGGTGTTGT TGCAATTATT GTTACAACAA TTTGTATTAG CATTCTCACC
 2100
 TTTAATCATC AAAGCGATGA AAGGTATACG TTAATATTGT TGGCCTAATT CAAAAACAG
 2160
 TAAGTCATTT AAATGGCTTA CTGTGTTTTT ATAGGTTTCT ATTAATTAAA TTCAAGATAT
 2220
 CAGTATAAAT AAAAGCTTAA TATGCTCGTT ATAGACAGCT ATAAGTATAT TTTCTCGTCC
 2280
 CACTCTATAG ACATCAATGT CAGTTATTAC CATTTTCTCT ATTTAAAAAC ATATTTTGG
 2340
 TATTAACAAT TAAAAGTGGG TATATATATT TAATGAACCA ATTTTGTAGAA AGTAGGCTAA

2400
ACTATGGAAA ATAAATATAC ACATGGTGTC CTCTTTTACC ATGAACACAG TGGATTAAAA
2460
AATATTAATC AAGGTATTGG GGAAGTTACA ACAGCATTAA GTTCAATTTG TAAGCATCTT
2520
TCTATTCAAT TGAGTGAAAA CGAAGGTGAC ATTATTAAAT ATTGCCAAGA AATCAAAACT
2580
AAAAACTATC CAAAAGATGT AGATAG
2606

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

CTACGATGGC ATCTAAATCT GCGGTGTCGT CAATAATCAG TGCTATTGNC TGGTGGNCCT
60
GCNATGTGAG CAATACGCTA CCTGTCCAAA TAAANATTTT GNNGNAGATG CAACAAATTG
120
GGTACCTGGA CCNACAATCT TATCAACTTT AGGTATCGTN TCTGCNCCAT AAGTCAATGN
180
AGCAATACTN TGAGCACCAC CNNCTNGANA CACTTGAGTA NCTTGCGTAA GATAACATGC
240
AGCTAATACC TCTTGGGATA CTCCGTTAGG GTGAGGTGGT GTCACANCAN CAATATTTTC
300
TACACCCGCT ACTTGTGCTA AAGTACNCTG TCATTAGANC CGTTGATGGA TAACTTGCTT
360
TGCCACG
367

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

GGCACGAGCG ATATTTGTCA GGAAGTTAAA GTTCATGGAG ATAAGGCTTT GAAAATGTAT
60
AATCTAACAT TCGATCATAC GAAAACAGAT CATTTAGAAA TTAGTCATGA ACAAATTAAA
120
GCAGCATTTG ACACATTAGA TGAAAAAACA AAACAAGCAT TACAACAAAG TTATGAAAGA
180
ATTAAAGCAT ATCAAGAAAG TATTAAGCAG ACGAATCAAC AGTTAGAAGA ATCAGTGGAG
240
TGTTATGAAA TATACCATCC ACTAGAAAGT GTGGGTATTT ATGTGCCTGG TGGCAAAGCA
300
AGTTATCCAT CAACGGTTCT AATGACAGCG ACTTTAGCAC AAGTAGCGGG TGTAGAAAAT
360

ATTGTTGTTG TGACACCACC TCAACCTAAC GGAGTATCCC AAGAGGGTAT TAGCTGCATG
 420
 TTATATTACG CAAGTTAATC AAGTGTTCCTA AGTTGGTGGT GCTCAAAGTA TTGCTGCATT
 480
 GACTTATGGA ACAGAAACGA TACCTAAAGT TGATAAGATT GTAGGTCCAG GTAACCAATT
 540
 TGGTNGCATA TGCCCCAAAA ATATTTATTT GGACAGGTAG GTATTGTTCC ANATTGCAGG
 600
 ACCANCAGAA ATAGCACTTG ATTATTGACG ACACCGCCAG ATGTAGATGC CANCGNCTNT
 660
 NATGTTTTTG GGCAAGCNAG AACATNATGA ATTAGNACGT CCATNTNTCA TTGGTGAAGA
 720
 TGCGCAAGTC CTNAAAGATT TNGAATCACN TATTGCTAAN GCATTGCCTA ATGTGGACAG
 780
 ANACGACATT GTTTCTANAA GTATCGCNAA TCAACACNAC CTNATCCANN ATNGTAATTN
 840
 NGATNTGGGN GAAGCATCNC CANCTCATGA ATACAATCGC GCCTGAACAT GCGTCGATTC
 900
 AACAGTAAA TCCTCAACCA GGAATTCTTG TTGAACGAAT AATTTCTATC TCGTTATCAT
 960
 CGTAAGCGTC ATTATCAACT TGTGTTTCTT GCATTTCTTG TAATTCGGCA ACAAACACTT
 1020
 CTTGATCTCC TCGATCACGG CTCTTACGAT TAATACGTGT TTTATATTTT CGAACTTGTC
 1080
 TTTCAAGTTT ATTATTAATT AAATCAATAC CTGCGTATAA ATCATCGTTT CGCTCTTCAG
 1140
 CTCTTAACGT AACATTTTTC AATGGAATTG TTAATTCAAT TTTAGTAGCT GAATNTGAAT
 1200
 AAGTTTTAAC TTAAACATGC GCCACTGCAT NTGGTACGTC ATTAAAATAA CGTTCCAAC
 1260
 TACCAATTTN CTCCTCAAAT ATAGNTGCGA ATAGCATCTT GTGATAGGGG AGGGNTATCT
 1320
 CCAATGAATT TNCAAATCTA TATCATANGG GAATCTCTCC CTTAAACCTC TTTATTGGTA
 1380
 ACTCTTTATT ATATTNNNAC ATTNNNACGC TATCGNGCAA ACGCAAACAC TTTGGATTCT
 1440
 CTGATATTNT NNAGCATATT AATTTACAAC CCTGCACGAT GATTG
 1485

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

ATGATGTAAA CCCAGTTCCN ANCTTCATCA TTCAGTTGAT GCAATAATGT CACNNAACT
 60
 CTACCACCAA GATGCACCAA TAGGTTGTCC CTAAATGCAA TAAGCGCCAC CCTTTAACAA
 120
 TTCACCTTTT TCAGGGAGGT NATTTTAAAT TCACCGATCC AACAGCTAAT GATTGTCCTN
 180
 CAAATGCTTC AATTTAATTC CAAATACATC AATATCGCTT AATTCTTTTT TACTACGTTT
 240
 CCAAAGCCTT TTCTACAGCG CCAACTGGTG CAATACCCAT AATAGAAGGA TCTACGCCAT
 300

GACTTCCCAA AGCCATCCAA GCACTGCCAA TGGTTCGATA TTTAATTCTT TAGCTTTGTC
 360
 TTCTGACATG ACTAACATCA TCGCAGCACC ATCATTGATT CCTGATGCAT TACCTNCTGT
 420
 AACTGTCCCG TCTTTTTTGA AAGCTGGTCT TAAGCGACTT AATTTTTCGA CTGATACATT
 480
 TTCACGGACA CCTTCATCCT TAGTGACTAA GATTGGTTCA CCTTTACGTT GAGGAATCGA
 540
 TACTGGAAC TTTCACTAT CAAATTCACC ATTTTGCTGT GCACGTACTG CTTTATTGTT
 600
 GTGAGATTAC CAGCAACATG TATCTTTGTT CTTCTCTTGA AATACCATAT TGCTCCTACT
 660
 AAATTTTCAG CAGTAATACC CATATGATAT TGAGTAAATA CATCTGTAA ACCATCATAT
 720
 ACCATGCTAT CAACCATTGA GTGATGTCCC ATTTTAAAAC CGAAGCGACT GTTGTTGNCA
 780
 AGCATTGGTG NCTGAGACAT ATTCTCCATA CCGCCAGCGA GCACGATGCT CATGCCCACC
 840
 AGTCAGCNAT AGATTGATAT GCTAATTGAN TCGACTTTAA CCCAGAGCCC ACATACTTTA
 900
 TTCACTGTAA ATGCAGGTGC TGTTTCTGGC AAGCCACCTT TCATAGCAGC AATTCGTGCT
 960
 GGATTTTGTC CTTGTCCTGC TTGTAGTACG TTACCGATGA TAACTTCATC AATCTCACTT
 1020
 GGATTCAAAC CCGTCTCTTT AATAATATGT TCTATTAAAG TCGCACCTAA ATCATAGGCT
 1080
 GGCACGTCTT TAAACGCACC TCCAAAAACG CCAATAGGTG TCCTGTATGC TGCTGCTAAT
 1140
 ACGACTCTCG TCATGTCATA TTCATCTCCT TATGATATAT ACAATTTTAT TACTAATACG
 1200
 TCTAATGAAC CAATACGCCA CTAACATCCA ATTTATGAAA CCAATTGCTA CGTATGTTAC
 1260
 ATTTTCATTC TTGTTATGCA TTTAACAAAT CATATTATAC AATGATGTAA TTTGTTTGGG
 1320
 CAATCGGAAA CGTAAACGGT TTCACTTTAA CATTTACAC TCTTAAATAT GCTCTATCAT
 1380
 CCTCATCTAT AGTACAAAAT TATGCTTTGA TTTACCACAA ATTATCATT ATCATTTTCG
 1440
 TCGTGCCTCT AATTAAATTC TTTCTATCAT TGGATCGNTA TCACAGGTGG NTTCACCACA
 1500
 ATTCTCATCA ATTT
 1514

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1000 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

GGCACGAGCT CAAGTAAAGT GCTACCATTT TTCTTACAGA CATTTGCCGA NATCTTAAAC
 60
 TAAGACATAN CCCCTAAAAT ACTCNCTANA GNACCGNACA ACCNCAACAC AATTCCTGTC
 120
 ATGATCTTAG GCTTTGTGCC ACCTNCCCCA GTTGNCAAAT GCTTTGTCCA TCCTTCTTGT
 180

AATGACTGAA ATCCTTCTTG ATACATNCGA AATGCAACAA ATGGAAATCC TTCATAAACT
 240
 GTTACGGGCA ATGATTGTGA AGTAGATGCA CTTCTTAAAG CAAATCCTTC AATAAAAATG
 300
 ACGGGTCGCA CTTTTATGAC CTCCAGTTGC ATAATAATCT TCTTTATTTG TTAATGTCAC
 360
 CGGTCCAAAT GCATGCTGGT TAGTCCGCAC CGTCGTCTAA GGTANAAAAT ACATTCATAC
 420
 CACCGACTTG TCATTAAATT AAATATCGCT GAAAACCCCT CGTAGAAACG CTTTGTTATA
 480
 TGATAAGGCT GTACGCTTAA CAATCCTTTT TCACCTTGTA ATTGATACTG ATTAATCAAC
 540
 GTTTCAACAG CATCTTTCCT TAAGAAAGTT ACATCAGCAT CTACAAAGGC AATACGATTC
 600
 GTACATGCAT GCGTCACACC TTGATAACAA GCATGTGATT TCCCCATACC ATTTGCCGTC
 660
 AGTATCATCA ACAACATCTA CTACAGTCGC ACCATATGAA CGTGCTACAC GTGCTGTTTC
 720
 ATCTGTGAT CCGTCATTCA TAACAATGAC ATCTACTGGA ACTTGCTGTT GTATTATCGA
 780
 ATGTAGTAAA TGACCTATTC TTTTTTCTTC ATTTCTAGCC GGAATAATAA TTGTTAATGC
 840
 TTTATGATTG AAGTTCAGCG TTTTCGTCTT TAGCTGATGT CTACGATTAA ATATCAATGC
 900
 ACCACACGCC ATAGACATGG TCACTATTAC TGTTAATATT CGTGATAACC ATTTCATAGA
 960
 TATCACTTCC TATTCTTCGC TTCTCGCGCG AGCCCGNGCC
 1000

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1047 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

GGCACGAGCT ATATCCAATT GGGGTAAAGC GGGTAAAGAC CAAGAGAAGA ATTTAAGAAG
 60
 ACATTAGCAG AAATTGAAAG GACACCGGCA CGAGCTAGCG CAACAAGTTT AGCGATTGAA
 120
 GCATTTGGTG CAAAAGCAGG TCCTGATTTA GCAGATGCTA TTAAAGGCGG TCGCTTTAGT
 180
 TACCAAGAGT TCTTAAAAAC TATCGAAGAT TCGCAAGGAA CCGTCAATCA GACATTTAAA
 240
 GATTCTGAAA GTGGCTCCGA AAGATTTAAA GTAGCAATGA ATAAACTTAA ATTAGTAGGT
 300
 GCTGATGTAT GGGCTTCTAT TGAAAGTGCG TTTGCTCCAG TCATGGAAGA ATTAATCAAA
 360
 AAGCTATCTG TAGCAGTTGA TTGGTTTTCA AGTTTAAGTG ATGGATTTAA AAGGTCGATT
 420
 GTTATATTCG GTGGTATTGC TGCTGCAATT GGCCCTGTAG TTTTGGGAT TAGGTGCATT
 480
 CATAAGCACA ATTGGCAACG CAGTAACTGT TTTAGCTCCA TTATTAGCTA GTATTGTAAA
 540
 GGCTGGCGGA TTGATTAGTT TTTTATCAAC TAAAGTGCCT ATTTTAGGAA CAGTCTTCAC
 600

AGCATTAAC T GGTCCAATTG GTATCGTGTT AGGTGTACTG GCTGGTTTAG CAGTCGCATT
 660
 TACAATAGCT TATAAGAAAT CTGAAACATT CAGAAATTGT GTTAATGGTG CAATTAACAG
 720
 TGTTAAACAA ACGTTTAGTA ATTTTCATTCA ATTTATCCAA CCTTACATTG ATTCCGTTAA
 780
 AAACGTCTTT AAACAAGCGG TTTCAGCAAT CGGTGATTTT GCTAAAGATA TTTGGAGTCA
 840
 AATTAATGGA TTCTTTAATG AAAACGGAAT CTCTATTGCA CAAGCGCTTC AAAATATATG
 900
 CAATTTTATC AAAGCTATAT TTGAATTTAT CTTAAAATTT TGTAATTAAA CCAATCATGT
 960
 GTGCGATTTG GCAAGTGATG CAATTTATTT GGCCGGCGGC TAAAGCCTTG ATCGTCAAGT
 1020
 ACTTGGGAGA ATATAAAGA GTAATAC
 1047

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

GGCACGAGCG GTACGAGTTC ACTGTTAATC TGCATTCAA TGTGATTATG ATCTGAGTTA
 60
 TCCTGCATTT CGTAACCGAT AGCGATGTTT GTTACTTTTT CAAAATTAAT ATCACTATTG
 120
 TTCGCTAAGC TTGAACGTAC AGACTCTAAT TTCGGCAACG TTTTATTATC CTCACTATTT
 180
 AACACAACGT CGGTGCGCAA TAACGAACGA CGATAATCAA AGACGCCTTT TTCACCCCAA
 240
 GTGACTTGAA TTTGATTAGA GCCTTCTTTA TTAAACGTTG GATAACCGTT AAGGAAACGT
 300
 TGATATGTTA ACTCGCCTGA CTGATGGCAT TCGTACTAAA CAATCTGAAG TCTTCGTTTA
 360
 AGAAACCACC ATGACCATTA ATAAAATCAA AGGTTCTTGG AATCGTTTCT TCCATTGTGC
 420
 TGGAACCTGC TTCATCTTCG GACAGGTTTT TATAATGATA TTTNCATTT TTATCGTTAT
 480
 AGTGTGNGAC ACCTGTATTA TTGNTGTAGG TTGTAACACC ACTCTNTGAN CTACGAACGA
 540
 TGGNTGANTC GACAAATAGT ATAGCATNCA TTTTCTCAAC ACTAATCGTG TTAAATACCA
 600
 TGCGATATGT TTTTANCTTN NCAGGTTTAC CTTGGGTGCA AAAACATGCG TCGNACGATC
 660
 AATTGTATCT NTGTGTGTGA TGATATCTTG TGTATGGGTT GCATATCTTT TCACACTGCT
 720
 GCTTAATGCA TCTTAAAAA TGNATCATTT CGCGGTGGTA GNTGNTTAAT TTTACGGTAA
 780
 TCGGGGCGGT CTTTACTTAT AGCATAAAGC ACGATATTAT CATCAGCATC ATGATCTATG
 840
 ACTAAACGAT TGAAATTGAA ATGATTTGGT ACTTTCGCAT TCAATGTTCA NGAACCTGGC
 900
 CAAGATATGT TGATAACGGT AAATCAAACG TAAAATCGAA TAATGTAAAA TCACTGCTTA
 960

AATCCGGAAT CATCAAGTTA TGATCACGAC GAACATGTTC CACGGACNTC ACTTCTTTAT
 1020
 TTTTCAAAGG TTTCGTCAGT TTATTCACAT TAGATACCGT CGCAATCGTA CCTTCTGGAT
 1080
 GATCATTTTT CGAATGAATA ATCTGAAATG GCGTAATAGT TGTATCCATT TTGGCTGTCA
 1140
 TAGGTGTCGT TAAAGGTTTC GTTTCACTCT TCTTACTATC TGTATTGTCTG ACATTTGCAA
 1200
 TATCAGGAGA AAAGTTCCAT ACCATATATG TCAATACGAC ACTCATCAAG ACGAGTAGCG
 1260
 CTAAAATGAC AGATTTAATA TGTTCCCTTAT TATTCATCCC AATCACCGTC TTCAATGACT
 1320
 TCACATGGAA GTGTGATAAA GATAGATGTA CCTTGACCTT CTACACTGTT TGCCCAAATA
 1380
 CGACCATTGT GCGCTTCCAC AATCTCTTTC GAAATGGCTA GTCCTAATCC AGTACCACCC
 1440
 ATTTTACGCT CGTGCCGTNC CTTATCTACA CGATAGAATC GGGNCGGAAT ATCTTTATCG
 1500
 ACTTTATTGG ATAGGAATTC CCGATG
 1526

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

GGCACGAGCG AGCAATATCA AATAATAAAT CATCATCAAT AGTTCTTCCT TGGAAACGTT
 60
 CAGGGATGAT GTTGAATAAT AATGACGTAT CTAATATATG GTCATATAAA GAGAAATCAC
 120
 CAACTGGGAT GCTATCTAAG TGATAGTACT TTTGTAATAA TAAATTTTCT TTATGTAGAT
 180
 CAGGNAATGN ATGCATCTAN CNACTCNTCN TTAGANNTCN TCNTTGCCCA ANAACTTTCTG
 240
 ATGGCTTTTC TCCATTCCCT TTCTCNACCT AATCTTGGA ANCCTAAGTT TGATGTTTTA
 300
 ATTGTTGACA TAATATTGCC TCCTTGAGAG CAGGTAATAG ATTTNGAGTA TGCTGCAAGT
 360
 TCTAATGAAT CTTGACATT TNGANACGGT GTGATAATGT ATAAACCATN AAAATATTCA
 420
 TGAACAGTAT CGATTAAATC CTTTGAAAGC TTAAGACTTA GTTCTCGCGT TTTGGCTTTA
 480
 TCATCTCTAA CTGCTTCAAA TTGGTGGAAA ATTTCANCTG ACATCTTGGA TTCCNGGCAC
 540
 TNCATTATGC AAAAAGAGTG CGTCNTTGTA ACTTGCGATA GGCATAATGC CTATGAAAAA
 600
 TGGNTTGNTC AAGTGCTTAG TGGCATGGTA AATTTCAATG ATTTTCTCTT TGCTGTACAC
 660
 GGGTTGTGTT ATNAAATAAG ACATTCCGCT TNCTATCTTT NTNCTCTAAT CTTNNGACGG
 720
 CACCATCTAA TTTACGAACA TCAGGGTTAA AGGCGCCAGC GATGTTGAAG TGTGTACGTT
 780
 TCTTCAGCGC ATCACCCCCA GNGTTAATAC CCTGATTAAA TCTTAGAGCG AGTTCANCNA
 840

ATCCTTTAGG AATTAACATC ATAGACATTG GTTGACCTG GTAAGTGACC AACTTTGGAA
 900
 GGATCACCAG TTATGGCTAA TATTTCTGTTA ACGCCAATGA GCGATAATCC AAGTAAATGG
 960
 GACTGCAAGC CGATTAAGTT TCGGTCTCGA CATGTAATAT GTACGAGTGG NTCAATATTG
 1020
 TAATATTGCT TAATTAAGCT AGCAGCAGCA ATATTGCTAA TTCTGACAGT TGCCAATGAA
 1080
 TTATCTGCGA GTGTTACCGC ATCTACATTA GCTTTATCAA GTTTAGCGAT ATTTTCAAAA
 1140
 AATCTATCCG TGTCTAAATG TTTCGGTGTA TCCAATTCGA TAATAACGGT TGGACGTTCT
 1200
 TGAACCTTAG ATGTTAATGA TTGTCTAACT TTATTTTGAG ATGGATTGAA AAGTGCTTTC
 1260
 GTTGGTATCG GAATCACTTT TNTGNCANTA ACAGGTTTAA GTGTCNGAAT AGATTCTTTA
 1320
 ATAAATTTGA TGTGCTCTGG CGTTGTACCA CAGCAACCAC CAATTAAACG AACACCTTCG
 1380
 CGAATTAGTG CCATTNTGGN GNAACTTGAC CGAAATATTG T
 1421

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1886 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

TTATTTAAAA GTATCCAATA GCCAACAATC TCTTTCATCT TTGAGTAGTA TCCCACGTAT
 60
 TTCGGGATTG CATCCGAGTT GATTTTTATN ATTTTCTTCA ATGCTATCAA GCGCAGCTCG
 120
 TTTACGTCTT ACTTTAGGTT TTATTTGCTC AATTGCCTTG ATTGTTTGAT TTCTAACATC
 180
 AGTAACAGCA GCATCTTGAT TTGTATTTTC TATTTCTTGT TGCGCTTGTT TGAGTGTGTC
 240
 GCTAATTAAT TGATTGCTT CATCTAATTC ATCAACTGTT GCATGTGGTG TATCTTTTAT
 300
 TGATTCTACT TGATTTTCTG CAGTTGCTTT TATTGCTTGT TGTGCTTCAG GCTTAATTAC
 360
 AATATGAGGT TGCACGAGCA CCTTTTAGTG TAGCAATGCC ATTNNGTTTCA ACACGTTTCA
 420
 CATCATTANT CGTGACTGCT TGATTGAGGT TTTGTAATGC AAGTTTTTCA TTATTCGCTA
 480
 ATTGATTTAA AGCAACTTGT TTTTCTTCAT CAGTCNCATG TTCAGCTTGC TCTATTTCTT
 540
 GCTTTTTCAG CTCATATTGT TGCTTTACTG CATCTCNAGC AGCTGCTCTA AAAATATGTT
 600
 CAGGCGCTAC TAAAGCAATG CTATCAAGCG CTTGACTTGT TGTATCATCA ACTTGTTGAT
 660
 TTGTTCTATT ATTCGTAATA TCTGTCATGG CTTGATTTAC AAATTCNTAT GNTNTTATCT
 720
 AGTGCTACGT TGTCNNTCNG CCTGCTGTTG CNTCTTTATC CCTGANTAAT CGTAGCACAG
 780
 TAAATCATTC GCNTGTTGGA TTGAGTTTTT CCACGTTGCC AGCTGGNGGT AACTTTTTGT
 840

TTCAGGGTGA ATAATNTTAA TCGCTGATAC ACCATTTGTT CCTGCTTGAT TCACCTGACN
 900
 ATTCGTTTGA GCNTGGTCAA TANCTCCAAG TGCTTTTTCT TTTTCTTTAG CTAATGCTTG
 960
 TGAAGCAACT TCTTTCTCAT NATCTGTTGA ATCAAGACTA TTATCAATTT GCTGTTGCTT
 1020
 TTCTTTAACA GCTTTTTTCAA NATCTGCAAT TGCCTTTGGT TTAATTACTA CTTCAGCTNC
 1080
 AACATTATCT ATAGCATTTA CCGCTTGATT TGTAGTTGTG TCTACCTGAT CATTTGTTTG
 1140
 GTTTTGATTA ATTTGATTAA TTGCTTGATC TTAAAGTTGA GTGATTTGAT TAACAGCAGC
 1200
 CTGCTTTTCT TCGTCAGTTG CATTAGGTGT TTGTTTAACC GCTTCAATAC GCTTCGCCAC
 1260
 TTCAGCAGTG ATTTTATCTC GCGCTGCTTG TTTTTTACT ACATCAACTT GAACAGCATC
 1320
 GATATTATTC TCTGCTACTG TCGCAGCTTG GTCTACTTCT GCATTTGTGT TAGCTTGTTT
 1380
 AATACTTCNA ATAGCTNGTT GTCTGTCTTG ATTTAAAGTA TAGATCGCAG CATTTNTCTC
 1440
 AGCATTCGTT GCATCTGGTG TAGCATTGAT TTCAGCTAAT TTAGCATTAT AATGCTGATT
 1500
 GATTTGTGCT AATGCTGCAG GTTTATTAAAC AATATTTGGC TGAATCGCAT TAATTGCTTT
 1560
 TGTACCTAAT TGTTGCGCTT GATCTACTTC CGCATTTGTA TCAGCTTGAT TTATATTATT
 1620
 AATTGCCGTT GCTAACTCTT GATCCACTTG ATTTAAAGCC ACTTGCTTTT CTTCAGTTGT
 1680
 TGCATTTGTG TTTTGATTAA TTTCTTGCTT TTTAGCAGTT GCTAAATCAT TTAATACACC
 1740
 TGTAGCAGGT TGTTTCTTCG TTACATGCGG TTGACTGCGC CGATTTGATG ACTGCATCGN
 1800
 CTCTAATACT ATTGACCACC GAGTAGTAGA CGTCACACAA TATCAGTAAT GCTCTATTTT
 1860
 AGTGATTGAA ACGAATATCG GTCTTG
 1886

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GGCACGAGAC AATATATCTA CCGTGAATAA CTGTGCAAAT AGTGAAGTTG TAGCCGCCAT
 60
 ACGCATTTCA TTTTCATCAG TTCTGCCATA AATCAATGCA TAGTCGGCAA TTTGAGCCAC
 120
 GTGCCGATTA TTCGGCACGA GCTGTACTAG ATATAGTTAT GATGGGAATA CTGTAATGTG
 180
 TGGCCACCTG TGCAATTGAC TGCAATTCAC TATGACTACC TTGATTCGTC AAAAAATCA
 240
 TGCAATCTCT ATCATCATGC GTCGCAAATG TTGACACAAG TAAATGCGTT TCATGTAATA
 300
 ACCTGACATT TAAGCCAATA CGAGATAACT TTTGAAAAAG ATCACCAATA GTCAAACTCG
 360

ATGCGCCAAA TCCAAATAAA AATATTGTCC TGGCATTTTT CAACACATCA CAAATTGCAT
 420
 CAATTTGCGC ATCCATAATA TTAGTAGCTA CAAATCGCAT CCGTATTCCG TTGCTCTAGC
 480
 AATCATTTTA TTTTCAAAG TTTCTACAGA TTCATTTTCA ATCAATTCTA AATGTGGATT
 540
 GGTTGCAATA TCTTCGGGTA AGTATCGAGA TATCGCAATC TTTAGCTCTT GAAAACCTTG
 600
 ATGTGTCATT TTCCGACTAA ATCTAACAAT TGATGCTGTA CTAACATTCTG TAACATCTGC
 660
 CAAATCATTC ACCGTCATAT CAATGATTTT ATGTGGATT CTTAAAATGT AATCAGCGAT
 720
 TATCTTTTCT GTCTTCGTAA AATCACTCAA CTGTTTATCA ATGCGATATT AAAATATTTG
 780
 TCATCATTAA TCACCCAACA AATCTGTCTT GTCGCATCGC CTTTGTCGGT CCAAATAAAT
 840
 ATGTACAAAC GAATCCACCA GCATATGCAG CAAGTAATCC TGCAATATAA CCTAAATACA
 900
 TATTATCTGA GATTAATGGT AAGAGTGACA CACCACTTGG GCCTATTGCT TTGGCACCAA
 960
 TATGTCCAAT TCCACCTATT ACAGCGCCAC CAATACCACC ACCAATACAA GCAGTTAAGA
 1020
 AAGGTGGAAC TAATGGGCAA AGTCACACCA TAGATTAATG GTTCTCCGAT ACCTAGGAAA
 1080
 CCAACTGGCA ATGCACCTTT TAAAGTATTA CGTAATGTTG TGTGCGTTT ACATCTTACC
 1140
 CAAAGTGCTA ATGCGGCACC TACTTGTCCA GCACCCAGCC ATCGCTGCAA TTGGCAATAA
 1200
 GTAAGTAGCA CCAGATTGGT TAATCAATTT CTATATGAAT TGGCGTNAAA AATATGATGA
 1260
 AGGCCCTAAC AATAACTTAA CGGTAGGAAG CTTGGTCCAA ATGATAAATC CACTTAAATT
 1320
 ACGNCACCCA ATACTTAATA ATCCCCGTTA CTACTGAAAC TTAANTTGTC TTTGAAACAA
 1380
 A
 1381

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

GGCACGAGCG TTTTAGTTGA TGTGTATCAC TAATATCTTT GAAAATTTTA ATCAGGTACT
 60
 ACGACAATAT GATGTCTGTT TTGTGTCTGA AAGTTTTACA GTTTTAAAA TAAAATGGT
 120
 ATAAAGTGTG ATTTGTATAA AAAAGAGTCT CGACGGATAA GAATTGATTA ATAACAGTTA
 180
 GCATTTTATT AATTACCTTA ACAATGATTC AAGTTTAGTT AAATGAGGTT TAATTTGAAA
 240
 GGGGATAGCG CCTCAATATA ATGTAGGTAG ATTGTTTATA TTACGTAATT GAAAAATCAA
 300
 ATTTAAATAN ATAGGGTGGG GCTNNAAATT ATGAAATTTA AAGCGATAGC AAAANCAAGT
 360

TTAGCATTGG GAATGTTAGC AACAGGTGTA ATTACATCGA ATGTACAATC AGTACAAGCG
 420
 ANAACAGAAG TTANACAACA AAGTGAATCA GAGTTGANAC ACTATTATAA TAAACCGGTT
 480
 TTAGAGCGTA AAAATGTTAC TGGATATANA TATACTGAAA AAGGTAAAGA TTATATAGAT
 540
 GTCATAGTAG ACAATCAATA TTCTCAAATT TCTTTAGTTC GGATCTGAAT AAAGACANAT
 600
 TTNAAGATGG AGACAACCTCG NATATAGATG TGTTTATCCT TAGAGAAGGT GACAGTAGAC
 660
 AAGCAACNAA TTACTCAATT GGTGGCGTAA CACAAACAAA CAGTCAACCT TTTATTGACT
 720
 ATAG
 724

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

CCTTCACCAA TACGTGTANT ATCNTTATTT GGGCGNTTGT CCACTTACCC ATGTAATCGT
 60
 GGCATCTGGA ATGGCACTAC CATTAGATAA CTAAAGTAA TCTGCTGCAC TAGAACCATT
 120
 ACCTGCTGGG AAGTCTTGGC CTTGTACAGT GTAATGCGAA TGTGCAACGA TTTCTGGAAT
 180
 GACATGCTTT ACAGGTACAG TCACTGTTGA TGTTGTTCCA TCTTGATGAG TAACAGTTAC
 240
 TGTGACATTG GCATTATTTT CAGTACGACT GACATTACTA ACTGTTTTAC TAGTGATTTT
 300
 ATTTGCGCTT GCTGTTGCAT AGTTTCTATT TGGTGCATTA CTTGTAAACG TTAACGAATT
 360
 AATAATTGTC GCTTGATCAG CTTGTGATAC TGTCGCATTA TTCGAAATAT TGGCAATTCT
 420
 AACAGGATTA GCAGNCCGTT GATGAAGTAC CAACTCGATA TTTATCACGC AAAGGTTTCA
 480
 CTGTTACATT GAATGAAGTT GTAGCTGTAT TACCACTNGT ATCAGTTGCT AATAAATTGA
 540
 TTGTCTTACT AGTTGCTGAT GTCACATTTG GTGCCGTTGC AGAAACATGT TGATGGTTAT
 600
 TATCAACAGT CTCGTGCC
 618

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1005 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

TTGTGAGACA CACGCTTAGT GCACATGACA ATGTGAATGT TGTTGCACAA ATTATTAAAA
 60
 GAAGACTTAC CACTGTTAAG TTGTATCGAG CCGAATGATA CATTTGATTT TCCACNAAAC
 120
 TAGGGAGTGT AAGAAGTGAT GGAAAATAGT AGGCCCGAGC GTAATGAAGC GACGATGCAT
 180
 CTTGATGAAA TGA CTGTGGA AGAGGCTTTA ATTACGATGA ATAAAGAAGA TCAGCAAGTC
 240
 CCGTTAGCAG TTCGAAAGGC AATACCACAA TTGACAAAAG TAATAAAAAA AACAAATTGCA
 300
 CAGTATAAAA AGGGTGGACG ATTGATCTAT ATCGGTGCAG GTACAAGTGG AAGATTGGGT
 360
 GTCTTAGATG CAGCGGAGTG TGTACCTACA TTCAATACTG ACCCTCATGA AATTATAGGT
 420
 ATTATTGCTG GTGGACAACA TGCTATGACG ATGGCTGTAG AAGGTGCGGA AGATCACAAA
 480
 AAATTAGCGG AAGAAGATTT GAAAAATATA GATTTAACAT CAAAAGATGT CGTTATAGGA
 540
 ATTGCCGCGA GTGGCAAAAC GCCATATGTT ATAGGCGGTT TAACATTTGC TAACACAATC
 600
 GGTGCTACAA CAGTATCTAT TTCATGCAAT GAACATGCAG TTATAAGTGA AATTGCGCAG
 660
 TATCCAGTAG AAGTTAAAGT TGGTCCAGAA GTATTAAC TGTTTAAAGTCT
 720
 GGTACAGCAC AAAAGTTAAT TTTAAATATG ATTTCAACCA TCACAATGGT TGGTGTGCGGA
 780
 AAAGTTTACG ATAACCTCAT GATTGATGTT AAAGCAACCA ATCAAAAACT GATCGACCGT
 840
 TCAGTGCGTA TTATTCAAGA AATATGTGCT ATCACAATATG ATGAAGCAAT GCGGTTATAT
 900
 CAGGTATCTG AGCATGATGT TGAAAGTTGC GACAGTTATG GGTATGTGTG GCATTTCTAA
 960
 GGGAAGAAGC AACAAGACGG TTATTAAAC AATGGTGACC TTGTT
 1005

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

GGCACGAGCG ATGACAGGAA TATGATATTG TTTTGCAGCT AACGCAACGC CTACGGGTGT
 60
 TTTACCAAAG ATGGTCTGAT AATCCATGCG TCCTTCTCCA GTAATAACGA GGTCTGCATC
 120
 TTTAATTCTT TGATGAAAAT CTGTAATGTC AAAGACGACA TCAATACCTT TTGTTAAAGT
 180
 TGTCTCACAA AACGCTAATA ATGCTGCGCC CATACCGCCA GCTGCACCGAG AACCTGGTAT
 240
 TTGATTATAC GGACTTTCCT GTGCACATTT TTATCTTATC ATGACAATGN GACATTGCGA
 300
 AATCCAAATT AGGTATGCAT CTTTGCATCA GCGCATTTTT GAGGACCATA AATATAGGTA
 360
 GCACCATTTT CACCCAATAA AGGATTTGAA ACATCACAGG CCACTTTAAA GGTCACCTCT

420
 TTTANTCGCG AATCGGCCAG ATTGGTTATA TCGATTTGTG CAATGTGAGC AAGATTAGCA
 480
 CCATTCATTT GTAATAAGTC CCCGTTTACA TCAGTAACT TTACGCCTAG TGCACCTAGC
 540
 ATACCTGTAC CACCATCATT TGTTGCACTG CCACCAATCC CTAAAATAAT GGTCTTAGCA
 600
 CCATGATTTA ATGCATCTTT AATTAGTTCA CCGGTACCAT ATGATGATGT GTATAAAGGA
 660
 TTACGTTCCCT CTTTTTCTAA TAAATCCAAA CCTGACGCTG CCGCCATTTT AATAATTGCA
 720
 ATTTGTTGTT CGTCTGCGCG TGCATAACAT GCTTCAATAG GTCGCATTAA AGGGTCATTA
 780
 ACGATGACTG TATACTTAGT GGCANCTGNT GCATGAATTA ANGCATCTGN GGTACCTTCA
 840
 CCACCATCAG GCATCGGAAT GATATCATAA TGAAGGGTAT TCCCATAAAC ATTAGTAAAT
 900
 GCCTGTTTTTA TAATATTGNC AACTTGGTGT GNGGNCATAC TTTCTTAAA TGAGTCAGGA
 960
 GCGATGACAA TTTGTTGGGA ATGGATGGNA GNCACCNCTC AATATGNNGG CGNTCTTTTG
 1020
 GTTTTANATT NTAGTGACTN
 1040

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

TGTATAGGCC TATTTGTATA NAAAGTAATA TGATGTTTAG TGGCTATGTA AGTGAAGCAA
 60
 TGTATAAATA ATGATGAGTG GTTTGTTACT AATGATAATG GCTATGTAAA AGAGCAGTAT
 120
 TTATATTTNG CGGGACGTCA ACAGGATATG TTAATTATTG GTGGGCGAAA TATATATCCA
 180
 GCACATGTTG TNCGCCTTTT AACGCAATCT TCGAGCATTG ATGAAGCAAT TATCATCGGT
 240
 ATTCCACATG AGCGTTTTGG TCANATAGGC GTATTGCTTT ATTCTGGTGA TGTGACACTT
 300
 ACACATAAAA ATGNAAACA ATTTTTNAAA AAGAAAGTGA AACGCCATGA AATTCCATTC
 360
 GATGATTCAT CATGTAGAAA AGATGTATTA CNCTGCAAGT GGTAAAATTG CTAGAGAAAA
 420
 AATGATGTCG ATGTATTTGA GAGGTGAATT ATAATATGAA TCAAGCAGTC ATAGTTGCAG
 480
 CTAAACCGAA CTGCATTTGG GNAATATGGT GGCACCTTAA AACATTTAGA GCCAGAACAA
 540
 TTGCTTAAAC CTTTATTCCA ACATTTTAAA GAGAAGTATC CAGAGGTAAT ATCTAAATA
 600
 GATGATGTAG TTTTAGGTAA TGTTGTTGGG ANTGGTGGCA ATATTGCAAG AAAAGCATTG
 660
 CTTGAAGCGG GGCTTAAAGA TTCAATACCT GGCGTCACAA TCGATCGGCA ATGTGGGTCT
 720
 GGACTTNGAA AGTGTTCAAT ATGCATGTCG CATGATCCAA GCCGGAGCTG GCAAGGTATA

780
 TNTTGCAGGT GGTGTTTGAN AGTACAAAGTC GAGCACCTTG GAAAAATCAAA CGACCCGCANT
 840
 CTGTGTACGA AACAGCATT A CCNGAGTTTT TATGAGCGTG CATCATTTGC ACCTGAAATG
 900
 AGCGACCCAT CACATGATTC AAGGTGCTGA AAATGTGGCC AAGATGTATG ATGTTTCAAG
 960
 AGAATTACAA GATGAATTTG CTTATCGAAG TCATCAACTG ACAGCGGAAA ATGTAAAGAA
 1020
 TGGAAATATT TCTCAGGAAA TATTACCTAT AACCGTTAAA GGAGAAATAT TCAATACTGA
 1080
 TGAAAGTCTA AAATCACATA TTCCGAAAGA TAACTTTGGC CGATTTAAGC CCGTAATCAA
 1140
 AGGTGGGACC GTTACCGCTG CGAATAGTTG TATGAAAAAT GATGGTGCAG TTTTATTGCT
 1200
 TATTATGGAA AAAGATATGG CATACGAATT AGGTTTCGAG CATGGTTTAT TATTTAAAGA
 1260
 ATGGTGTTAC GGTAGGTGTT GATTCTAATT T
 1291

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

CATTCACTA ACCTNTTCAT CAGTTGAGTG ATTTTAATCT ATCCTTCAAA AGTTNGNGGA
 60
 TCAGGTCCAA TTCTCTTATC TAGATTTAAA CCAGGCACGA GCGTCATTTG TTCATCTGAT
 120
 AATTGCAAAAT CAAATATTTG GAAGTTTTCA GAGATTCTGT TTGGTGTTAC CGATTTAGGG
 180
 ATTATAACCA CACCATGCTG CACATTCCAT CTAAAAACAA CTTGGGCAGG TGACTTTCCT
 240
 AATTCTTGAG CAATGTCTTT AATTGTCTCA TCATTTAAAA TTTGTGCATT CATCAATGGT
 300
 GACCAAGATT CCATCACGAT ATGTTGTGCT GCCAAATATA ATTTCAATTT ATGTTGCGTT
 360
 AAATATGGAT GATATTCAAC TTGATTAAIT ACAGGTTTAA TTGACACTTG TGCCAACAAA
 420
 GCTTCCAAAT GTTCAGGTTC AAAAAATTGCT GACACCTATA TTTTATAGCTT TATTATTTTT
 480
 ATATAAATCT TCCATACCTT TCCATGTTAT CAACCATTAC GGCTTCGTTT GTGCCTGGCC
 540
 AATGTTACTA RRDCTNS
 557

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 904 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

GGCACAATTC GGCACGAGCG TTGGTATGTA GAATATGATG GTGAATGGTA TGTGTATAAC
60
GATGGGAGGC TTGAATAAAT GAACTGGAAA CTGACAAAGA CACTTTTCAT TTTCGTGTTT
120
ATTCTTGTCA ACATCGGGTT AGTATCGATT TATGTTAATA AAGTCAATCG CTCACACATT
180
AATGAAGTTG AGAGTAACAA TGAAGTTAAT TTTCAGCAAG AAGAAATTAA NGNACCGGCT
240
AGTATATTGA ATAAATCAGG TAAAGGTATA AAATGAGAGC AAATTACAGG GCGATCAAAA
300
GACTTTAGTT CTAAAGCTAA GGGCGATTCTG GATTTGACCA CATCAGATGG TGGAAAATTA
360
TTGAATGCGA ACATTAGTCA ATCGGTAAAG GTCAGTGACA ATAACTTAAA AGATTTGAAA
420
GATTATGTTA ACAAACGTGT GTTCAAAGGT TCAGAATATC AATTAAGTGA AATTAATTCT
480
GGTTCTGTAA AATACGAACA AACGTATGAT AATTTCCCGA TTTTGAACAA TAGTAAAGCG
540
ATGTTGAACT TTAATATAGA AGATAACAAA GCGGCTAGTT ATAAACAATC AATGATGGAT
600
GACATTAAGC CCACAGATGG TGCAGATAAG AAGCATCAAG TTATTGGAGT GAGAAAAGCA
660
ATCGAGGCAT TATAGTATAA TCGTTACTTG AAAAAAGGTG ATGAAGTCAT TAATGCTAGA
720
CTCGGTTACT ACTCAGTCGT GAACGAAACG AATGTTCAAT TGTTACAACC AAAC TGGGAA
780
ATTAAAGTGA AGCATGACGG TAAGGACAAA ACGAATACTT ACTATGTCGA AGCGACAAAT
840
AATAACCCTA AAATTATTAA TCATTAATAT GAATCGTAAT AAGCTAGTAT TGCAAGCTCG
900
TGCC
904

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

TTGTACCACC ACAGTTGTCA CGGAGACCAT AAAGATGCCG AGGAGTAAAA GTAAAAAGAA
60
CCAAATAGAA TTGATACCAG CGGCTGATAT GTTAAACTTG TTAGGGTTTG AATTACAACC
120
AACTAATGAT GGATTGATTA TTCATCCGTC AAGAATTTAA AACAAATGCA ACAGTTGATA
180
GTTTAACTGA TCATCGAATA GGAATGATGC TTGCAGTTGC TTCTCTACTT TCAAGCGAGC
240
CTGTCAAAAT CAAACAATTT GATGCTGTAA ATGTATCATT TCCAGGATTT TTACCAAAAC
300
TAAAGCTTTT AGAAAATGAG GGATAATATA AAATGGAAGA TATCTATAAA TTAATAGACG
360

ATATCAATCT ACAAAACTA GAAAATTTAG ACTCTCGTGT TAATGAAGCA ATAACACTG
 420
 ACAACGATGA CGCATTATTT ATTCTAGGAG AGACACTTTA CAATTTTGGA TTAATGCCAC
 480
 AAGGTTTGGA AGTATTCCGC TCGTGCCATA TCNCAAATAT CCAGNCGANA GTGANGTGCT
 540
 GATTTATTTT ATTGAAGGTT TAATGTCTGA NAATCAACCT GCCGAAGCGT TAGAANANTT
 600
 AAGTTATGTT GATCCATCAC CTGCNNAGTT GATGTTNAAG AAATAGTTTT GCGANNTGAT
 660
 TATCTAAAC AGTATTCAGA ANTTATTTGG TAGAAAATA
 699

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

CCAAACAACC TATCCTTCAA ACAATTATCC AATATTTGTT GAACATGGTG CAATTGACCA
 60
 TATTAGCACG TATATTGATC AGTTTGATCA AAGTTTTATA TTAATTGACG AGCATGTAAA
 120
 TCAATATTNT GCTGAAAANT TTGATTGAAA TTTTAATCAA ATTGAAAATG TCCATAAAGT
 180
 TCATTAATCC NAACCTGGTG AAAAAGACGG AAAACATTTG ACCAATATCA AAGAAACATT
 240
 AGAATACATT NTGGTCACAT CATGTAACGC GTAATACAGC GATTATAGCT GTTGGTGGTG
 300
 GTGCGACAGG AGATTTTGCA GGATTTGTAG CAGCAACACT ATTAAGAGGT GTCCATTTTA
 360
 TACAAGTTCC TACAACGATT TTGGCGCATG ATTCTAGTGT TGGCGGTAAA GTGGGTATTA
 420
 ACTCAAAACA AGGTAAAAAC CTTATCGGTG CATTTTATCG TCCAAGTCT GTGATTTATG
 480
 ATTTAGACTT TTAAAGACG TTACCATTTG AGCAAATATT AAGTGGCTAT GCAGAAGTTT
 540
 ATAAGCATGC GTTATTGAAT GGTGAATCAA CGACGCAAGA AATCGAACAG CACTTTAAAG
 600
 ATAGAGAGAT ATTACAGCCA TTAAATGGTA TTGGATAAAT ATATTGCTAA AGGT
 654

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 880 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

CTAACTTTTCG CTTTTTCTTT TTCTTCAATG TCTTGCACTT GTCTTTCAAC AATGTTAAAT

60
 CTTTGGTTGTA AACCTGCTTT TTCTGTTTCT AGTTGTTTGA TGTCTTCCAT ATCAATATTT
 120
 GGATCTGTTG CTTTCTGACT CAATTCATCA TTTTATTTT TTAATTGNTG TCCAATCATA
 180
 CCTAAGGATT GTTTNAATTC ATATAATGTC GGCATNTCAT TTCCTCCTAA TAANTCATTG
 240
 TCATTTTTTAA AATTTGCGAT TCGAGCGTAC AATNTNNTCT CTNTNNTCTT NCTCTTCTAG
 300
 CGACATACTT TCTTTAGGTG GTTTCACCA ATCCAGATCG TATCTNACAT CATCAATTTT
 360
 AGTGATTTTN TCTACATCTT TCTTTAAATC TTCTGGGACN TTCTCNAAC GCCTACATTG
 420
 CTCTTTAGAG ATACTAGCAG CTATTTTATT AGCTCCTAAA ATTTTATCTA TCAAGCCGAA
 480
 AGACAAGGCT TCTTCTGCAG TAAGCCAAGT TTCTGCATCT AACATCTGTT TTAAGTGTTT
 540
 TTGATCTAAA TCTNTTGNTT TATCTAAATA AGCTGAATTA CTAACAGCAT CTGTTTTTTC
 600
 AAGTAAATCC GCTGTCTTTC TTAATTCTTC TGCATTACCT ACAGTCATAA CCCATGAATT
 660
 ATGAATCATT AAAAACTAT TNNTGGGGCA TAAAAATAGT GTCACCACTC ATAGGGATAA
 720
 CAACTAGCAA TTGGATGCCG CTAAGGCATC GACATAGATA TTANTTNNTG GAGGATGCAT
 780
 TTNTAGCATA TTGGNTTTTT GGATGNTCCN CAAATACANT GGCTCCAGAT GAATTTATAT
 840
 TGAACAACCT TTTCAACTGA TGTCTCCNNG GTCAACTTAG
 880

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

AGTATTTTTT TGACCGAGAC ATGCAAGCCC TCCTGGTTGA TTATCATTTA CATATCGTAT
 60
 CATAACCAAT CATAACAAT AGTTTTATTA ACTTGTAGAC ACAATGTTTG CTAAAGTCAT
 120
 TTTTAAAAAA TATAGCCAAA AAATTAGCTA TATATTATAA AAGCGTGATA TAAATGTTTT
 180
 ATATAACAAA GAAATAAAAA TCATTTTTTTA CAAATGGTTG TAAGAAAAAG ACATGCAGAT
 240
 GTTGTTAAAA TTTTAATAAG AATCAAGGAG GCTATATTAT ATGGCTAAAC TAAATGTAGA
 300
 AGTATTTGCG GACGGTGCAG ATATTGAAGA AATGAAAGCA GCTTATAAAA ACAACAAGT
 360
 GGATGGTTTT ACAACAAATC CTAGTTTAAT GCCGAAAGCG GCCGTAAGCA GATTACAAAG
 420
 CTTTTGCTGA AGAAGCTCGT GAAAGAAATT CCAGATGCTT CAATTTTATT TGAAGTATTT
 480
 GCAGACGATT TAGAACTAT GGAAAAAGAA GCAGCAATTT TAAACAATA TGGCGAAAAT
 540
 GTATTTGTGA AAATTCCTAT TGTAATACA AAAGGTGAAT CAACGATTCC TTTAATTTAA

600
AAACTTTTCAG CTGACAATGT GAGATTAAAC GTTNCGGCTG TTTACACAAT TGAACAAGGT
660
AAAGAAATAA CTGAAGCAGT AACTGAAGGT GTGCCCAACA TATGTTTCAG TATTTGCAGG
720
ACGTATTGCA GATACAGGCG TAGATCCATT ACCATTAATG AAAGAGGCTG TAAAAGTTAC
780
GCATAGTAAA GACGGCGTTA AATTATTATG GGCAAGTTGC CGCTCGTGCC
830

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

NTTAATTTTA AAATGTACAA TGATATNTGT GAAAGCGCTT GCTTAGGAGG TGTATNTGAG
60
AGTGAATGAA ATGAATGCTA AAGAACNATT AGTGGACNAT TTAATGAAAA CATCATCGCA
120
ATTATTTTAAA TTNCACGGTG AAGTTGNCAT GCAGCTTNTC TTAAATGATG AATTAAAATT
180
ACCTTCTATT GNTGAAATAT GCGTGGAACG TAAGCGTTTA AGTGATATTG TGAAAGTTAT
240
TCCGCAATCA TATGCGTTAC TATACATAGA TAAGCAAGAT CAAGCAAGAG CTAAAGANNA
300
TTTATCACTT NCAAAAATTG CAAAAGTTTA TGTGCAATAT GATGATACAA CAATAATGAG
360
TATTTTCGTT TATGATGTAG TAAACGATGA ATGGATTTTA AGATTGGATC CGAATATACG
420
TATACCTAAG AGTAACATAT ACTTCCATAG TTAAATTGG GATGTGGATT ATATTAAACC
480
GGAGATCGTT CTAATGTATG ATCTAATGCA ACACCATCAG TATCATCATT ATTCCAATTA
540
TAAACGAGTC ATAGATGCNT TAAGCTACTA TCAATTTTTT ATTTTAAAT TTGTAGTAGG
600
TGAGCNACGT ATTAAGGATG CAATCCAGAA GAACAATAAA TAATTAAGAA AAAGCAATTC
660
ATAACGCAGT TGAATACATG TGTTACGAAT TGCTTTTATA TTAGTTTTTA TCACACAAGT
720
TTTTTAATGC AACNCCGTGA TAGCAAACT CATATGTAGA TAATACAGCT TTTTCAGCAT
780
CATCTACAT
789

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

ATATTCGAGA CGACCTAAN TAATTGTGTT GTCTGTCATA CTGGGNCANG ATTTGTGTGN
60
CTANATACNA CTNATCATTA GCANTAGATT GTTTATATGT TGTTGAGTGG CAAAATTGTT
120
GTGGTGCGTG TGGGGTTGCN TGCTGAGATG AGTGAGTATA TTGTTGAGTA TTATATGGCT
180
CTGGTGTTGG GTGTTGCGCC TGTGGCACGT TAGNCTCGAG CCGCTGGGTG TGTATTATCA
240
TCAGTTTTCT TCTGAGTATC ATCTGAGNTA TCTTGAGATG CATTGTCATC CTTATCTTTC
300
GACTCATCCT NTGATGCTTT ATCATCATTC TCNTCTTTAG CAGGACGTTG CTTTGTAGGT
360
GCTTGTTGCT GAGGTGGCAC ATATTGATAT TGATTCTGCT GTGGCAATTG CTGATATTGG
420
TTTGCTTG TG AATCTAGCTC AGCCTGCTTT TTTTCTCTT GTTGCTTTNN CTTTCTCTCT
480
TTATCTGCAA TTTCTTTTTG ACGCTTTTCT TTTTGTTTCT GCTTTTTGTT CGTTCAACAT
540
ACGTTCTTTA GCTTTATTCG AATGAATCTA CATATGCAAA AATTGCAAAT ACTAAATCCT
600
CCCGA
605

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 683 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

GGCAGGAGAC TGGTGGAGGT TCAGGTAACG CGCCGGCACG ATTAATGCCT GATAAAATAT
60
TGGATTTAAA GTATAAGTTG CGTGTTAATA ATGTACCGAC ACCAAGAACA GTAACATTTA
120
ATGATACATT AACATATAAA ACATATACAC AAGATTTTAT TAATTCACCT GCTGAAAGTC
180
ATACTGTAAG TACAAATCCA TATACAATCG ATATCATCAT GAATAAAGAT GCATTACAAG
240
CCGAGTTGA TAGACGCATG GCAACAAGCT GATTATACAT TTGCATCATT AGATATCTTT
300
AATGATCTTA AAAGACGTGC ACNAACGATT TTAGATGAAA ATCGTAACAA TGTACCATTA
360
AATAAAAGAG TTTCTCAAGC ANATATTGAT TCATTAACTA ATCAAATGCA ACATACGTTA
420
ATTGGAAGTG TTGATGCTGA AAATGCNGTT AATAAAAAAG TTGACACAAA TGAAGATT
480
AGTTAATCAA AATGATGANT TGACAGATGA AGAAAAACAA GCNGCAATAC AAGTTATCGA
540
GGAACATAAA AATGAAATAA TTGGTAATAT TGGTGACCAA ACGACTGATG ATGGCGTTAC
600
TAGAATCACA AGATCAAGGT ATACAGACCT TAAGTGGGGA TACTGCAACA CCGGTTGT
660
AACCAAATGC TAGGAAAAGC AAT
683

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 932 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

TGATGATTAG ATAAATTGAA ACAACAACGT ATTGAGTTGA ATGAACAAAT CGATGCGCAG
60
GAAGCTACAT ACAAGTTTGT CACCAAGATA TTTTAGCTAT CGAAAATCAC TACCAAGATA
120
TTAAAGCTGA ACAATCAAAG TTAGGATGTA TTAATTCATC ATGCGATAGA TCATTTAAAT
180
GATGAATATC AATTGACTGT TGAACGTGCG AAATCTGAAT ATACGAGTGA TGAATCGATT
240
GACGCATTAC GTAAAAAAGT TAAGTTAATG AAGATGTCCG ATTGATGAAC TAGGTCCTGT
300
AAACTTAAAT GCAATTGAAC AATTTGAAGA GTTAAATGAA CGTTATACAT TTTTAAAGTGA
360
ACAACGTACA GATCTTCGTA AAGCTAAAGA AACATTAGAG CAAATTATAA GTGAAATGGA
420
TCAAGAGGTT ACTGAAAGAT TTAAAGAAAC TTTCCATGCT ATTCAAGGAC ATTTTACAGC
480
TCGTGCCCAA ACAATTGTTT GGTGGAGGCG ATGCAGAATT GCAATTAAC TGAAGCCGATT
540
ATTTAACAGC TGGTATTGAT ATTGTGGTAC AACCACCGGG TAAAAAGTTG CAACATTTAT
600
CGTTACTGAG TGGTGGTGAG CGTGCATTAA CTGCTATTGC TTTACTATTT GCAATTTTAA
660
AAGTAAGATC TGCACCTTTT GTTATATTAG ATGAGGTTGA AGCTGCACTA GATGAAGCAA
720
ATGTTATTAG ATACGCAAAA TATTTAAATG AGTTATCAGA CGAAACACAA TTCATTGTTA
780
TTACACACCG TAAAGGAACA ATGGAATTTG CAGATAGGTT ATACGGTGTA ACAATGCAAG
840
AATCAGGTGT TACTAACTT GTGAGTGTGA ATTTAAATAC AATAGATGAT GTGTTGAAGG
900
AGGAGCAATA ATGAGCGGCA CGAGCTCGTG CC
932

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

CGGTTAATCG GTAGTATTTT AGGTTCTGTT GTTATTAAGA TTTGGGAAGA TTTGATCTTC
60
CATCCCCCAA AGGGNTTAAC CGTATGGGGA TNCNTCANAA TCATTTGCCC AAGCTAAACC

120
 ACCAAAGAAT GGATATTTGA ATCCGGTTGC ATTTAAGNTC AATTGGGATG ATTTTTAGCC
 180
 TCCAGTTATT AAGTTCAAGT GTTAAATACC CTGTTCTAAT TTTAATTAAT TCTATTAATT
 240
 TAAGATACTT AAAATGATAA GACACTAAGA AAGGGAGGCT ATTAGTAATA ATGCCCCAAA
 300
 ATAAAAGCAA ATGAAGCATT AGTTAAAGCA TTACAAGCAT GGGATATAGA TCACTTGTAT
 360
 GGTATTCCAG GAGACTCAAT CGACGCAGTT GTCGATTAGT TTAACGTACA GTGAGAGATC
 420
 AATTTAAATT TTATCATGTA CGTCATGAAG AAGTAGCAAG CTTAGCGGCT GCTGGTTACA
 480
 CAAAATTAAC TGGTNAAATC GGTGTGGCAT TAAGTATCGG TGNCCCTGGT TTAATTCATT
 540
 TATTAAATGG TATGTACGAT GCCAAAATGG ATAATGTACT CGTGCCAATT AATATTATCT
 600
 GGACAAACNG AATAGTACAG CACTTGGAAC GAAAGCATTT CAAGAAACAA ATTTACAAAA
 660
 ATTATGTGAA GATGTAGCCG TTTATAATCA CCAAATTGAA AAAGGTGACA ATGTGTTTGA
 720
 AATCGTTAAC GAAGCAATTC GTACGGCATA TGAACAAAAA GGTGTCGCTG TTGTTATTTG
 780
 TCCTAACGAC TTATTAAGT AAAAAATTAA AGATACAACG AATAAACCAG TAGATACATC
 840
 AAGACCAACA GTTGTATCAC CAAAATATAA AGACATCAAA AAAGCGGTTA AACTAATTAA
 900
 TAAAGTAAA AAGCCTGTCA TGTTAATTGG TGTAGGTGCA AAACATGCGA AAGATGAGCT
 960
 CGTGCC
 966

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

CTGTGAAATT AAGTCGNTAT TACCCGCAAG GATTAAGAAG TTTGAATGGT GGTCGCATGG
 60
 CAAGATTTGG ACGTACACCA TTACTTGATG CAATGGAGAT GGCTAATGAG CATATTATGG
 120
 TGATTGCCAT GATAGAAGAT GTTGANGGGG TTATGGCCAT TGACGATATA GCTCAAGTCG
 180
 AAGGTTTAGA CATGATAGTC GAAGGTGCCG CAGGATTTAT CGCAGTCACT TGGCATACCA
 240
 TNGCAAACGA GCGTGATGAT CAAGTAACAT CACATNTTCA ACATATTTNT GNGGTTGTGA
 300
 ATGCACATGG TAAACATTTN TGTGCATTAC CACGTGAAGA TGAAGATATT GCAAAATGGC
 360
 AGGCACAAGG TGTACAAACA TTTATTTTAG GCACGAGCGG AAAAATATAT CGCCATTTAA
 420
 GTGCATCTCT AGCGACGTCT AAACAGAAAG GGGATGATGG CTAATGCGTA TAGTTCAACC
 480
 TGTTATTGAA CAATTAAAAG CACAATCTCA TCCAGTTTGT CATTATATCT ATGATTTAGT

540
 CGGACTGGAA CATCATTTC AACATATTAC ATCGTCATTG CCGAGTAATT GTCAAATGTA
 600
 CTATGCAATG AAAGCAAATA GTGAACGAAC AATCCTAGAT ACAATTAGTC AGTATGTTGA
 660
 AGGATTTCGAA GTTGCATCTC AAGGTGAAAT AGCAAAAGGT CTTGCTTTTA AACCAGCAAA
 720
 TCATATTATT TTTGGTGGCC CTGGTAAGAC AGACGAGGAA CTAAGATATG CAGTAAGTGA
 780
 AGGTGTTTCAG CGTATTCATG TTGAAAGTAT GCATGAATTA CAACGGCTAA ATGCCATCTT
 840
 AGAAGATGAA GATAAGACAC AACACATTTT ATTGCGTGTT AATTTAGCAG GACCATTTCC
 900
 CAATGCAACG TTGCATATGG CAGGACGCCC AACACAATTT GGTATTTCTG AAGACGAAGT
 960
 TGATGATGTC ATTGAAGCTG CGCTAGTAAT GCCAAATATT CATCTAGATG GCTTTCATCT
 1020
 TCATTCCCTAT TTCTAACAAT TTAGACTCGA ATTTACATGT CGATGTAGGG GAAACTTTAT
 1080
 TTTAAAAAG CAAAATCATG GCCTTGAAAA ACATCGATTT CCACTCAAAC ATATCAATCT
 1140
 TGGTGGGTGG CATAGGCGGT CAACTATGCA GATTTAACTA GGCCAACTNG AGTGGGATAA
 1200
 TTTTGNGGAA AATTTNAAAA CACTTATCGT TGAGCAAGAA ATGGAAGATG TGACATTGAA
 1260
 CTTTGAATGT GGGCGCTNTA TTGTGGCACA TTGGGGTTAC TATGTGACAG AAGTGCTAGA
 1320
 TATTANGAAA GNGCATGGCG CTTGGTATGC CATTTNAAAG GGAGGTACGC AACCAACNTAG
 1380
 CCTGCCGGNA TCTTGC
 1396

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3918 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

ACCAAAGCCA AATACTTGCA TTAANNCGGG GTAATTCCAA CAACTTAAGA ACNGTGCGAA
 60
 ACNAGCCTGC GGAACNACAA GCGATTACCA AATGCTTCGG GACNTTAAAA TACCACAACA
 120
 CAAAGAAGCA TTGTAAGCAC AAGTAACAAG TGCAGGACGC GTATCTGCAG CANATGGTGT
 180
 TGAACATACT GCGACTGAAT TAAATACTGC GATGACAGCT TTAAAACGTG CCATTGCTGA
 240
 TAAAGCTGAC ACACAAGCTA GTGGTAATTA TGTCAATGCT GATGCGAATA AACGCCAAGC
 300
 ATATGATGAA AAAGTGACAG CTGCAGAACA TATCGTTAGT GGTACACCAA CACCAACGTT
 360
 AACNCCATCA GATGTTACAA ATGCAGCAAC GCAAGTAACG AATGCGAAGA CGCAGTTANN
 420
 CGGTAATCAT AATTTAGAAG TAGCGACNCA AAATGCTAAC ACAGCAATTG ATGGTTTAAC
 480
 TTCTTTAAAT GGTCTCTCAA AAACCCAAAA CTAAAGAAG AAGTGGGTCA AGCGACNGAC

540
GTTNCCAAAT GTTCAAACCTG TTCGTGATAA TGCACAAACA TTAAACACTG CAATGAAAGG
600
TCTACGAGAT AGCATTGCGA ATGAAGCAAC GATTAAAGCA GGTCAAAACT ACACAGATGC
660
AAGTCAAAAC AAACAAAATG ACTACAACAA TGCAGTCACT GCAGCANAAG CAATCATTGG
720
TCAAACAAC AGTCCATCAA TGATTGCGCA AGAAATTAAT CAAGCGAAAG ACCAAGTGAC
780
AGCTAAACAA CAAGCGTTAA ACGGTCAAAG AAAACTTAAG AACTNCGCAA ACCAAATGCG
840
AAGCAACAAT TGAATGGCTT AAGTGAAGTA ACTTAATGCC CCCCAGAGAT GNAGCGANAC
900
CNCCAAATCG AGGTGCAACG CATGTTAATG GAAGTAAACA CCCAAGCCCA CAATAATGGG
960
GACGGCATTAA AAATACAAGC TATGNCGGNA CTTGTNAAAT GGTAATTCAA AGACTCACAA
1020
TNCGGATTAA GCAAGGTGTT AACTTCACTT GATGCAGATG AAGCGAAACG TAATGCATAT
1080
ACAAATGCAG TGACGCAAGC TGANCAAATT TTAAATAAAG CACAAGGGCC AAATACTGCA
1140
AAAGACGGTG TCGAAACTGC GTTACAAAAT GTACAACGTG CTAAAAACGA ATTGAGCGGT
1200
AATCAAAATG TTGCGAACGC TAAGACAACG GCGAAAAATG CATTGAATAA CCTTACATCA
1260
ATTAATAATG CACACAAAGC AGCATTGAAA TCACAAATTG AAGGTGCGAC AACAGTTGCA
1320
GGTGTAATC AAGTGTCTAC AATGGCATCT TGAATTAAAT ACCTGCAATT GAGCAACTTA
1380
CCAACGTGGT ATTAATGACG AAGCAGCTAC AAAAGCAGCT CAGAAATATA CTGAAGCAGA
1440
TAGAGATAAA CCCANCCTGC ATACAATGAT GCTGTAACAG CAGCTAAAAC GTTATTAGAT
1500
AAAACAGCTG GTTCAAATGA CAATAAAGTA GCCGTTGAAC AAGCATTACA ACGTGTGAAT
1560
ACTGCTAAAA CAGCATTAAA TGGTGACGCG CGATTAAATG AAGCGAAGAA CACAGCTAAA
1620
CAACAATTAG CGACAATGTC ACATTTAACT AATGCTCAAA AAGCAAACCTT AACAGAACAA
1680
ATTGAACGTG GTACAACCTG TGCTGGTGTT CAAGGCATCC AAGCAAATGC TGGTACTTTA
1740
AATCAAGCAA TGAATCAATT AAGACAAAGT ATTGCTTCTA AAGATGCGAC TAAATCAAGC
1800
GAAGATTATC AAGACGCGAA TGCAGATTTA CAAAATGCAT ACAATGATGC GGTAACATAAT
1860
GCTGGAGGTA TTATTAGTGC ANCGAATAAC CCTGAAATGA ATCCTGATAC AATTANCCAA
1920
AAAGCGAGCC AAGTGAACAG TGCGAAGTCT GCATTGANCG GTGATGAAAA ATTAGCAGCA
1980
GCAAAACAAA CTGCGAAATC AGATATCGGT CGTGTGACAG ACTTGAACAA TGCACAACGA
2040
ACTGCGNCAA ATGCTGAAGT GGATCAAGCA CCAANTCTTG CAGCTGTCAC AGCGGCTAAA
2100
AATAAAGCAA CATCGTTAAA CACAGCGATG GGTAATGTGA AACATGCACT TGCTGAAAAG
2160
GATAATACGA NACGTAGTGT CAATTACACA GATGCGGATC AACCAANACA ACAAGCGTNT
2220
GATACTGCAG GTACACAAGC AGAAGCAATT ACTAATGCAA ATGGCAGTNA CGCGAATGAA
2280
ACACAAGTTC AAGCAGCGCT TAACCAATTG AATCAAGCTA AAAACGACTT GGAATGGGTG
2340

ATAATAAAGT TGCTCAAGCG AAAGAAACAA CAAAACGTGC ATTAGCTTCA TATAGTAACT
 2400
 TGAATAACGC GCAATCAACT GCAGCAACTA GTCAAATTGA CAATGCAACG ACAGTAGCAG
 2460
 ACGTAACTGC TGCACAAAAT ACTGCTAATG AATTAAATAC AGCAATGGGT CAACTTCAAA
 2520
 ATGGTATTAA TGACCAAAAC ACTGTTAAAC AACAAGTGAA CTTTACAGAT GCTGACCAAG
 2580
 GTAAGAAAGA TGCTTACACA AATGCTGTTA CGAATGCTCA AGGTATTTTA GATAAAGCAA
 2640
 CACGGTCCAA AATATGNCAA AAGCACAAGT TGAAGCTGCA TTAAATCNAG TANCNCTGC
 2700
 TAAGAATGCT TTAAACGGTG ATGCAAATGT NAGACAANCA AAATCAGATG CGAAAGCAAA
 2760
 CTTAGGTACA TTAACACACT TANATAATGC AAAAAACAA GATTTAACAT CACAAAGCGN
 2820
 NGGTGCAACA ACAGNCAACG GTGTAAATNG TGTTAAACG AAAGCACNAG ACTTAGATGG
 2880
 TGCAATGCAA CGATTAGAGT CAGCAATCGC AAATAAAGAC CAAACTAAAG CGAGCGAAAA
 2940
 CTACATTGAC GCAGATCCAA CTAAGAAAAC AGCATTTGAT AATGCCATCA CACAAGCTGA
 3000
 ATCTTACTTA AATAAAGATC ATGGTACGAA TAAAGATAAG CAAGCTGTTG AACAAGCAAT
 3060
 TCAAAGTGTA ACGTCTACTG AAAATGCTTT GAACGGTGAC GCGAACTTAC AACGCGCTAA
 3120
 AACTGAAGCT ACACAAGCTA TCGATAACTT GACACAATTG AATACACCGC AAAAAACAGC
 3180
 ATTGAAACAA CAAGTGAATG CTGCACAACG CGTATCAGGT GTAAGTGATC TGAAAAATAG
 3240
 TGCTACATCA CTTAATAATG CGATGGATCA ATTAAAACAA GCAATTGGTG ATCATGACAC
 3300
 AATTGTAGCT GGTGGTAATT AACTAACGC AAGTCCTGAT AAACAAGGTG CTTACTACTGA
 3360
 TGCATATAAT GCTGCGAAGA ATATCGTAAA TGTTTCACCT AATGTGATTA CAAATGCAGC
 3420
 AGATGTTACT GCGNCAACAC AACGTGTCAA TAATGCTGAA ACAAGTTTAA ATGGTGAGAC
 3480
 AAACCTTAGCA ACTGGCGAAG CAACAAGCTA AAGATGCATT ACGTCAAATG ACACATTTAT
 3540
 CTGATGCACA ANAAACAAAG TATTACTGGT CAAATTGATA GCGCGACACA AGTAACTGGT
 3600
 GTACAAAGTG TGAAAGACAA TGCAACAANT CTTGACAATG CAATGAATCA ACTTCGAAAT
 3660
 AGTATTGCGA ATAAAGATGA AGTAAAAGCG AGTCAACCAT ATGTTGATGC AGATACAGAT
 3720
 AAACAAAATG CATACAATAC AGCAGTTACA AGTGCTGAAA ATATCATTAA TGCAACGAGT
 3780
 CAGCCAACAC TTGATCCATC TGCAGTAACA CAAGCAGCTA ATCAAGTGAA CACTAACAAA
 3840
 ACTGCGCTTA ATGGTGCGCA AAACCTTAGCA NATAAAAAGC AAGAAACAAC TGCTAACATC
 3900
 ACCCGATTAA GTCATTTA
 3918

(2) INFORMATION FOR SEQ ID NO:244:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1265 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

ATGCGATACG CTTAACCAGC AATGCATGGT TTAAGACAGA GCATTCAAGA TAACGCAGCA
60
NCTAAACCGA ATAGCAAATA TATCAACGGA AGTCCACGAG AGCAACCAAA ACTATGATCA
120
AGCTGTTCAA GCCCCAAATA ATATTATCAA TGAACAAACT GCAACATTAG ATAATAATGC
180
GATTAATCAA GTAGCGGCAA CTGTGAATAC AACGAAAGCA GCATTACATG GTGATGTGAA
240
ATTACAAAAT GATAAAGATC ATGCTAAACA AACGGTTAGC CAATTAGCAC ATCTAAACAA
300
TGCACAAAAA CATATGGAAG ATACGTTAAT TGATAGTGAA ACAACTAGAA CAGCAGTTAA
360
GCAAGATTTG ACTGAAGTAC AAGCATTAGA TCAACTTATG GATGCATTAC AACAAAGTAT
420
TGCTGACAAA GATGCAACAC GTGCGAGCAG TGCATATGTC AATGCAGAAC CGAATAAAAA
480
ACAAGCCTAT GATGAAGCAG TTCAAAATGC TGAGTCTATC ATTGCAGGAT TAAATAATCC
540
AACTATCAAT AAAGGTAATG TATCAAGTGC GACTCAAGCA GTAATATCAT CTAAAAATGC
600
ATTAGATGGT GTTGAACGAT TAGCTCAAGA TAAGCAAACCT GCTGGAAATT CTCTAAATCA
660
TTTAGATCAA TTAACACCAG CTCAACAACA AGCGCTAGAA AATCAAATTA ATAATGCAAC
720
AACTCGTGAT AAAGTGGCTG AAATCATTGC ACAAGCGCAA GCATTAAATG AAGCGATGAA
780
AGCATTAATA NAAAGTATTA AGGATCAACC ACAAACTGAA GCAAGTAGTA AATTTATTAA
840
CGAGGATCAA GCGCAAAAAG ATGCATATAC GCAAGCAGTA CAACACGCTC GAAGATGCCT
900
TGNTTAACAA AACAACTGAT CCTACATTAG CTAAATCAAT CATTGATCAA GCGACACAGG
960
CAGTGACTGA TGCTAAAAAC AATTTACATG GTGGATCAAA AACTAGCTCA AGATNAGCAA
1020
CGTGCAACAG AAACGTTAAA TAACTTGTCT NACTTGAATA CACCACAACG TCAAGCACTT
1080
GANAATCAAC TCAATTCNTG CAGCAACTCG NCGNGANGTA GCACANAAAT TTAATGANGC
1140
ACANGCACNT TATCCACGCA ATGGANGCTT TNCGTCATAG CATTACGNN NCAACAAACA
1200
AAACAGATCT GGTNTGCAAN TTTTTTATTG AAGGTTNNNC CNCACCCCGG TGCTTCCNGC
1260
GCCAC
1265

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 791 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

TTCATTAGTG GTGTGGCAGC ATAGCTCAAN GATAACCAAA CTCCTGGAAA TTCTCTAAAT
60
TCATTTAGAT CAATTAACAC CAGCTCAACA ACAAGCGCTA GAAAATCAAA TTAATAATGC
120
AACAACTCGT GATAAAGTGG CTGAAATCAT TGCACAAGCG CAAGCATTAA ATGAAGCGAT
180
GAAAGCATT AAGAAAGTA TTAAGGATCA ACCACAACT GAAGCAAGTA GTAAATTTAT
240
TAACGAGGAT CAAGCGCAAA AAGATGCATA TACGCAAGCA GTACAACACG AGCGAAAGAT
300
TTGATTAACA AAACAACTGA TCCTACATTA GCTAAATCAA TCATTGATCA AGCGACACAG
360
GCAGTGACTG ATGCTAAAA CAATTTACAT GGTGATCAAA AACTAGCTCA AGATAAGCAA
420
CGTGCAACAG AAACGTTAAA TAACTTGTCT AACTTGAATA CACCACAACG TCAAGCACTT
480
GAAAATCAAA TCAATAATGC AGCAACTCGT GGTGAAGTAG CACAAAAATT AACTGAAGCA
540
CAAGCACTTA ACCAAGCAAT GGAAGCTTTA CGTAATAGCA TTCAAGATCA ACAACAAACA
600
GAATCTGGTA GCAAGTTTAT TAATGAAGAT AAACCGCAAA AAGATGCTTA CCANGCAGCA
660
GTTCAANATG CAAAAGATTT AATTAACCAA ACAGGTANTC CAACGCTTGA TAAAGCACAA
720
GTTGAACAAT TGACACATGC TTTTAAACAA GCTAAAGATA ACCTACACGG TGATCAAAAA
780
CTTGCAGACG A
791

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

CTATTAAGGA ATCCTTGNN AATTCACATT AGCAAGTTGG ATTGTCCACC TTATTAATTG
60
ATAAAGTATG CAAATAATTT CACAGTGTTT CCAGCGGGGC CAANTTATGA TTGCAAGTAA
120
CCTATAGCAA TCGTATTCTT GTTCTTGCCA ACGCTATTTA AGTATCAGGT TTAACCAACA
180
GGTGCGACAA AAGGTTAGTT TGAAATTAGG GAGTGGGGCA GAATTGATAA AGAACCACTA
240
ATGACGATAA AGATTAAAAG GGAGGACGTT ATGATGACGG ATTAAAGTTG GAATCATTGG
300
GTGTGGTGGT ATTGCGAATG GCAAGCAACA TGCCAAGTTT ACNAAAAGTT GAAAATGTTG
360
AAATGATCGC ATTTTGTGAC GTAGACATTT CGAAAGCAGC GAGTGCGGCA GAAGCATACG
420
GAACTGACAA TGCAAAGGTT TATGATGATT ACAAAGCATT GTTAAAAGAT GACACGATTG
480
ATGTTATCCA TGTTTGTACG CCAAATGACT CGCATTGTGA AATTACTGTA GCAGGGTTGC
540

ATGCCGGTAA GCATGTGATG TGTGAAAAAC CAATGGCTAA AACGACAGCA GAAGCTCAAA
 600
 AAATGATAGA TACAGCTAAA TCAACAGGTA AAAAATTAAC AATAGGTTAT CAAAATCGCT
 660
 TCAGACCAGA TAGTCAATTT TTACATCAAG CAGCGCAACG TGGCGACTTA GGAGACATTT
 720
 ACTTCGGAAA GGCACATGCC ATTCGTCGTC GTGCAGTACC GACATGGGGT GTCTTTCTAA
 780
 ACGAAGAAGC CCAAGGTGGA GGACCTTTAA TCGATATTGG TACGCACGCA TTAGATTTAA
 840
 CGTTATGGAT GATGGATAAT TATGAACCAG AATCAGTGAT GGGTTCAACA TTCCATAAAT
 900
 TAAATAAGCA GCATGATGCG CCAAACGCTT GGGGTTTCATG GAATCCAGAT GAATTAACAG
 960
 TTGAAGACTC TCGGTTTGGC TTTATTAAAT GAAGAACGGA GCGACGATCA TTTTAGATCC
 1020
 GCTTGGGCGA TTAATTCTTT AGAAGTGGAT GAGGCAAAAT GTTCATTATT AGGAACGAAA
 1080
 GCAGGTGCTG ATATGAAAGA TGTTCTACGT ATTCATGGTG AAGATATGGG CACACTTTAT
 1140
 ACCAAACACG TTGAATTNGA AAACAAAGGC GTCGACTTTT ATGAAGGTAA TGAAGTGGAT
 1200
 GAAGCTGAAG AAGAANCAAA AGCTTGGATT GATGCAGTTG TAAATGATAC TGAACCAAGT
 1260
 GTGAAACCGG AACAAGCAAT GGTAGTTACA AAAATTCTTG AAGCGATTTA TCAGTCTGCA
 1320
 AAATCAGGCA AAGCAATTTA CTTTGAATAA CATCATACGG TAAGGAGGCA CATCATGACA
 1380
 AAATTAATAAG TTGGTGTGAT AGGTGTTGGT GGCATTGCAC AAGACCGTCA TATTCCAGCA
 1440
 TTGCTGAAAC TCAAAGACAC AGTCTCATTA GTTGCAGTAC AAGATATTAA TACAGTGCAG
 1500
 ATGATTGATG TTGCGAAGCG CTTTAATATA CCTCAGGCAG TTGAGACACC TAGCGAGCTG
 1560
 TTTAAACTTG TTGATGCGGT GGTCATTTGT ACACCCAATA AATTCCATGC TGATCTTTCT
 1620
 ATAGAAGCAT TGAACCATGG TGTCCATGTC TTATGCGAAA AGCCAATGNC AATGACGACG
 1680
 GAAGAGTGTG ATCGCATGAT TGAAGCGGCT AATAAAAAATC ACAAATTATT AACTGTGCGT
 1740
 TATCATTATC GTCACACAGA TGTCGCTATG ACTGCTAAAA AAGCAATTGA AGCAGGTGTG
 1800
 GTTGGTAAAC CATTAGTAGC ACCGTTGTCC AANCGATGCG TAGGCGTAAA GNACCTGGGT
 1860
 GGGGCGTTTT TACCCAATAA AACCGTTGCA AGGTGGCGGT AGTTTAATCG ATTATGGTTT
 1920
 CCCACTTGTT AAGACTTATC TTTGTGGCTA TTAGGTAAAG ATATGGTGCC GCATGAAGTG
 1980
 CTAGGAAAAA CATATAATCA ATTGAGCAAA CAACCGAATC AAATTAATGA TTGGGGAACA
 2040
 TTTGATCACA CTAAATTTGA TGTCGATGAT CATGTTACTA GTTATATGAC ATTTGCCAAT
 2100
 CGAGCAAGCA TGCAGTTTGA ATGTTCTGGT TCTGCAAATA TAAAGGAAGA TAAGGTACAC
 2160
 GTTAGTTTAT CAGGAGAAGA TGGCGGTATC AATTTATTTT CATTTGAAAT ATATGAGCCC
 2220
 CGCTTTGGAA CTATTTTTGA AAGCAAAGCT AATGTTGAGC ATAACGAAGA CATTGCTGGT
 2280
 GAGAGACAGG CGCGTAACTT TGTCAATGCG TGTTTAGGTA TAGAAGAGAT TGTGGTGAAA
 2340
 CCGGAAGAAG CACGCAATGT AAATGCCCTT ATAGAAGCGA TTTATCGTAG CGATCTTGAT

2400
 AACAAAGAGCA TACAACCTTTA ATGATTATTA TATATAATAC AAAATTCTCA ATATAAAAAG
 2460
 ANGGAGTGCT TTTCAATGAA AATAGGTGTA TTTTCAGTAT TATTTTACGA TAAAAATTTT
 2520
 GAAGATATGT TAGATTATGT CGCAGAATCT GGATTGGATA TGATTGAAGT TGGAACAGGT
 2580
 GGTAACCCAG GAGATAAATT TTGTAAGTTA GATGAGTTGT TAGAAAATGA AGACAAGCGA
 2640
 CAAGCATTTA TGAAGTCAAT CACAGACAGA GGCTTACAAA TAAGTGGTTT CAGTTGTCAT
 2700
 AACAAATCCAA TTTCTCCAGA TCCGATAGAA GCGAAAGAAG CCGATGAAAC GTTACGTAAA
 2760
 ACAATCCGTT TAGCAAATCT ATTAGACGTG CCAGTTGTGA ATACATTTTC TGNCAATTGCA
 2820
 GGGTCAGATG ATACCGCTAA AAAGCCTAAT TGGCCTGTGA CACCTTGGCC AACAGCCTAC
 2880
 TCTGAAATTT ATGATTATCA GTGGAATGAA AAGTTGATAC CATATTGGCA AGATTTAGCT
 2940
 GAGTTTCCNC AAGAGCAAGA TGTNNAAATT GCCATNGAGT TACATNCAGG ATTTTTAGCT
 3000
 CANACACCAA ATACGATGTT NAAGTTACGT GAGCCAACAA ATGAATATAT CGGTGCTAAC
 3060
 TTAGATCCTA GTCATTTATG GTGNCAAGGT ATTGACCCAA NTCCTGCGAN TCGCATATTA
 3120
 GGCCCNANCA AATNCAATTC ATCACTTCCA TGAATTCCG AAGAAACGTA TGTTANTCNA
 3180
 GGGNATGTAA ANATGTATGG TCTAGCTGAT NTCCAGCCAT ATGGTNACGT TGCGACANGN
 3240
 GCATGGACAT TCCNTACAGN TGGNTATGGA CATAGTCCAT ATGNATGGGC AGATNTCATA
 3300
 AGTCAACTTA NTATTAGATG GAG
 3323

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 641 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

TCCATTTAAT TCCACCTTGC CCCGACAGGT TTTNCCGACC TGGAAAGCGG TCAGTGAGCC
 60
 CNAACNCAAT TAATGTGAGT TAGCTCCACT TCATTAGGCC ACCCCAGGCC TTTACACTTT
 120
 ATGCTTCCGG CTCCGTATGT TGTGTGGAAT TTGTGAGCGG ATAACAATTT CACACAGGAA
 180
 ACAGCTATGN CCATGATTAC NCCAAGCTCG AAATTAACCC TCACTAAAGG GAACACAAGC
 240
 TGGAGCTCCC ACCGCGGTGG CGGCCGCTCT AGAACTAGTG GATCCCCCGG GCTGCAGGAA
 300
 TTCGACGAGA ACGCGTGCAG CGTTTACAGT TGCGTCTATT GATTTAGGTG CGCATCCAGA
 360
 ATTTTtaggg AAAAATGATA TTCAATTAGN CAAAAAGAA TCTGTAGAGG ATACTNCNAA
 420
 AGTATTAGGT AGAATGTTCG ATGGTATTGA ATTCAAACCT TAACTGAGCT TCATGGGGCA

480
 CCAGGTTTTG AAGAAGAAGT AAAAAATTAT ATGACTCAGC AAATGGCGCC GTATGTAGAT
 540
 GGAATTTATT GAAAATCGTA TGGGTGGATT TTTTGGGTGT GAAAAAATCT AAAAAATCCAA
 600
 ATGCAAAACG TGTAATGATT GCAGNACATA TGGATGAAAT C
 641

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

CTGCTTAAAT TCGAACGTGT CATTGACATT TTCAATAAGA AAAACAACGG AGCATGGAAT
 60
 TTCTGTCCGC AAAACGCCGG TTATTGGGAA CATATCCCTA AGAGTATTAC AAAATTATCA
 120
 GATTTAAAAA TCGTTGGTTT AGATTTCTAT ATCACTACTG AAGAATCAAA ACGATTTACT
 180
 GATTTTCCTA AAGACTTTAA AGGTATTGCA GGTTCGATAT TAGAAGTAAA ATCGAATACA
 240
 CCAGGTAACA CAACACAAGT ATTAAGACGT AATAACTTCC CGTCTGCACA TCAATTTNTA
 300
 GTTAGAAACT TTGGCACGAG ACTGGTGGCG TTGGTAAATG GGAGTTTATT CGAAGGAAAG
 360
 GTGGTTGAAT AATGATAGTA GATAATTTTT CAAAAGACGA TAACTTAATC GAGTTACAAA
 420
 CAACATCACA ATATAATCCA ATTATTGACA CAAACATCAG TTTCTATGAA TCAGATAGAG
 480
 GAACTGGTGT TTAAATTTT GCAGTAACTA AGAATAACAG ACCGTTATCT ATAAGTTCTG
 540
 AACATGTTAA GACATCTATC GTGTAAAAAC CCGATGATTA TAACGTAGAT AGAGGCGCTT
 600
 ATATTACAGA CGAATTAACG ATAGTAGACG CAATTAATGG GCGTTTGCAG TATGTGATAC
 660
 CGAATGAATT TTAAACAT TCAGGCAAGG TGCATGCTCA GGCATTCTTT ACACAAAACG
 720
 GGAGTAATAA TGTGTTGTT GAACGTCAAT TTAGCTTCAA TATTGAAAAT GATTTAGTTA
 780
 GTGGGTNTGA TGGTATAACA AAGCTTGTTT ATATCAAATC TATTCAAGAT ACTATCGAAG
 840
 CTGTCGGTAA AGACTTTAAC CAATTAAAGC AAAATATGGC TGATACACAA ACGTTAATAG
 900
 CAAAAGTGAA TGATAGTGCG ACAAAGGCA TTCAACAAAT CGAAATCAAG CAAAACGAAG
 960
 CTATACAAGC TATTACTGCG ACGCAAACTA GTGCAACACA AGCTGTTACA GCTGAAGTCG
 1020
 GATAAANTAG GTGGGAAAAA GAGCAAGCGA TTGGGGACCG TTTTAACGAA GTNGGACAAC
 1080
 AAATCAATGC GCCTGGCCTT GTNAAGGTAA TNCAACAACA AATTGGGAAA
 1130

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

```
CCTCAGCATA TGGTTGAACC CCTTCTTGAT AACCCATATC TGTTAGTTTT CCCCAATGAT
60
TGCTCGCATA GCTAATTGTG CCAATTGGAAT ATCAAGTAAT TTTACTTAGG CACGAGAATG
120
GTNCCGTTCT ACTAGAACGG TGGGTTTACT TCTAAAACAA TATACACCAT CGTGAGCTAT
180
AACGAATTGA ATGTTGATTA AGCCAATGAT GTTTAAACCT TTAGCTAATT TTATAGTATA
240
GTCCTCAAGT GTTGCTAACT CGTCTTCTGT CAAAGTTTGT GCGGATATA CAGCGATTGA
300
GTCACCACTA TGTACACCAG CAGTTTCAAT ATGTTCCATG ATTCCTGGAA TAATGACCGT
360
TTCTCCATCA CAAATCGCAT CAACTTCAAT TTCTTTACCA GTTAAATATC TATCGACTAG
420
TACCGGATGT TCCGGACTCG CTTTTACAGC CTGGGTCATA TAGTTTTCTA ACTCTTTGTC
480
ATTGTCTACA ATTTCCATTG CGCGACCACC TAATACATAA GAAGGTCTTA CTACAACCGG
540
ATATCCGATT TCTGCAGCAT TCGCTAATGC TTCCTCAGGT GATGTAGCTG ATTTCCCTTG
600
TGGCTGTGGC ACGTTAATTT TTCTTAATAG TGCTTCAAAT TCTTTTCTAT CTTCAGCACG
660
ATTTAGATTT TCTAGTGAAG TACCAAGTAT TTAAACACCA TGTTTAGCCA ATTTGTCTGC
720
TAAATTAATC GCTGTTTGTC CTCCAATTG TACAACGACA CCTTTAGGTT TTTCTAAATT
780
AATGATATTC ATCACATCTT CTTCAAGTAA AGGTTCAAAG TATAATTTGT CAGAAATTGA
840
AGAAGTCTGT TGAAACTGTT TCTGGATTGT TATTCACAAT TATCGCTTCG TACCCTGCTT
900
TTTGAATTGC CCAAACGGCG TGAAGTGTG CATAGTCAAA TTCTACACCT TGGCCGATTC
960
GAATTGGTCC AGAGCCTAAT ACTAAGATTT CTCTTTGTCA GTAACATATG ATTCATTTTC
1020
AGTTTCGTAT GTACCATAAT AATATGGTGT TGAGATCAAA TCAGCTGCGC AGTATCAACA
1080
TCTGTAACAG GTTAATATCA TTTC
1104
```

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1995 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

CTATCATAAA AACATAAAGT ATTGTAAGCT TTTTATCGAT ATTTTTTATT TATAAAAAATA
 60
 AAATGAGATA ACTNTGTGAA TTTTATTGA GATAAATTAG ATAGTGNTGT TTTTGTGATG
 120
 TTTAATAATA TCTTGGGTGT GTTAATACTA GTAATGCTTT CAACTGATGC ATTAAGACTG
 180
 TGACATCATA ACTCATTTAA GAACTTCGCT TATTAATTTT CTACCAATAC AATCCCTTCT
 240
 AAGTGCACATA AAAAATCCTT ACTGCTAAGT GATTAAACTT AACAATAAGG ATTTATTTAT
 300
 CGCTAATGCA TGATTATTAA CGGAATCTCA TACCACCATC TACAATAATT GTTTGTCCAG
 360
 TAATGTAATC AGAGTCTTTA CCAGCTAAGA AGCTCACTAC ATTTGAAACA TCTTCTGGTT
 420
 GAGAACTCT GCCCAAAGCA ATCTGACTTG TAAATTGTTT CCAACCCCAT GCTTCAGGTT
 480
 TACCTGCTTC TTCGGCTGTT GCCACTGCGA TACTTTCCAT CATTGGTGTT TGAACGATAC
 540
 CAGGTGCGAA TGCATTCACA GTAATACCTT CAGACGCTAA ATCTTGTCG GCTACTTGTG
 600
 TTAAACCTCG CACTGCGAAT TTTGTACTGC AATATAAAGA CAAGCCTGGG TTACCCCTCAA
 660
 CGCCTGCTTG AGATGTTGCA TTGATAATTT TACCGCCATG ATTGAATTTT TTAAATTGTT
 720
 CATGTGCGGC TTGAATACCC CATAGCACAC CTGCAACGTT CACGCCATAT ACTGTTTTAA
 780
 ACTGTTCTTC AGTAATTGTA TCGATTGGTG TTGTTGGTCC AAGGCCGGCA TTGTTAACCA
 840
 TGACATGGAA ATCGCCAAAT TGCCTCGGA GTTGCTGTC TTAGTGCCTT AAATACATCA
 900
 TCACGGTTTG ATACATCTGC TTTGATAGCA ATAGCTTTTG TACCATCACT TGATAATTTA
 960
 AGTGCAGCTG CTTTTGCCCC TTCTTCATTG AAATCAACAA CTGCTACTTT GAAACCATCT
 1020
 TCCACTAAAC GTTCTGCAAT TTTAAAACCA ATCCCTTGTC CTCCGCCAGT TACTAATGCT
 1080
 ACTTTGTTGT TTGTCATAAA GATCACTCCT CAAATTTCTT TCCTTTAATT ACATTTTACT
 1140
 CCTCTTCATT TGAATAGTAC AACAAAGGTA GCTCCATTTA ACAAATATT CAGATATTTA
 1200
 AGGTATAGTT AAACGCACTA CCATTAGTGA TTGGCAATGC GTTTAAATGT CGTTTTAAAA
 1260
 GTTCTTATGT TGAATATTAT TTTTAAAGT CTCTCGATTA GTTTGTCATC AATCTTTTTT
 1320
 CGAGACATGG GCCTTTTGAT TCAATCGGCG GNTTCCGTGT TATCACTGAC AACTTTAGTT
 1380
 GTAGCTTCAT CTTTATGTAT TTCTTCGCTA AATCCTTCAA GGTTTTTAGT CGTGGGATTT
 1440
 TTAACCTCAG GATGTTCCAT CATGTCTTTG ACTATCAAGT TCCTTTTTAC ACGTGTCTTT
 1500
 ATGGTGATGC TTGATTTGGC GTTCCCTTTT ACTTTTTTTG AATAGTGGGT AGGTATCTGC
 1560
 TGCAGCTACT AATTTNCTTC TTACCCTTAA AATAGATATT GGCTTGGAAG CAAAACCAGA
 1620
 GTATTTGCAG ATACAAAGTT GCATTAATAC TTAAAGCAAT AATAGCCAAT ACAAATTAAT
 1680
 ATTGACACCT NTTGAAATCC CTTCTTTTAA ATTAAGTCAG ATGCCAATAC GATGACAGGG
 1740
 TACGGATTGA AAGTATAATT ACAAATATAG AAATTATTGC CGATATAACT ATTGTTACTA
 1800
 TTAAATAATC AGCTCTGCTA CCTGATAATA AATAGAAAAG GCGAAAATTA GTCCATAGCA

1860
AATTACAAAC CCACATAAAG TTATAGCCAT GAGTACTATA TAAGCTATTT GAAAATATAA
1920
ACCTATCTTT ATGAATGATT TTCTACATTT TTTCCATGTC TATCCCCATT ATTAATATTA
1980
TACTTACCTA ATATA
1995

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1940 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

TGTACTTGAA CACTGTACTG CGGATGAGTT TTTTATTGAC ACGGAATTAT TAGGGTTCAA
60
CGGTGACTTA CCACGTTTCG TAATTACCTC CAAACGACAG CTAGTACGTT TATAAGATGG
120
TGTATCCGTG TATTGATCAA CATCACTATT AGTTAATAAG TTAATTGCAC CTAGATCTCC
180
ATTTTCCATC GCATCATTAT TTAATGGAAT ATAGATTTCT TTACCTTTAA CACGATCTGT
240
CACGTGAACT TGTAATACCG CTTCTCCTGT TTCAGAAATC AGCTTAACTT CTGCACCTTC
300
ATGAATGCCT CTATCTTCAG CAAGCTCTGG AGAAATTTCA ACAAATGCAC GTGGCACTTT
360
GTATTTAATC ATTGGTGTTT GATAAGTCAT ATTACCTTCA TGGAAGTGCT CTAACAATCG
420
ACCATTGTTT ACATGAATAT CATAAATTC ATCTTGCTTA AAGTAATTAT CAAATGATAA
480
TGGAATAAT TTTGCTTTAC CATTATCAAA ATTGAATCCT TCTAAGTATA GAATAGGCTC
540
ATCAGTNCCA TCCNGNTTGT ACTTGNCAT TGTAAACTAT TGAATCCTTC TANNCGATTC
600
ATAACTTACC CCAGCATATA GAGGTGTAA GCGTCCTACC TTCAATCCAT AATTTCACTA
660
GGATGCTTGT AATTCCAATC CAAATCCCTA ATCTATTAGC AATTGCTTGG AAAATTTTCC
720
AGTCAGGTTT TGAATACCA AGAGGTCTTA ATGCTTGGTA TAAACGTTGA ATACGACGTT
780
CGGTATTTGT AAAAGTACCG TCTTTTTCAA GTGAAGGACT TGCTGGCAAT ACAACATCTG
840
CGTATGTTGC TGTGAATGTT AAAAATTCAT CTTGGACTAC CATGAAATCT AATTTTTCAA
900
ACGCAGCTTG TACAAAATTA ATATTTGAAT CCACAATACC CGTATCTTCA CCATATAAGT
960
ACAATGAGTG TACTTCTCCG TCATGTATAC CTTCTACCAT TTCATGATTA TCTTTACCAG
1020
CTTTTGGATT CAATTTAACG CCATATTCTT TTTCAAATTT AGCACGAGCG AATATCATCC
1080
GCTTCAATAC TTTGATAACC AGTAATCTTA TCAGGCATAC TTCCCATATC ACTACATCCT
1140
TGAACATTAT TATGTCCACG TAATGGATAC GCACCAGTAC CAGGACGACG ATAATTACCT
1200
GTTACTAATA ATAAGTTTGA AATCGCTGTA CTTGAGTCAC TACCAATGTC TTGTTGTGTA

1260
 ATACCCATTG CCCAACAAAT TACAACAGAT TCAGCTTTAG CACATTCTTC AGCAAATTTA
 1320
 ATCAATTCTG ATTCAGGAAT ACCTGTTGCT TCTTCAGCAA AAGCCATTGT AAATGTTTCT
 1380
 AATGATTTGT AATATTCATC AAAATCATCT ACCCACTCAT CAATAAATGC TTTATCGTGT
 1440
 AAATCATGAT CAATAATATA CTTAGTCACT GCACTTAACC ACGCTAAATC CGTACCTGGT
 1500
 TTAGGTTGAT AAAAACGATC CGCACGTTCT GCCATTTTCAT GTTTTCTAAT ATCAAATACA
 1560
 TGTATTTTTT GTCCAAATAA TTTTGTAGCA CGTTTCATGC GTGATGCGAT AACTGGATGA
 1620
 GCTTCGGCTG TATTGGTACC TATCAATACA GACATTGCCG CTTTTTCTAA ATCTTCAATA
 1680
 CTACCTGAGT CACCGCCGTG TCCAACCGTT CTAAATAAGC CTTTTGTTGC AGGTGCTTGG
 1740
 CAATATCTTG AACAGNTATC AACGTTATTT GTGNCAATAA CTTGGTCTTG CTTAATTTNN
 1800
 GGGATGNAAA TACGATTCTT CCATTCCGGC CGGTTTTAGA AGAAGGAAAT GAATTGATAG
 1860
 TGCATCTTGG GCCAATACTT NNNCTTTNAA TAGATGTAAA ATTATCTGCA AATGACAATT
 1920
 TAAAGGTTCC ATCCCATCTT
 1940

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 847 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

GATTCAACAT AACGTCGTGT CCTTCAGCAT ATATAGTATC GAATGCTATG GACGATTAAC
 60
 CTGACCCAGA TAAACCTGTC ATAACAATTA ATTTATTTTT AGGTAGTTCG GATATCAATA
 120
 TCTTTCAAGT TATGCGCAGC AGCACCTTTT ACTACTATGG ATGGNTCTTT CATTTACTTG
 180
 TCACCCNTCT GCTTTTAATT CAAATAACAT ATCTCTTAAT TCNGTAGCTT TCTCGAAATC
 240
 TAAATCTTTC GCTGCTTGTT TCATTTCTTT TTCTATATTG TCGATTGTCT TTNGACGTGC
 300
 TCTTTTCGGC ATCTTCTTAG GTATCACAGT TTGTGCTTNG TCATNATTTT CGTCATTTTC
 360
 AACAGTAGCA CTAATTAAAT CATGTACTTN TTTATTAATT GTTTTAGGTG TAATACCATG
 420
 TTTTTCATTA TGTTTCATCT GTATTTCTCG ACGACGTTGT GTCTCATCAA TTGCATACTT
 480
 CATNGAATCA GTCATATTAT CGGCATACAT AATGANTTCA CATTTATCGN TACGCTCGTG
 540
 CCGAATCGGC ACGAGCTCGT ACCTATTGTT TGAATTAATG AGCGGNTAGA ACGTAAAAAT
 600
 CCTTCTTTAT CTGCATCTAA TATGACAAGT AGAGAACTT CTGGTATATC AATACCCTCT
 660
 ACTTAATAAA TTAATACCTA CGATAACATC ATATGTACCC ATTCGTAAGT CTCTAATTAT

720
TTCGATTCGT TCGTAATGTC TTGATTTCTG AATGCAGATA ATTAACTTTA ATACCCGCTT
780
CTTTCATGTA TGTGGTTAAA TCTTCACTCA TCTTTT TAGT GAGCGTTGTA ACAAGTACGC
840
TCGTGCC
847

(2) INFORMATION FOR SEQ ID NO:253:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1300 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

CCGCTTCGCA CGAGCNAAGG CTTTTATTGC ANCCCTCGCA TCTTCTTTAG CTTACACTAA
60
ATCTTTGATG TCTTGTAATG CTTGTGCAAG TTGTGCTTTG GCTTGTTCAA TTTCTTCTTT
120
AGTCATCGCA TTGTTAATGT CGTTATGACC TTGTTGAAGT ATTTGANTAA TTCGATCTTT
180
AAGCGCTTGT TTNTCCTTAT CTGTTAGATT TGGATTGTGA TCGATTTTCGN CAATTAATGC
240
TTGAACTTGT TTATCAACAT CTTGTTTCGC ATCTTCTTTA GCTTACACTA AATCTTTAAT
300
GTCTTGTAAT GCTTGCGCAA GTTGTGCTTT AGCTTGTTCA ATTTCTTCTT TAGTCAGCGC
360
ATTGTTAATG TCGTTATGAC CTTGTTGAAG TATTTGATTA ATACGATCTT TTAAGTGCTT
420
GTTTTTCCTT ATCTGTTAGA TTTGGATTTT GATCAATTTT GTCAATTAAT GCTTGAACCT
480
GCTTATCAAC GTCTTTATTG GCATCAATTT TNGCTTTNGG TATTTTATTA GCANGCACTN
540
GTTCAATCGC GTGGTTGCCT GCTGTTTGAA CTTGAGATAC AGCCTGATTA CTTGTTGCTT
600
TATTAATGTT GTTGATGATG CTGGTTTGCC AATTCTTCTT GCTTTATTTT TTCGGCAATA
660
AGCTTGCTTT GATCCGTCGC ATTTGAAGCT TCGATTTCTT TTAGCTTATT AGCTAAAGCT
720
TGATTAATTG ATTGAATTGC CTTGTCTTTA GCATCTTGTA GTCGTTGATC ACCATTAAGA
780
TTATGGATTG CATCATTGAC TGCTTGGATT GCGCCATTGA TATCATTAC ATTTGTGTTA
840
TCACTATTTA GCAATGTATT TGCTAGACGT TTGGCATCAT CGAAGTTTGT TTTAGCATTA
900
TCGTCAGCGT TTTGGTAATT GACAGTTTGC TCTGCATTTG GAATTTTCATT GTCAACTAAA
960
TGTTTCAATG TTTCCATTGC ATCATTTAAG TCAATTTGAT TATTAACAAT ATCTGTTACA
1020
TCTGATACAG TATCGGCATT GTTAATTGCT TTATGTGCAA GATCTTGTTG CTGTTGATTT
1080
AATCCATTTA ACGAATTAAC AAACGCATTT GCTTTATCCT TTGGCATTTG CAAGGTTTTG
1140
GTCTCCATTT AATGCATTTT GAGCATCGAT AATATTTTGT TTCAATTGCT CTGCTTCAGC
1200
TTTTGCAATT GCATTACTTG CACTTTATCT AACTCATGTG CTGCATTCGC AATGCATATC

1260
ATAATTTGCT TTCAATGTCA TCTGCATGAT GTATTGTGCT
1300

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

CTTTTCATCT CTTGACCTG TGTAATACCT TTGATCAGCT GCACAAATAG ACAAGTATAA
60
AGGTCTTACG ATGACATGAT TACCATAAAT ATCAACATTA TTATATGTGA CGTCGAACTG
120
TCTCGGTGCA ACGAGTTGAT ATACTTGATT AATCATCGGC AATATCACCT TGAATAATGG
180
NATTTGCTAC TTTNAANTCA TNCGGGGTTG TCACTTTAAT GTTGTATAGT TCTCCACGTA
240
CCAATTTAAC TGCATGTCCA GATTGACAA TTATTTTACA TGCATCTGAT AAGATTTCTT
300
TNTGGTTCAC TACTTAAGGC GCGATAACTA TCTTGTAATA ATTTAATATT AAATGATTGT
360
GGTGTGTTGGC CTTGATACAT TTCATTCTT ACAGGGATAC TGTGTATGTT CTGTTTATCT
420
TTAGACATTA CAATCGTATC AATTGCTTCA ATGACTGTAT CTACTGCACC ATATTNNGCT
480
GCTACTTCAA TGTTCTCTTT AATAATACGT TGAGTTAAAA ATGGTCTTAC GGCATCATGA
540
GTTACAATCA CATCATCATT ATTAATTCCA TTTACATTGC GAATATGGTC GATAATGTTC
600
ATAATTGTTT CGTTTCGATC CGNACCACCT GCAACTACTT TGACACGTTG ATCTGTAATG
660
TTATATTTTT TTAATAATATC CTGTGTATGG GAAATCCACT GTGCTGGCGT TGCGATAATA
720
ATCTCATTAA ATTCACTCAC TAAAATGAAC TTCTCAATTG TATGGATTAA AATCGGTTTA
780
TTATCAATAT CTAAAAATTG TTTTGGGTAA TGGCACGTTC CCCATTCTCG AACCAATACC
840
TCCTGCTAAA ATACCTGCAT AAATCATGTT GGCCTCCATC CTGTCATTAC ATCATTTCCA
900
TTTATACATT ACTGACCTAT GCCCGCACAT AAGCCTAACC TATTGCTCAC TNGNCTCTTN
960
TATTAATCCA AAGATAGTTG TCACAATAGT GTGATAATTN TTTATAAAAA TGTATTTNTG
1020
NNACTGACCA NTCTAAGTTG TTTTGGCATG CAGCTAATCA TTAACCTCTGA CGATATTAAA
1080
TTGTAAAGG TATTAATGTT TACTCTTTCA CAAATTCATT ATTACTGCCA TCATTTNNCC
1140
ATATATTATA ATAAATTTAT CTTATTAAGT GGCTGNACTT GATTTTCACT TAAAAATTA
1200
TCAATATTG CCATCTCATT TTAAGNATAC AAAATGCAAA ACAACCGATT CACAAGCATA
1260
TTTCACACAA GTAAACCGGC TATTTATCAA CGTATATTCG AAGATGAATT ATTTGATAG
1320
TATCTTGTAG ACCAGNCGGC ATTCGCACTT TCAATAGCNT ATTAACCTAT ACCAGNGGTT

1380

TCGTCCTCNA NGGTGCATAC TAATAAATCG TAAACNTGAC TTTAG

1425

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

TTTCTTACCT TTAATAATTG GTAATTCATC TTCCATCCTC TTGTTTGATC TGTGTCGCAT
60
AAGCTTCATC AAATAGTACA TCAGTACGTG GAACACCTGT AGGCACTACA TTTTCTCTT
120
TAATACCAA TGCTTCAGCG TAGAATGGAA TATCGGTTTC AGATGATACA TAAGCTTTGG
180
CACGAGCTAC GATGATTTAA TGAATCAATA AATGGTCCAC CCTTTTACC AGTACGACTA
240
AAGCCAACTG TTTTAAAGGC ACCAACGGCA TGCCATACTT GAATAACTTC TTGAGAACGT
300
CTAAAACGCA CTGTATAAAT CAAGGGGTGA AAGTCATCAA CAAAGATGTA GTCTGCCTTC
360
CCAAGTAAAT ATGGCAATCT AAACCTGTCTG ATGATGCCAC GTCTATCTGT AATATTCGCT
420
TTAAAACAG TGTGAATATC ATACTTTTTA TCTAAATTTT GACGTAACAT TTCGTTATAG
480
ATGTATTCAA AGTTTCCAGA CATCGTTGGT CTAGAGTCTG ATGTGAACAA CACCGTATTC
540
CCTTTTTTCA AGGGTGAAAA ATTTGTCGTG ATTAATATC GCNTNAAAAA TAAATTGTCT
600
TTGTTATTAA ATGAATGTTT GCGGAAATAC NTACGTAATT CTTTAATATT TACGAACGAA
660
AATAAATACT TTTAACTTCC GGAGTCGTTA CNACCAACAT CAAGGACAAA TTCATTAACA
720
TTTCGNAGAA ATTTCAGGGT GTAACAGTAT AAACCGTTTT CTTCGAAATG CCGCCTTTTC
780
TAAATTCTTT TAGGTAAGTC TGCAATAAGA AATTGATTTT ACCATTTTGT GTTTCTAATT
840
CGTTGTATTG TTCTTCTTGT TCTGGCTTTA GATTTTGATA TGCATCATTA ATCACATCTG
900
GGTTTANCTG TGCAATATAA TCAAGTTCTT GCTCATTAC TAATAAGTAC TTATCTTCAG
960
GTAAGTAATA ACCATTATCT AAGATAGCTA CATTGAAACG ACAAACGAAT TGATTCCCAT
1020
CTATTTTGAC ATCATTCGCC TTCATTGTAC GTGTCTCAGT TAAATTTCTT AATACAAAAT
1080
TACTATCTTC TAAATCTAGG TTTTCACTAT GTCCTTCAAC GAATAACTGA ACACGTTCCT
1140
AATAGATTTT ATCTATATAT ATCTTACTTT TANCCAACGT TAATTCATCC TTTTCTATTT
1200
ACATAATCCA TTTTAATACT GTTTTACCCC AAGATGTAGA CAGGTCTGCT TCAAAGCTT
1260
CTGTAAGATC ATNAATTGTT GCAATTTTCA ATTCTTGACC TTTTAACAAC GCTAATTTAT
1320
CTACAATATC TGGGTATTGA ATGTATAAGT CTACAACATC TTGGAAATCT TGTGACCCAC

1380
TTCGACTACT ACCAATCAAC GTTAGTCCTT TTTCCAATAC TAGACGTGTA TTAACCTTCTA
1440
CTGGGAACTC ACTTACACCT AACAGTGCAA TGCTTCCTTC TGGTGAAATA TANTCAATCA
1500
TTTGATTTAT TGCTGATTGG NTACCACGCC CACCAACGCA CTCAAATGCA TGATCANATG
1560
TTAAGCCTTC AGGTATTTTA TTAATAAAGA AGACATCATC AACAAATGAG AAGTGACTIONA
1620
ATTTATAATC TTGGTNNACC AAAGACATAT ATGGNAGACT TCTGGATATT AATNGACGGA
1680
ATAAAATGGC TGTAATGTAA CCTAAGTTAC CATCACCCCA AATACCAAAT GTATTTTTAT
1740
TTGAAATAGA TTTCTTTTCA ACAACGACGA ATAGCATGCA AACTTACTGT TACAAGCTCT
1800
GTAGATGAAA TAATACTTAA ATCAATATCA TCAGGTAGTG GTACAGCTCT ATCATGATTT
1860
AGCAACACAA AATCTTGCAAT AAACCCATCA TGTCCACTTG ATCTGAAGTA GCTCGATTTT
1920
AAATAGTTTT CAGCAATGAC ATCGTCTTTT TCTGTCGGCG TATTCGGTAC CATAACTACT
1980
TTTGTACCTT TATTAAACAC ACCTTTACTG TCAAATACGA CCTCACCAAC ACCTTCATGA
2040
ATTAAAGACA TTGGCAATTT CTGAGATAAG ACATTCTCAT CACGGCTACC AGTATAATAT
2100
CTTTGATCGG CAGCACAAAT TGACATATAT AAAGGACGTA CAATGACATA GTCACTGTAA
2160
ATATCTACGT TGTTATACGT AACTTCAAAT TGTCTAGGTG CAACTAATTG ATATACTTGA
2220
TTAATCATCG GCCAATACCA CCTCGAATAA TAGCATTTCG TACTTTTAAA TCGTAAGGTG
2280
TTGTTACTTT AATGTTATAT AACTCACCTT TTACAAGTCG AACCGGTTTG TTTGTTTCTA
2340
CAATAATCTT ACAAGCATCA GATAAAATAC TCTTTTGCTC ATCACTCAAC TGTGCATAGC
2400
TTTCTTTTAA TAAATTAATA TTAAACGATT GAGGTGTTTG ACCTTGGTAC ATTTCAATTAC
2460
GCACTGGAAT TGCATCAATC GTTTGATTAT CTTTAGATGT AACAATCGTA TCTATAGCAT
2520
CAATCACTGT ATCTACTGCA CCGTACTCTA AAGCAGCTTG AATATTTTCT TTAATAATAC
2580
GATGCGTTAA AAATGGTCTA ACTGCATCAT GTGTCACAAT GACATCGTCA TCGTTAATAC
2640
CATTTGTTGA TTCAATATGT TTAACGATAT TCATAATTGT ATCGTTACGA TCGCTACCAC
2700
CTTGAATGAC TTCAATTCTT TCATCAGAAA TTTTGAATTT TCTAAGTGTA TCTTTCGTAT
2760
GCGTCATCCA TTGTTGTGGC GTCGCGATAA TAATTTTTTC AAAATCATTAA ATTAAAATAA
2820
ATTTTTCTTA ATGTATGGAT TAAAATCGGN TTGTTGTCTA AATCTAAAAA TNGTTTAGGT
2880
AAAGGGTACG GTTACCCATT CCTTGAGCCT ATACCTCCAG CTAGAATACC AGCGTATTTT
2940
ATAAAATACT TCCTCCATTC AACTATATCT ATATTTAATT ATTTAAATTT CGTTGCATTT
3000
TCCAATTGAA AACTCATTTT AAAATCAAAA CTCTAAATGT CTGTGTATTA CTTAAAATTA
3060
TACATATTTT GCTTATATTT TAGCATATTT TGTTTAAACC TATATTACAT TATATCAGAC
3120
GTTTTCATAC ACAAATAATA ACATACAAGC AAACATTTTCG
3160

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1676 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

```
AAAAAACAA TTTANCCCAT NACNACTTGT CGTTAATTAT TCATACGAAA TACATGATTA
60
ATGTACCACT TTAACATAAC AAAAAATCGT TATCCATTCA TAACGTATGT GTTTACACAT
120
TTATGAATTA GATAACGATT GGATCGATTA TTTTATTTTA CAAAATGACA ATTCAGTTGG
180
AAGGTGATTG CTTTGTGATTG AATCGCCTTA TGCATGAAAA ATCAAAAGGT TATTCTCATT
240
GTATAGTCCT GCTTCTCATC ATGACATGTT GCTCACTTCA TTGTCAGAAC CCTTCTTGAA
300
AACTATGCCT TATGACTCAT TTGCATGGCA AGTAATATAT GCCAACATTA GCGTCTAAAC
360
AAATCTTNGA CTAAACGTTT ACTNGAGCGA CCATCTGGAT ATTTAAAANG TTTAGCTAAG
420
AATGGTACAA CTTTTTCAAC CTCATAATCT TCAGTGTCCTA AAGCATCCAT TAATGCATCA
480
AAGGATTGTA CAATTTTACC TGGAACAAAT GATCCATATG GTTCATAGAA ATCACGCGTC
540
GTAATGTAAT CTTCTAAGTC AAATGCATAG AAAATCATCG GCTTTTTTAAA TACTGCATAT
600
TCATATATTA AAGATGAATA ATCACTAATC AACAAGTCTG TAACAAAGAG AATATCGTTA
660
ACTTCACGAT GATCTGACAC ATCGATAAAG TATTGTCTAT GTTCACGTGA AATATTAAGT
720
CTATTTTTTA CGAACGGATG NATTTTGAAT AACACAACCTG NATTATGCTT CTCGCAGGAT
780
CTTGCTAAAC GTTCAAAATC AATTTTAAAA AATGGATAAT GTGCCGTACC GTGACCATTA
840
CCTCTAAATG TCGGTGCGAA TAGAATAACT TTCTTACCTT TTATAATTGG CAATTCATCT
900
TCCATCTCTT GTTTAATTTG TGTTGCATAA GCTTCATCAA ATAGTACATC AGTACGTGGT
960
ACACCTGTTG GTACAACATT TTCTTCTCTA ATTCCAAATG CTTCAGCATA AAATGGAATA
1020
TCGGGTTTCT GATGAAACAT ATGCTTTCGG TGTAACCTACG ATGGGTTTTA ATGAATCGAT
1080
AAACGGACCA CCTTTTTNAC CTGTACGACT AAAGCCAACT GTTTTAAAGG CACCAACAGC
1140
ATGNCACACT TGAATAATTT CTTGTGATGG TCTAAAGCGA ACCGTATAAA TTAATGGATG
1200
GAAATCATCA ACAAAAATAT AATCGGCCTT ACCAAGTAAA TATGGCAATC TAAACTTGTC
1260
TCTCCATTTG CGTCTATCCG TAATATTCGC CTTAAATACC GTTTTAATAT CATAATCAAA
1320
ATCTACTTTG TGGCGTAGTA ACTCATCATA TACATACTTG AAATTCCCTG ATAAATTCGG
1380
ACGCGAATCT GATGTGAATA ATATTGTTNT GCTTCTTTTA ATATGTAGTA ACTTTGTAAT
1440
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ATTAAAAATA GCTTTAAATA AGAAACTTCT ACTTTCAAAT GAAGCTTTAT GACCTTGTTT
 1500
 ATGAAGCCAG TGTGCACTTG GCGCAATGAC CCTGATTTCT CTTGAGGTAA GGTGATTTCA
 1560
 ATATCAAATA CAAATTCGGN TAACCGTCAC TTGGCTATCT CCGGAGTAAT GGTATTAGAC
 1620
 CGTATGTTGT GATACGCCAC CTTTACGGAA AACTTTAGCA TCATACGCTA ATAAAG
 1676

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3110 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

GATTTCGAGCT CGGTACCGGG GATCCTCTAG AGTCGACCTG CAAGCTATAC CAAGCTAGAG
 60
 TACTGCGACG CAAACTAGTG CAACACCTAA GGCTGTTACA GCTTGGAAGT CGATAAAATA
 120
 GTTGAAAAAG AGCAAGCGAT TTTTGAACGT GTTAACGAAG TTGAACAACA AATCAATGGC
 180
 GCTGACCTTG TTAAAGGTAA TTCAACAACA AATTGGCAAA AGTCTAAACT TACAGATGAT
 240
 TACGGTAAAG CAATCGAATC GTCTGAGCAG TCCATAGATA GCGTTTTAAG CACAGTTAAC
 300
 ACATCTAGGA TTATTCATAT TACTAATGCA ACAGATGCGC CAGAAAAGAC GGATATAGGC
 360
 ACGTTAGAGA AGCCTGGACA AGATGGTGTT GATGACGGTT CTTGTTCTGA TGAATCAACT
 420
 TATACATCAA GCAAATCTGG TGTGTTAGTT GTTTATGTTG TTGATAATAA TACTGCTCGG
 480
 TGCAACATGG TACCCAGACG ATTCAAACGA TGAGTTCACA AAATACAAAN TCTTACGGCA
 540
 CATGGTACCC GTTTTATTAA AAAGAATGAT GGAAACTTAA CTAGCAATTT GGTGAGGA
 600
 ACGTCTTACA ACGCTTTAAA TCAAGCTAAG CAGTATGTAG ATGATAAATT CGGAACAACG
 660
 AGCTGGCAAC AACATAAGAT GACAGAGCCG AACGGTCAAT CAATTCAAGT TAACTTAAAT
 720
 AATGCGCAAG GCGATTTGGG ATATTTAACT GCTGGTAATT ACTATGCAAC AAGAGTGCCG
 780
 GATTTACCAG GTAGCGTTGA AAGTTATGAG GGTTATTTAT CGGTATTCGT TAAAGATGAT
 840
 ACAACAAGC TATTTAACTT CACACCTTAT AACTCTAAAA AGATTTACAC ACGATCAATC
 900
 ACAAACGGAA GACTTGAGCA ACAGTGGACA GTTCCTAATG AACATAAGTC AACGGTATTG
 960
 TTCGACGGTG GAGCAAATGG TGTAGGTACA ACAATCAATC TAACTGAACC GTACACAAAC
 1020
 TATTCTATTT TGTTGGTAAG TGGAACCTAT CCAGGTGGCG TTATTGAGGG ATTCGGACTA
 1080
 ACCGCATTAC CTAATGCAAT TCAATTAACC AAACCGAATG TAGTTGACTC AGACGGTANC
 1140
 GGTGGCGGTA TTTATGAGTG TTTACTATCA AAAACAAGTA GTACCCACTT TAAGAATAGA
 1200

CAACGATGTG TATTTTCGATT TAGGCAAAAC ATCAGGTTCT GGAACGAATG CCAACAAAAGT
 1260
 TACTATAACT AAAATTATGG GGTGGAAATA ATGAAAATAA CAGTAAACGA TAAAAACGAA
 1320
 GTTATCGGAT ACGTTAATAC TGGCGGTTTA CGCAATAGTT TAGATGTAGA TGATAACAAT
 1380
 GTGCCTATCA AATTCAAAGA AGAGTTTGAA CCTAGAAAAGT TTGTTTTTCAC TAACGGCGAA
 1440
 ATTAAATATA ACAGCAATTT TGAAAAAGAA GACGTACCGA ATGCATCAAG CCAACAAAAGT
 1500
 GAATCAGATT TGAGTGATGA AGAACTTCGC GGAATGGTTG CGAGTATGCA AATGCAGGTG
 1560
 GCACAAGTAA ACGTATTAAC AATGGAATTA GCTCAACAAA ACGCTATGTT AACACAACAG
 1620
 TTGACTGAAC TGAAAACTAA CAAAACAAGT ACTGAGGGGG ACGTTTAATG ATGAAGATGA
 1680
 TTTATCCGAC TTTTAAAGAC ATCAAAACTT TTTATGTTTG GGGTTACTAT AAAAACGAGC
 1740
 AAATTAAGTG GTACGTAGAC AAGGGTTTAA TCGATAAAGA AGAATACGCT TTAATCACTG
 1800
 GAGAAAAATA TCCAGAAACA AAAGATGAAA AGTCACAGGT GTAATGCTTG TGGCTTTTTA
 1860
 ATTTAACAAA AAGTAGGTGG CGTAATGTTT GGTTTTACCA AACGACATGA ACAAGATTGG
 1920
 CGTTTAACGC GATTAGAAGA AAATGATAAG ACTATGTTTG AAAAATTCGA CAGAATAGAA
 1980
 GATAGCTTA GAGCGCAAGA AAAGATTTAT GACAAATTAG ATAGAAATTT TGAAGAATT
 2040
 AAAGCGCGAC AAGGTAGAAG ATGAAAAGAA TAAAGAAAAG AATGCCAAGA ATATTAGAGA
 2100
 CATAAAAATG TGGATTCTCG GTTTGATAGG GACTATCTTC AGTACGATTG TCATAGCTTT
 2160
 ACTAAGAACT ATTTTTGGTA TTTAAAGGAG GTGATTACCA TGCTTAAAGG GGATTTTAGG
 2220
 ATATAGCTNC TGGGCGGTCC TCCTGGTTGG GGGTAAATGT AAATAACAGT TAAGAGTCAG
 2280
 TGCTCCGGCA CTGGCTTTTT ATTTTGATTG AAATGAGGTG CATACTGGG ATTACCTAAT
 2340
 CCAAAGACTA GAAAGCCTAC AGCTAGTGAA GTGGTGGAGT GGGCAAAGTC GAATATTGGT
 2400
 AAGAGGATTA ATATAGATAA TTATCGGGGC AGTCAATGTT GGGATACACC TAACTTTATT
 2460
 TTTAAAAGAT ATTGGGGTTT TGTAAATGG GGCAATGCTA AGGATATGGC TAATTACAGA
 2520
 TATCCTAAGG GTTTCCGATT CTATCGTTAT TCATCTGGAT TTGTTCCGGA ACCCGGAGAC
 2580
 ATAGCAGTTT GGCACCCTGG CAACGGAATA GGTTCGGACG GACACACCGC AATAGTAGTA
 2640
 GGACCATCTA ATAAAAGTTA TTTTATAGC GTTGACCAAA ACTGGGTAA TTCTAATAGT
 2700
 TGGACAGGTT CTCCAGGAAG ATTAGTAAGA CACCCTTATG TAAGTGTTAC AGGCTTTGTT
 2760
 AGGCCTCCGT ACTCAAAAGA TACTAGCAAA CCTAGTAGTA CTGATACAAG TTCAGCATCA
 2820
 AAAAGCCAAT GACTCAACAA TTACTGGCGA AGCGAAGAAA CCGCAATTTA AAGAAGTTAA
 2880
 AACAGTAAAA TACACTGCTT ACAGCAATGT TTAGATAAAG AAGAGCACTT CATTGATCAT
 2940
 ATAGTTGTAA TGGGTGATGA ACGCTCAGAT ATTCAAGGAT TATATATAAA AGAATCAATG
 3000
 CATATGCGTT CTGTAGACGA ACTTTATACG CAAAGAAAATA AGTTTATAAG CGATTATGAA

3060
ATACCGCATT TATATGTCGA TAGAGAGGCT ACAGGAATTC CGGAATTCCG
3110

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

AAATTATATA TAATAACGTC GTTTTAACTA AGGCAACATA AGGAGGTGCG TCAATTGGCT
60
CAAGCAAAAA AGAAATCGAC AGCTAAGAAA AAAACAGCAT CAAAAAAAAG AACAAATTCA
120
AGGAAAAAGA AGAATGATAA TCCGATACGT TATGTCATAG CTATTTTAGT AGTTGTATTA
180
ATGGTGTTGG GTGTTTTCCA ATTAGGAATA ATCGGTCGTC TAATTGACAG CTTCTTTAAT
240
TATTTATTTG GGTACAGTAG ATATTTAACA TATATTTTAG TACTCTTAGC AACTGGTTTT
300
ATTACATACT CTAAACGTAT TCCTAAAACT AGACGAACGG CTGGTTCGAT TGTATTGCAA
360
ATTGCATTGC TATTTGTATC ACAGTTAGTT TTTCATTTTA ATAGTGGTAT CAAAGCTGAA
420
AGAGAACCTG TACTTTCTTA TGTATATCAG TCATACCAAC ACAGTCATTT TCCAAATTTT
480
GGTGCGGGTG TATTAGGTTT TTATTTATTA GAGTTAAGCG TACCTTTAAT TTCATTATTT
540
GGTGATGTA TTATTACTAT TTTATTATTA TGCTCAAGTG TTATTTTATT AACAAACCAT
600
CAACATCGTG ATGTTGCAAA AGTTGCACTG GAAAATATAA AAGCTTGGTT TGGTTCATTT
660
AATGAAAAAA TGTCGGAAAG AAACCAAGAA AAACAATTGA AGCGTGAAGA AAAAGCGAGA
720
CTTAAAGAAG AACAAAAGGC ACGTCAAAAT GAACAGCCAC AAATAAAAAGA TGTGAGTGAT
780
TTTACGGAAG TGCTCAAGA AAGAGATATT CCAATTTATG GGCATACTGA AAATGAAAGT
840
AAAAGCCAGT GTCAACCAAG TCGAAAAAAA CGAGTGTTTG ATGCAGAGAA TAGTTCGAAT
900
AACATCGTAA ATCATCAAGC AGATCAGCAA GAGCAATTAA CAGAACAAAC TCATAACAGT
960
GTTGAAAGTG AAAACACTAT TGAAGAAGCT GGTGAAGTTA CGAATGTATC GTATGTTGTT
1020
CCACCGTTAA CTTTACTTAA TCAACCTGCA AAACAAAAAG CAACATCTAA AGCTGAAGTA
1080
CAACGTAAAG GACAAGTACC AAAGAGATAC ATNAAAAGAT TTTGGGGTNA AATCCNAAAG
1140
TNGACACAAA TNAAATTGTC CTNCAGTAAC TCAATATGAA ATCCCACCCA GCTCAANGGG
1200
GGTTNAAAGT GAGTAAAATT GTAAACTTTG CATAATGATA TTGCATTAGC TTTAGCACCA
1260
AAAGATGTTA GAATCGAAGC ACCAATACCT GGTGCTCTG CAGTAGGTAT TGAAGTGCCA
1320
AATGAGAAAA TTTCATTAGT TTTACTAAAA GAAGTTTTAG ATGAAAAATT CCCGTCTAAT

1380
 AATAAACTAG AAGTTGGATT AGGAAGAGAT ATATCAGGTG ATCCAATTAC TGTTCCACTA
 1440
 AATGAAATGC CACACTTATT GGTGGCAGGA TCGACGGGTA GTGGTAAATC TGTTTGTATA
 1500
 AATGGTATTA TTACAAGTAT TTTATTAAAT GCTAAGCCGC ATGAAGTTAA ACTTATGTTA
 1560
 ATCGATCCGA AAATGGTTGA ACTAAATGTT TATAACGNNN NNNCACATTT ATTAATTCCG
 1620
 GTTGTTACAA ATCCTCATAA AGCTGCTCAA GCTTTAGAAA AAATTGTAGC TGAGATGGAA
 1680
 AGACGTTATG ATTTATTCCA ACATTCATCA ACTAGAAATA TTAAAGGTTA TAACGAATTA
 1740
 ATCCGTAAGC AAAATCAAGA ATTAGATGAG AAGCAACCAG AATTACCTTA TATCGTTGTT
 1800
 ATTGTAGATG AGCTTGCAGA TTTAATGATG GTAGCTGGTA AAGAAGTTGA AAATGCGATT
 1860
 CAACGTATCA CACAAATGGC ACGTGCAGCA GGTATACATT TGATTGTAGC AACACAAAGA
 1920
 CCTTCTGTGG ATGTAATTAC AGGTATCATT AAAAATAACA TTCCATCTAG AATTGCTTTT
 1980
 GCTGTGAGTT CTCAAACAGA TTCAAGAACT ATTATTGGTA CTGGCGGCGC AGAAAAGTTA
 2040
 CTTGGTAAAG GGTGACATGT TATACGTTGG AAATGGTGAT TCATCACAAA CACGTATTCC
 2100
 AAGGGGCGTT TTTAAGTGAC CAAGAGGTGC AAGATGTTGT AAATTATGTA GTAGAACAAC
 2160
 AACAGGCAAA TTATGTAAAA GAAATGGAAC CAGATGCACC AGTGGATAAA TCGGAAATGA
 2220
 AAAGTGAAGA TGCTTTATAT GATGAAGCGT ATTTGTTTGT TGTTGAACAA CAAAAGGCAA
 2280
 GTACATCATT GTTACAACGC CAATTTAGAA TTGGTTATAA TAGAGCATCT AGGTTGATGG
 2340
 ATGATTTAGA ACGCAATCAG GTAATCGGTC CACAAAAAGG AAGCAAGCCT AGACAAGTTT
 2400
 TAATAGATCT TAATAATGAC GAGGTGTAAA AAATTTGATT AAGCAAATA AATTGGAATA
 2460
 TGGTGACCAA CTATCCAAGT AATTTATCAA TTGCCAGAGA ATTAAATGTA AAAACCGACG
 2520
 ATGTTTATGA AGCAATTCAG GCATTGATTA CTG
 2553

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1664 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

CCGTACATTA ACAACCTGGA TTAATTACAG ATTACGTTTT GTCTCATCTA AAAATTGTTG
 60
 ATAATCTTTG ATCAATTTCC AAATCTGTAC GTATGTATTA TCTTAGTAGT AGTTTAATAT
 120
 GCACTAAATA CTTGCAATTG ATATTTACCA TATTTATTGT CAAATCCAAT TATCTTGTGT
 180
 TTTTCATAAA ACGATTGCTT TAAATAATCT TCTAACACAT CAAACATCGT ATTATCACCG

240
 ACATGGTGCC CGTATAAAAT AGTATTATGA TTTAAATTCT NCAATTCATT TCTAAAATCC
 300
 ATAAAAATAC TACCTTTACG TCGATGTTCT CGCTCAAAAT CTAAATTTAA ATAATCGTGA
 360
 TTTGTCTTAC CTTGTAGTAC TGGATAANTT AATGATGTTT CTGATAATTT TATCCATCCA
 420
 ACAATGTCTT TATTTATTTT TTCAAGTGAT TCAAATTGTG GTCTCACATG TTCTTGATGT
 480
 TTGNTCATCA GCATNTGAAA TTTNTGTTGT AATTTCTCAT AANTTGCGCG TTCTTGCTTG
 540
 TCTTCAATAT ATGTTTGAAC AATTTTGTAA CCAAAAATGA TAATAATTAC AACCAATAAA
 600
 ATTTGTACAA TAGTTAAAAA TCGCTTCATT CTCATAAAAA CCTCTTTAA TAAACAANTT
 660
 TCTTCAGTCA TCACTAAACC AGTTGTTGTA CCGTTTTAGA TTCGATTTCTG TTGACTTTGA
 720
 CAAATTAAGT AAATTAGCAT TGGACCACCG ACAATCATTA AAATAGCATT GGCTGGAATT
 780
 TCTAAAGGAG GCTGTATCAC TCGTCCTAAT AAATCAGCCA CTAACAATAG CCATGCACCA
 840
 ATAAGTGTAG AAAACGGAAT AAGTACTCTG TAATTGCCCC CAACTAGCTT TCTAACCACA
 900
 TGTGGCACAA TAATACCTAA AAAGGCTAGT TGTCCAACAA TCGCAACAGT TGCACTTGCT
 960
 AAAAATACTG CTAATAAACC TGTTAACCAT CTGTAACGAT CAATATTAAA ACCGATACTT
 1020
 CGCGCTTGTA TGTCGTCTAA ATTTAGTAAA TTCAATTTAG GGGACAATAG TAATGTTAAT
 1080
 ATTAATCCCA ATAATGCTGA TACTGCTAAT ATGTATACGT CGCTCCATAT TTTCATTGTT
 1140
 AAGCCTTGAG GAATTTTCAT TAAAGGGTTT TGAGTTAAAA TTTCTAAAC ACCATTTAAT
 1200
 AATACGNATA ACGCAACACC TACTAATATC ATACTTACAG CATTGAATCT AAATTTAGAA
 1260
 TGCAACAATA TAATTATTAA AAATGGTATT AAACCTCCAA TAAAACTTAA TAATGGTAAG
 1320
 TAAAAGTACA ATTGTGGAAT AAACAACATA CCAAGTGCTC TCATTATAAG TGCACCTGAG
 1380
 GAAACGCCAA TGATATTCGC CTCTGCCAAA GGATTTTGTA GTCCTGCTTG TAATAATGCT
 1440
 CCAGAACTG CTAACATTGC GCCANCCATC AATGCAANTA ATAGACGTGC CAATCCCCAA
 1500
 TCAATGATTG AATCCACTGC TTCATTGCTA CCAGTTGTAA ATTTTGTAAG TAGGTCATTA
 1560
 AATGACAATT TAATTGTACC GGTTACAAAC GAAATATAAG CAGTTGCGAT TAAAATGACT
 1620
 AACAAACATA AAAATAGTAG TTTCTTTTAA TTTTATCA TCAG
 1664

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

Val	Leu	His	Xaa	Ile	Arg	Glu	Ile	Leu	Leu	Gln	Leu	Val	His	His	Ser
1				5					10					15	
Asp	Xaa	Gly	Xaa	Gly	Ile	Gln	Pro	Pro	Lys	Phe	Phe	Gln	Pro	Gly	Asp
		20					25					30			
Xaa	Xaa	Lys	Val	Thr	Ile	Asp	Asn	Ile	Gly	Thr	Leu	Thr	Thr	Tyr	Ile
		35				40						45			
Xaa	Lys														
	50														

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

Val	Pro	Ile	Lys	Ala	Val	Ile	Ala	Gln	Thr	Met	Thr	Thr	Leu	Pro	Arg
1				5				10					15		
Val	Ile	Asn	Ile	Lys	Arg	Leu	Thr	Ser	Gly	Leu	Asn	Lys	Pro	Leu	Ser
		20				25						30			
Phe	Met	Met	Pro	Lys	Lys	Ile	Met	Ala	Xaa	Ile	Asn	Ile	Ile	Thr	Thr
		35				40						45			
Xaa	Met	Xaa													
	50														

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

Val	Ile	Lys	Phe	Lys	Asn	Val	Thr	Lys	Arg	Tyr	Gly	Lys	His	Val	Ala
1				5				10					15		
Val	Asp	Asn	Ile	Ser	Phe	Asn	Ile	Asn	Glu	Gly	Glu	Phe	Phe	Val	Leu
		20					25					30			
Ile	Gly	Pro	Ser	Gly	Cys	Gly	Lys	Thr	Thr	Thr	Leu	Lys	Met	Ile	Asn
		35				40					45				
Arg	Leu	Ile	His	Leu	Ser	Glu	Gly	Tyr	Ile	Tyr	Phe	Lys	Asp	Lys	Pro
	50				55					60					
Ile	Ser	Asp	Tyr	Pro	Val	Leu	Arg	Asn	Ala	Leu	Gly	Tyr	Trp	Xaa	Arg
65				70				75						80	
Xaa	Gly	Xaa	Arg	Leu	Glu	Leu	Xaa	Pro	Ile						
			85					90							

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

Val	Cys	Cys	Phe	Gly	Ala	Ser	Thr	Met	Leu	Ser	His	Ile	Thr	Ala	Tyr
1				5					10					15	
Glu	Ile	Leu	Ser	Glu	Ile	Xaa	Lys	Lys	Leu	Ala	Gln	Lys	Leu	Met	Arg
			20				25						30		
Leu	Pro	Leu	Xaa	Val	Val	Glu	Ser	Lys	Lys	Ile	Gly	Glu	Leu	Lys	Asn
		35					40					45			
Ile	Phe	Xaa	Asp	Lys	Val	Glu	Thr	Ile	Glu	Leu	Pro	Leu	Ala	His	Met
	50				55						60				
Ile	Pro	Glu	Val	Xaa	Gly	Asn	Leu	Leu	Val	Ala	Ala	Ile	Phe	Leu	
65					70				75					80	
Tyr	Ile	Met	Xaa	Xaa	Asp	Trp	Arg	Ile	Gly						
				85					90						

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

Val	Thr	Ser	Phe	Ile	Tyr	Lys	Ile	Leu	Tyr	Val	Val	Lys	Ile	Asn	Ala
1				5					10					15	
Tyr	Thr	Tyr	Asp	Ile	Met	Thr	Glu	Asp	Ile	Met	Xaa	Leu	Ser	Ile	Leu
			20				25						30		
Leu	Ile	Phe	Leu	Cys	Ile	Arg	Leu	Val	Ser	Leu	Lys	Ile	Cys	Ile	Xaa
		35					40					45			
His	Ser	Lys	Gln	Leu	Lys	Ala	Asp	Gly	Ala	Val	Glu	Tyr	Gly	Val	Lys
	50				55						60				
Asn	Ser	Lys	Phe	Leu	Ala	Ile	Thr	His	Val	Leu	Ile	Tyr	Val	Leu	Ala
65					70				75					80	
Gly	Val	Glu	Ala	Phe	Ile	Asn	Lys	Asp	Thr	Phe	Ser	Phe	Ala	Asn	Gly
				85					90					95	
Ile	Gly	Leu	Val	Ile	Leu	Ile	Phe	Ala	Tyr	Ile	Met	Leu	Phe	Met	Val
			100					105					110		
Ile	Lys	Thr	Leu	Gly	Gly	Ile	Trp	Thr	Leu	Lys	Leu	Phe	Ile	Leu	Pro
	115					120						125			
Asn	His	Pro	Ile	Ile	Lys	Ser	Gly	Leu	Tyr	Lys	Ile	Thr	Lys	Thr	Pro
	130				135						140				
Lys	Leu	Leu	Leu	Lys	His	His	Ser								
145					150										

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

```
Val Arg Val Thr Gly Ile Xaa Pro Tyr Gly Ala Phe Val Glu Thr Pro
 1          5          10          15
Asn His Thr Glu Gly Leu Ile His Ile Ser Glu Ile Met Asp Asp Tyr
 20          25          30
Val His Asn Leu Lys Lys Phe Leu Ser Glu Gly Gln Ile Val Lys Ala
 35          40          45
Lys Ile Xaa Ser Ile Asp Asp Glu Gly Lys Leu Asn Leu Ser Leu Xaa
 50          55          60
Asp Asn Asp Tyr Phe Lys Asn Tyr Glu Arg Lys Lys Glu Lys Gln Ser
 65          70          75          80
Val Leu Asp Glu Ile Arg Xaa Thr Glu Lys Tyr Gly Xaa Gln Thr Leu
 85          90          95
Lys Arg Thr Leu Thr Asn Leu Gly
100
```

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

```
Val Thr Xaa Gly Val Xaa Glu Leu Ile Ile Xaa Ser Gly Glu Glu Glu
 1          5          10          15
Ser Ser Ser Gln Leu Cys His Pro His Ser Val Lys Asp Val Thr Gly
 20          25          30
Ala Gly Asp Ser Phe Cys Ala Ala Val Val Tyr Ser Trp Xaa Asn Gly
 35          40          45
Met Ser Thr Val Asp Ile Leu Ile Ala Gly Met Val Asn Ala Xaa Lys
 50          55          60
Thr Ile Glu Thr Lys Tyr Thr Val Arg His Asn Leu Asp Gln Gln Gln
 65          70          75          80
Leu Tyr His Asp Met Glu Asp Tyr Lys Asn Gly Lys Phe Thr Gln Val
 85          90          95
Tyr
```

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

```
Val Asn Lys Asn Xaa Thr Thr Met Ser His Ile Thr Xaa Xaa Gln Ser
 1          5          10          15
Ala Ile Leu Ala Ser Lys Val Asn Ala Pro Ser Val Tyr Asn Xaa Asn
```

		20					25					30							
Asn	Met	Ser	Glu	Asn	Phe	Thr	Gln	Arg	Val	Lys	His	Xaa	Leu	Arg	Lys				
		35					40					45							
Asn	Glu	Ala	Thr	Thr	Xaa	Tyr	Gln												
		50					55												

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

Val	Ser	Ser	Arg	Asp	Ile	Gly	Glu	His	Val	Met	Asn	Leu	Leu	Met	His				
1				5					10					15					
Val	Asp	Gln	Val	Ser	Tyr	Val	Arg	Phe	Ala	Ser	Val	Tyr	Lys	Glu	Phe				
		20					25					30							
Lys	Asp	Val	Asp	Gln	Leu	Leu	Ala	Ser	Met	Gln	Gly	Ile	Leu	Ser	Glu				
		35					40					45							
Asn	Lys	Arg	Ser	Asp	Ala														
		50																	

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

Val	Ala	Xaa	Val	Xaa	Ile	Ile	Xaa	Phe	Met	Met	Leu	Xaa	Pro	Xaa	Gly				
1			5					10					15						
Gly	Phe	Ile	Ala	Leu	Glu	Gln	Ile	Gly	Glu	Arg	Met	Asn	Ile	Ala	Ala				
		20					25					30							
Ile	Glu	Val	Asp	Lys	Ser	Tyr	Arg	Phe	Asn	Gly	Ile	Gly	Ser	Ser	Ala				
		35					40					45							
Leu	Arg	Gln	Leu	Pro	Thr	Tyr	Leu	Arg	Lys	Asn	Tyr	Asp	Asn	Leu	Asn				
		50				55					60								
Val	Ile	Thr	Met	Ile	Leu	Phe	Gly	Glu	Asn	Asn	Asp	Phe	Lys	Pro	Leu				
65				70				75						80					
Cys	Leu	Asn	Ser	Asn	Phe	Val	Glu	Ile	Glu	Gln	Thr	Asp	Asp	Tyr	Val				
			85				90							95					
Val	Phe	Glu	Lys	Tyr	Leu	Asn	Tyr												
			100																

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

```
Val Glu Ile Lys Val His Ala Leu His Ser Gly Ile Thr Leu Ile Lys
 1           5           10           15
Asp Lys Gly Lys Ile Ile Asp Ile His Leu Ser Val Lys Ala Thr Glu
 20           25           30
Asn Ile Asp Gly Glu Val Leu Phe Lys Ala Thr Gln Pro Leu Gly Arg
 35           40           45
Thr Met Lys Val Gly Val Gln Asn Asn Ala Met Thr Ile Thr Leu Thr
 50           55           60
Lys Gln Asn Gln Trp Leu Asp Ser Leu Lys Phe Leu Val Lys Cys Ile
 65           70           75           80
Glu Glu Ser Met Arg Ile Ser Asp Glu Ala
           85           90
```

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

```
Val Glu Tyr Phe Val Ser Tyr Tyr Asp Tyr Tyr Gln Pro Glu Ala Tyr
 1           5           10           15
Val Pro Ser Thr Asp Thr Phe Ile Glu Lys Asp Ala Ser Ile Asn Asp
 20           25           30
Glu Ile Asp Xaa Xaa Arg His Ser Ala Thr Ser Ala Leu Phe Glu Arg
 35           40           45
Asp Asp Val Ile Ile Ile Ala Ser Val Ser Cys Ile Tyr Gly Leu Gly
 50           55           60
Asn Pro Glu Glu Tyr Lys Asp Leu Val Val Ser Val Arg Val Gly Met
 65           70           75           80
Glu Met Asp Arg Ser Glu Leu Leu Arg Lys Leu Val Asp Val Gln Tyr
           85           90           95
Thr Arg Asn Asp Ile Asp Phe Pro Thr Arg Asn Arg Phe Glu Cys Val
 100           105           110
Val Met
```

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

```
Val Gly His Ile Leu Ile Glu Ile Ser Xaa Asp Gly Pro Gly Phe Met
 1           5           10           15
```

Glu Asp Xaa Pro Tyr Glu Thr Leu Gly Xaa Gly Leu Ser Leu Pro Pro
 20 25 30
 Phe Leu Glu Asn Lys Arg Glu Tyr Ile Glu Ser Glu Ile Arg Pro Phe
 35 40 45
 Asn Thr Lys Arg
 50

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

Val Ser Ile Thr Leu Xaa Pro Ala Leu Ala Ala Thr Leu Phe Lys Lys
 1 5 10 15
 Gly Val Lys Arg Arg Asn Lys Gln His Gln Glu Gly Leu Gly Val Val
 20 25 30
 Ser Thr Thr Tyr Lys Xaa Val Xaa His Trp Val Thr Lys Ser
 35 40 45

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Val Val Gln Glu Thr Leu Asn Met Ser Lys Ala Arg Gly Tyr Glu Val
 1 5 10 15
 Gly Gly Thr Val Arg Ile Val Ile Asn Asn Gln Val Gly Phe Thr Thr
 20 25 30
 Ser Asn Pro Leu Asp Ala Arg Ser Tyr Ala Val Leu Tyr
 35 40 45

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

Val Glu Gly Asn Phe Gly Leu Ala Ile Asn Asn His Gln Asn Ile Val
 1 5 10 15
 Gly Thr Ile Gly Leu Ile Arg Leu Asp Asn Asn Met Ser Ala Leu Lys
 20 25 30

Lys Met Phe Val Asp Lys Gly Tyr Arg Asn Leu Lys Ile Gly Lys Lys
 35 40 45
 Leu, Leu Asp Lys Val Ile Met Thr Cys Lys Glu Gln Asn Ile Asp Xaa
 50 55 60
 Xaa Tyr Leu Gly Thr Xaa Asp Lys Xaa Xaa Ser Ala Gln Tyr Xaa Tyr
 65 70 75 80
 Xaa Asn Xaa Gly Phe Arg Xaa Asn
 85

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

Val Ile Gly Leu Lys Ser Lys Thr Ile Ile Ser Asn Glu Trp Gly Ala
 1 5 10 15
 Ile Met Ile Gln Ser Met Trp Phe Asn Leu His Val Gln Asp Leu Glu
 20 25 30
 Lys Ser Ala Gln Phe Tyr Lys Ala Leu Gly Phe Lys Ile Asn Arg Asn
 35 40 45
 Pro Gln Met Leu Asp Lys Met Val Gly Ile Gln Ile Gly Gln Thr Thr
 50 55 60
 Ala Ile Leu Ile Glu Asn Lys His Phe Gln Asn Val Ser Gln Gln Ser
 65 70 75 80
 Leu Asn Thr Glu Pro Asn Glu Val Met Ile Ser Leu Gly Val Thr Gln
 85 90 95

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

Val Ser Leu Met Thr Thr Phe Ser Glu Lys Glu Lys Ile Gln Leu Leu
 1 5 10 15
 Ala Asp Ile Val Glu Leu Gln Thr Glu Asn Asn Asn Glu Ile Asp Val
 20 25 30
 Cys Asn Tyr Leu Lys Asp Leu Phe Asp Lys Tyr Asp Ile Lys Ser Glu
 35 40 45
 Ile Leu Lys Val Asn Glu His Arg Ala Asn Ile Val Ala Glu Ile Gly
 50 55 60
 Asn Xaa Ser Pro Ile Leu Ala Leu Ser Gly His Met Asp Val Val Gly
 65 70 75 80
 Cys Arg Lys Ser Arg
 85

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

Val	Glu	Xaa	Met	Asn	Lys	His	Tyr	Xaa	Ile	Val	Ile	Ile	Gly	Gly	Gly	
1				5					10					15		
Thr	Ala	Gly	Val	Thr	Val	Ala	Ser	Arg	Leu	Leu	Arg	Lys	Asn	Xaa	Asn	
			20					25					30			
Leu	Lys	Glu	Lys	Ile	Ala	Ile	Ile	Asp	Pro	Ala	Asp	His	His	Tyr	Tyr	
		35				40						45				
Gln	Pro	Leu	Trp	Thr	Leu	Val	Gly	Ala	Gly	Val	Ser	Ser	Leu	Lys	Ser	
	50				55						60					
Xaa	Ser															
65																

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

Val	Leu	Arg	Asn	Lys	Ile	Lys	Arg	Ala	Ile	Arg	Glu	Asn	Phe	Lys	Val	
1				5					10					15		
His	Lys	Ser	Xaa	Ile	Leu	Xaa	Lys	Asp	Ile	Ile	Xaa	Ile	Xaa	Arg	Gln	
			20					25					30			
Ala	Ala	Lys	Asp	Met	Thr	Thr	Leu	Gln	Ile	Gln	Xaa	Ser	Leu	Glu	His	
		35				40						45				
Xaa	Leu	Lys	Ile	Gly	Lys	Val	Phe	Asn	Lys	Lys	Ile	Lys				
	50				55						60					

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

Val	Asp	Gly	Val	Ser	Leu	Ala	Val	Phe	Asp	Lys	His	Asp	Asn	Ser	Phe	
1				5				10						15		
Asp	Ile	His	Leu	Ile	Pro	Glu	Thr	Arg	Arg	Ser	Thr	Ile	Leu	Ser	Ser	
			20					25					30			
Thr	Lys	Leu	Gly	Asp	Lys	Val	His	Leu	Glu	Thr	Asp	Val	Leu	Phe	Lys	
		35				40					45					
Tyr	Val	Glu	Asn	Ile	Leu	Asn	Lys	Asp	Lys	Asp	Gln	Leu	Ser	Val	Asp	

50 55 60
Lys Leu Arg Ala Phe Xaa Phe
65 70

(2) INFORMATION FOR SEQ ID NO:281:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

Val 1	Xaa	Gln	Ser	Leu 5	Tyr	Glu	Phe	Leu	Glu 10	Glu	Asn	Ile	Asn	Tyr 15	Leu
Lys	Glu	Asn	Gly 20	Xaa	Tyr	Asn	Glu	Ile 25	Asp	Thr	Ile	Glu	Gly 30	Ala	Asn
Gly	Pro	Glu 35	Ile	Lys	Ile	Asn	Gly 40	Lys	Ser	Tyr	Ile	Asn 45	Leu	Ser	Ser
Xaa	Asn 50	Tyr	Leu	Gly	Leu	Ala 55	Thr	Asn	Glu	Asp	Xaa 60	Arg	Ser	Ala	Ala
Lys 65	Ala	Ala	Ile	Asp	Thr 70	His	Gly	Val	Gly	Ala 75	Gly	Ala	Xaa	Arg	Thr 80
Xaa	Asn	Gly	Thr 85	Leu	Asp	Leu	His	Asp 90	Glu	Leu	Glu	Glu	Thr 95	Leu	Ala
Lys	Phe	Xaa	Gly 100	Thr	Glu	Ala	Ala	Ile 105	Ala	Tyr	Gln	Xaa	Arg 110	Ile	Xaa
Leu	Xaa	Ile 115	Trp	Leu	Leu	Xaa	Gln 120	Leu	Val	Xaa	Glu	Xaa 125	Lys		

(2) INFORMATION FOR SEQ ID NO:282:

- ```
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
```

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

[illegible]

(2) INFORMATION FOR SEQ ID NO:283:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 32 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Lys | Glu | Asn | Asp | Val | Lys | Lys | Phe | Lys | Tyr | Lys | Asn | Phe | Xaa | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Ile | Glu | Ile | Asp | Phe | Thr | Asp | Ser | Asn | His | Leu | Ala | Ala | His | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Pro | Asp | Ala | Asn | Gly | Lys | Val | Ala | Phe | Asp | Gly | Leu | Glu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Phe | Thr | Gly | Thr | Pro | Ala | Val | Asn | Asp | Ser | Phe | Thr | Leu | Lys | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Ser | Asp | Ala | Ile | Val | Asn | Met | Asp | Val | Leu | Ile | Thr | Asp | Glu | Ala |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Ile | Ala | Met | Ala | Ser | Glu | Glu | Asp | Ala | Gly | Asp | Ser | Asp | Asn | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Asn | Gly | Gln | Ala | Leu | Leu | Asp | Leu | Ala | Lys | Gln | Gln |     |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Leu | Pro | Leu | Val | Phe | Ile | Ser | Val | Leu | Ile | Gly | Ile | Phe | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Ile | Lys | Val | Leu | Pro | Phe | Ile | Ile | Lys | Tyr | Val | Gly | Ile | Ala | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Lys | Ile | Thr | Arg | Met | Gly | Arg | Leu | Glu | Ser | Tyr | Phe | Ala | Ile | Ser |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Ala | Met | Phe | Gly | Gln | Pro | Glu | Val | Tyr | Leu | Thr | Ile | Lys | Asp | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Pro | Arg | Leu | Ser | Arg | Ala | Lys | Leu |     |     |     |     |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

```
Val Ile Ile Ser Asn Asn Val Gly Asp Met Ser Ile Gly Phe Ser Ser
 1 5 10 15
Asp Asp Asn Glu Leu Thr Met His Phe Arg Asn Asn Glu Lys Val Asn
 20 25 30
Ile Lys Lys Gly Lys Lys Val Val Leu Ala Ala Gln Ile Leu Asp Glu
 35 40 45
Leu Glu Thr Arg Trp Gln
50
```

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

```
Val Thr Tyr Xaa His Met Ser His Arg His Thr Leu Ile Ser His Ser
 1 5 10 15
Phe Lys Phe Xaa Arg Leu Pro Gln Asp Ile Asn Phe Phe Ser Trp Xaa
 20 25 30
Gln His Val Lys Asp Ser Asp Lys Thr Asp Glu Leu Thr Tyr Ser Glu
 35 40 45
Ser Leu Xaa Pro Glu Gly His Pro Thr His Pro Leu Thr Pro Thr Lys
 50 55 60
Leu Pro Xaa Thr Met Glu Glu Xaa Arg Ala Tyr Ala Pro Glu Phe Asp
 65 70 75 80
Xaa Arg Asn Pro Phe Ala Thr Leu
 85
```

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

```
Val Ile Ser Leu Leu Lys Asp Ala Lys Leu Pro Ser Ser Val Thr Arg
 1 5 10 15
Gly Asp Tyr Leu Ala Ile Leu Ser Xaa Gly Ala Tyr His Tyr Ser Met
 20 25 30
Xaa Ser Asn Tyr Asn His Met His Lys Pro Ser Val Phe Phe Leu Lys
 35 40 45
Asp Val Thr Ala Arg Val Val Ile Lys Arg Gln Ser Leu Arg Gln Leu
 50 55 60
```

Ile Ile Asn Xaa Thr Gln  
65 70

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gln | Phe | Val | Asn | Lys | Leu | Phe | Asn | Val | Ser | Ser | Ala | Ile | Ile | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Glu | Tyr | Asp | Gly | Val | Val | His | Ile | Gly | Tyr | Asp | Asn | Asn | Phe | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Lys | Thr | Glu | Gln | Phe | Lys | Met | Ser | Lys | Ser | Arg | Asn | Leu | Leu | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Arg | Ser | Gln | Asn | Xaa | Val | Leu | Ile | Arg | Leu | Leu | Asn | Trp | Leu | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Thr | Xaa |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gln | Leu | Gly | Leu | Thr | Asn | Ser | Val | Val | Ala | Ile | Ile | Ile | Ile | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Glu | Xaa | Ala | Val | Thr | Gly | Leu | Arg | Leu | Leu | Gln | Ile | Glu | Gln | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Xaa | Gly | Lys | Cys | Ser | Trp | Xaa | Ile | Arg |     |     |     |     |     |     |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asp | Val | Asp | Asn | Met | Ser | Asp | Tyr | Lys | Leu | Lys | Ile | Ile | Xaa | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Xaa | Ser | Asp | Ile | Thr | Gly | Tyr | Gln | Ile | Pro | Asn | Gln | Xaa | Gly | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

Ala Gln Tyr Val Ile Ser Gln Leu Ser Gln Gly Lys Arg Glu Val Asp  
           35                          40                          45  
 Asn Leu Thr Leu Asn Xaa Xaa Glu Xaa Leu Tyr Ser Tyr Xaa Arg Gln  
           50                          55                          60  
 Val Leu  
 65

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

Val Lys Gln Thr Xaa Val Glu Glu Ile Xaa Ala Ser Ile Asn Xaa Ala  
   1                          5                          10                          15  
 Gly Leu Xaa Xaa Glu Ile Pro Asp Phe Lys Xaa Glu Val Xaa Xaa Xaa  
           20                          25                          30  
 Xaa Lys Lys Trp Arg Leu Cys Tyr  
           35                          40

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

Val Ser Thr Asp Phe Ile Leu Cys Lys Leu Gln Ala Phe His Ile Ile  
   1                          5                          10                          15  
 Lys Phe Glu Lys Arg Tyr Ile Glu Val Glu Lys Asn Glu Tyr Thr Ala  
           20                          25                          30  
 Lys Tyr Asn Glu Tyr Ser Gln Leu Leu Asp Ala Thr Tyr Ser Gln Ala  
           35                          40                          45  
 Val Ala Tyr Leu Leu Asn Lys Tyr Gly Ala Val Thr Asp Asp Tyr Tyr  
           50                          55                          60  
 Lys Glu Lys Ser Tyr Thr Arg Phe Leu Asn Gly Glu Ile Lys Ser Ile  
   65                          70                          75                          80  
 Ser Lys Gly Lys Tyr Thr Arg Ala Ser Glu Gly Leu Tyr Cys His His  
           85                          90                          95  
 Ile Ser Glu Asp Lys Phe Gln Asn Leu Ser  
           100                          105

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

```
Val Ile Leu Ser Ser Ile Xaa Phe Tyr Met Gln Leu Leu Gln Lys Asn
 1 5 10 15
Pro Met Ala Ile Gly Val Trp Ala Gly Leu Cys Gln Met Ile Lys Pro
 20 25 30
Thr Val Ile Asp Trp Asp Ile Ser Glu Tyr Thr Pro Lys Pro Ala Trp
 35 40 45
Met Gln Ala Thr Lys Ala Arg Ala Tyr Val Pro Arg Ile Leu Val Glu
 50 55 60
Lys Leu Leu Ile Xaa Ile Asp Asp Met Leu Glu Gly Ile Glu Ile Tyr
65 70 75 80
Asp Xaa Xaa Glu Ser Arg
 85
```

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

```
Val Xaa Thr Tyr Val Asn Asp Tyr Leu Asn Glu Ala His Ile Thr Asn
 1 5 10 15
Lys Trp Ser Glu Met Met Leu Trp Ser Ser Gln Gln Arg Ser Gln Tyr
 20 25 30
Thr Val Gln Leu Ile Asn Lys Ile Glu Thr Asp Asp Ser Tyr Ile His
 35 40 45
Ile Ser Lys Gly Glu Leu Gly Ile Ser Leu Met Pro His Ile Gln Leu
 50 55 60
Lys Lys Ala Met Ser Asn Thr Ala Ser His Ile Glu Asp Leu Ser Cys
65 70 75 80
Gly Leu
```

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

```
Val Cys Lys Lys Tyr Val Leu Gly Gln Phe Lys Pro Gly Met Thr Ala
 1 5 10 15
Pro Gln Cys Ala Gly Ile Ile His Thr Asp Phe Xaa Arg Gly Phe Ile
 20 25 30
Arg Ala Gly Ser Asn Lys Leu Leu Met Thr Met Tyr Asn Met Ala Ala
 35 40 45
Lys Val Ala Leu Lys Lys Arg Ala Asp Thr Asp
```

## (2) INFORMATION FOR SEQ ID NO:297:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

```

Val Leu Thr Leu Ala Glu Met Lys Arg Thr Ile His Asp Ile Leu Asp
 1 5 10 15
Phe Arg Asp Glu Asp Ile Trp Xaa Cys Tyr Leu Gly Thr Leu Ala Val
 20 25 30
Ser Pro Xaa Leu Xaa Asp Asp Xaa Gly Xaa Xaa Leu Leu Ser Arg Xaa
 35 40 45
Xaa Asn Ala Tyr Asn Xaa Tyr Xaa
 50 55

```

## (2) INFORMATION FOR SEQ ID NO:298:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

```

Val Phe Asn Tyr Gly Gln Ser Val Phe Glu Gly Leu Lys Ala Tyr Lys
 1 5 10 15
Arg Asp Gly Glu Gly Cys Thr Xaa Pro Xaa Pro Glu Glu Asn Phe Lys
 20 25 30
Arg Leu Asn Asn Ser Leu Ala Arg Leu Glu Met Pro Gln Val Asp Asp
 35 40 45
Ala Glu Leu Leu Glu Gly Leu Lys Xaa Leu Val Asp Ile Glu Arg Asp
 50 55 60
Xaa Xaa Pro Glu Gly Glu Gly Gln Ser Leu Tyr Xaa Xaa Pro Phe Gly
 65 70 75 80
Xaa Ala Thr Glu Gly Ala Xaa Gly Val Gly Ala Ser His Gln Tyr Xaa
 85 90 95
Ile Tyr

```

## (2) INFORMATION FOR SEQ ID NO:299:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Arg | Phe | Ile | Leu | Glu | Asp | Pro | Pro | Arg | Asp | Leu | Asp | Ile | Tyr | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Ile | Ala | Glu | Arg | Ala | Gly | Gln | His | Pro | Xaa | Val | Glu | Arg | Ile | Xaa |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Asp | Gly | Xaa | Gln | Arg | Arg | Ile | Asp | Ile | Xaa | Thr | Val | Glu | Ser | Cys |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Lys | Thr | Arg | Ile | Leu | Lys | Val | Asp | Asn | Pro | Glu | Ile | Thr | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Leu | Lys | Pro | Thr | Gly | Ser | His | Phe | Gln | Gln | Cys | Val | Trp | Asn | Glu |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Leu | Arg | Gln | Val | Pro | Tyr | Gly | Thr | Leu | Thr | Thr | Tyr | Gly | Ala | Ile | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Lys | Val | Gly | Lys | Val | Leu | Asp | Lys | Pro | Gln | Met | Ser | Ala | Gln | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Val | Gly | Gly | Ala | Val | Gly | Ser | Asn | Pro | Leu | Ser | Ile | Ile | Val | Pro | Cys |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| His | Arg | Val | Val | Gly | Lys | Thr | Gly | Ser | Leu | Thr | Gly | Phe | Gly | Gly | Thr |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| Ile | Asn | Asn | Lys | Ile | Lys | Leu | Leu | Glu | Leu | Glu | Asn | Ile | Asp | Met | Ser |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Lys | Leu | Tyr | Ile | Pro | Lys | His | Ser | Thr | Lys | Pro |     |     |     |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Cys | Leu | Val | Glu | Cys | Met | Met | Ala | Leu | Asn | Thr | Ala | Gly | Xaa | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Arg | Thr | Val | Glu | Thr | Leu | Ala | Glu | Tyr | Ser | Gly | Val | Pro | Val | Trp |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Asn | Gly | Leu | Thr | Asp | Glu | Asp | His | Pro | Thr | Gln | Xaa | Leu | Ala | Asp | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Thr | Ala | Lys | Glu | Val | Phe | Lys | Lys | Arg | Leu | Cys | Arg | Tyr |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Leu | Pro | Asp | Phe | Pro | Pro | Lys | Ile | Gly | Val | Asn | Lys | Ser | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ser | Arg | Tyr | Xaa | Xaa | Gly | Ser | Arg | Xaa | Ile | Pro | Met | Glu | Asp | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Glu | Ile | Ala | Asn | Ala | Leu | Lys | Val | Thr | Pro | Glu | Tyr | Leu | Leu | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Xaa | Asn | Arg | Gln | Pro | Glu | Xaa | Glu | Val | Gln | His | Arg | Ala | Ala | His | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Gly | Glu | Leu | Thr | Asp | Asp | Glu | Cys | Gln | Arg | Val | Leu | Asp | Tyr | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asp | Tyr | Ile | Arg | Ser | Lys | Arg | Lys |     |     |     |     |     |     |     |     |
|     |     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Lys | Pro | Xaa | Cys | Ala | Lys | Lys | Asp | Arg | Tyr | Pro | Ile | Asp | Pro | Met |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Arg | Leu | Asn | Gln | Glu | Ile | Ile | Asp | Tyr | Ile | Asp | Thr | Leu | Asn | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Asp | Gln | Tyr | Ser | Ser | Ala | Gly | Ser | Phe | Arg | Arg | Phe | Lys | Glu | Met |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Lys | Asp | Leu | Asp | Phe | Ile | Ile | Ser | Thr | Asp | Asn | Pro | Gln | Ala | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Gln | Gln | Leu | Leu | Asn | Ile | Pro | Asn | Lys | Val | Lys | Glu | Val | Ala | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Asn | Thr | Gln | Val | Ser | Leu | Glu | Leu | Ala | Tyr | Asp | Asp | Glu | Thr | Ile |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Gly | Val | Asp | Phe | Arg | Leu | Ile | Glu | Pro | Arg | Ala | Phe | Tyr | His | Thr | Leu |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | His | Phe | Thr | Gly | Ser | Asn | Arg | Thr |     |     |     |     |     |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Phe | Asp | Ile | Tyr | Ser | Glu | Xaa | Asp | Leu | Ile | Glu | Ile | Thr | Asp | Tyr |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Pro | Xaa | Ser | Ile | Ser | Phe | Asn | Phe | Ala | Ser | Tyr | Met | Ser | Ala | Ser | Lys |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Phe | Phe | Lys | Asp | Tyr | Ala | Leu | Xaa | Thr | Asn | Asp | Lys | Ser | Gln | Tyr | Leu |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Glu | Asp | Tyr | Asn | Gln | His | Val | Ala | Ile | Val | Ala | Leu | Tyr | Leu | Ala | Xaa |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Gly | Asn | Lys | Ala | Gln | Ala | Lys | Gln | Phe | Ile | Ser | Ala | Met | Val | Glu | Gln |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |
| Arg | Tyr | Xaa | Pro | Ala | Thr | Pro | Thr | Phe | Leu | Asn | Ala | Xaa | Arg | Ala | Arg |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Arg | Gly | Glu | Leu | Val | Ser | Cys | Phe | Xaa | Xaa | Lys | Lys | Trp | Val | Xaa | Xaa |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Leu | Asn | Ser | Xaa |     |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Met | Glu | Val | Thr | Cys | Leu | Lys | Gln | Ile | Thr | Trp | His | Asp | Leu | Gln |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| His | Ile | Ile | Lys | Asp | Gly | Asp | Val | Ile | Gly | Leu | Pro | Ala | Leu | Ala | Val |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ala | Asn | Leu | Pro | Ala | Glu | Val | Leu | Arg | Ala | Val | Leu | Ala | Gln | His | Asp |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Thr | Tyr | His | Thr | Pro | Lys | Asp | Leu | Thr | Phe | Ile | Leu | Ala | Asn | Asp | Ile |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| His | Ser | Leu | Gly | Ala | Ala | Pro | Asp | Leu | Asp | Asp | Phe | Ile | Glu | Arg | Arg |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Met | Ile | Lys | Arg | Val | Ile | Met | Ser | Ile | Leu | Thr | Ala | Ser | Ser | Lys | Thr |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ala | Gln | Ala | Met | Lys | Asn | Asn | Asp | Ile | Glu | Ala | Tyr | Phe | Leu | Pro | Gln |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Gly | Ile | Ile | Ala | Thr | His | Tyr | Arg | Gln | Ser | Asn | Gln | Leu | Leu | Pro | Gly |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |     |     |     |  |
| Val | Ile | Thr | Lys | Ile | Gly | Leu | Asn | Thr | Ala | Val | Asp | Pro | Arg | Tyr | Gly |  |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |  |
| Gly | Gly | Lys | Val | Asn | Thr | Arg | Thr | Thr | Asp | Asp | Leu | Val | Ser | Leu | Val |  |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |  |
| Thr | Ile | Asn | Asp | Glu | Thr | Tyr | Leu | His | Tyr | Thr | Phe | Pro | Ser | Val | Asp |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Val | Ala | Leu | Leu | Arg | Gly | Thr | Tyr | Ala | Asp | Gln | Gln | Gly | Asn | Ile | Tyr |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Leu | Xaa | Gln | Glu | Ala | Tyr | Leu | Ser | Glu | Cys | Tyr | His | Val | Ala | Leu | Asn |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Ala | Lys | Ala | Asn | His | Gly | Lys | Val | Ile | Xaa | Gln | Val | Lys | Ala | Leu | Val |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Asp | Asp | Tyr | His | Leu | Lys | Pro | Asn | Glu | Val | Val | Ile | Pro | Gly | Asn | Leu |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |

Val Asp Tyr Val Phe Val Thr Glu Asp Glu Lys Asn His Arg Gln Val  
245 250 255  
Ile Gln Ser His Tyr Leu Pro Ala Leu Ser  
260 265

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

Val Val Lys Ile Val Xaa His Gln Lys Asp Ser Asn Xaa Glu Lys Asp  
1 5 10 15  
Asp Lys Ala Arg Thr Xaa Gln Gln Asp Xaa Lys Xaa Xaa Asp Ser Ser  
20 25 30  
Xaa Asp Lys Lys Asp Asn Xaa Asp Asp Ser Xaa Asp Val Xaa Lys Asp  
35 40 45  
Asn Lys Asp Asn Ser Ala Asn Asp Asn Gln Gln Gln Ser Asn Ser Lys  
50 55 60  
Cys Asn Lys Gln  
65

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

Val Arg Arg Phe Pro Asp Ile Glu Arg Arg Val Gln Thr His Asp Phe  
1 5 10 15  
Thr Trp Gln Ala Glu Ile Met Ser Lys Pro Val Lys Asn Met Thr Val  
20 25 30  
Ala Ile Ile Gly Thr Gly Arg Ile Gly Ala Ala Thr Ala Lys Ile Tyr  
35 40 45  
Ala Gly Phe Gly Ala Thr Ile Thr Ala Tyr Asp Ala Tyr Pro Asn Lys  
50 55 60  
Asp Leu Asp Phe Leu Thr Tyr Lys Asp Ser Val Lys Glu Ala Ile Lys  
65 70 75 80  
Asp Ala Asp Ile Ile Ser Leu His Val Pro Ala Asn Lys Glu Ser Tyr  
85 90 95  
His Leu Phe Asp Lys Ala Met Phe Asp His Val Lys Lys Gly Ala Ile  
100 105 110  
Leu Val Asn Ala Ala Arg Gly Ala Val Ile Asn Thr Pro Asp Leu Xaa  
115 120 125  
Ala Ala Val Asn Asp Gly Thr Leu Leu Gly Ala Ala Ile Asp Thr Tyr  
130 135 140  
Glu Asn Glu Ala Ala Tyr Phe Thr Asn Asp Trp Thr Asn Lys Asp Ile  
145 150 155 160  
Asp Asp Lys Thr Leu Leu Glu Leu Ile Gly Thr

## (2) INFORMATION FOR SEQ ID NO:308:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

```

Val Val Val Leu Met Cys Cys Leu Lys Tyr Glu Asn Asp Tyr Tyr Glu
 1 5 10 15
Glu Val Arg Ala Gln Leu Pro Asp Ile Gly Glu Ala Ile Glu Thr Pro
 20 25 30
Asp Gly Asn Arg Glu Ser Ser Cys Phe Lys Tyr Ile Arg His Phe Tyr
 35 40 45
Ala Gly Glu Ala
 50

```

## (2) INFORMATION FOR SEQ ID NO:309:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

```

Val Asn Thr Xaa Leu Leu Asn Xaa Arg Val Glu Pro Ala Ile Val Lys
 1 5 10 15
Ile Pro Val Ser Val Asp Glu Asn Ile Asp Asn Val Glu Lys Lys Leu
 20 25 30
Asn Thr Leu Phe Thr Ile Leu Cys Val Val Asn Xaa Xaa Leu Phe Val
 35 40 45
Ser Asp Pro Val Val Ile Gly Ile Asp Ala Phe Glu Asp Thr Arg Val
 50 55 60
Ile Leu Xaa Val Ser Ala Glu Thr Ile Pro Gly Xaa Gly Phe Ser Gly
 65 70 75 80
Ala Arg Ile Ile Arg Lys Glu Val His Lys Met Phe Leu Gln Glu Gly
 85 90 95
Ile Lys Thr Pro Xaa Pro Ile Met Thr Pro Phe Asn His Ser Glu Xaa
 100 105 110
Gly Val

```

## (2) INFORMATION FOR SEQ ID NO:310:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Gln | Leu | Leu | Lys | Asn | Ala | Xaa | Lys | Lys | Xaa | Asn | Asp | Leu | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Glu | Glu | Ala | Glu | Ile | Val | Lys | Asn | Asp | Asp | Leu | Pro | Xaa | Xaa | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Ile | Xaa | Gly | Xaa | Gln | Tyr | Asp | Xaa | Arg | Trp | Arg |     |     |     |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Arg | Phe | His | Asp | Gly | Xaa | Thr | Phe | Asp | Ala | Asp | Ala | Val | Lys | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Ile | Asp | Ala | Xaa | Gln | Gln | Asn | Lys | Lys | Leu | His | Ser | Trp | Leu | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Ser | Thr | Leu | Ile | Asp | Asn | Val | Lys | Val | Lys | Asp | Lys | Tyr | Thr | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Leu | Asn | Leu | Lys | Glu | Ala | Tyr | Gln | Pro | Ala | Leu | Ala | Glu | Leu | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Met | Pro | Arg | Pro | Tyr | Val | Phe | Val | Ser | Pro | Lys | Asp | Phe | Lys | Asn | Gly |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Thr | Thr | Lys | Asp | Gly | Val | Lys | Lys | Phe | Asp | Gly | Thr | Gly | Pro | Phe | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Leu | Gly | Glu | His | Lys | Lys | Asp | Glu | Ser | Ala | Asp | Phe | Asn | Lys | Asn | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Tyr | Trp | Gly | Glu | Lys | Ser |     |     |     |     |     |     |     |     |     |
|     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Ile | Asp | Tyr | Ile | Xaa | Gln | Thr | Gly | Asp | Ile | Val | Glu | Ile | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Ser | Lys | His | Ser | Tyr | Gly | Pro | Ser | Arg | Asp | Trp | Leu | Xaa | Ile | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Lys | Ser | Ser | Ser | Ala | Lys | Gly | Lys | Ile | Lys | Ser | Phe | Phe | Xaa | Xaa | Gln |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Asp | Arg | Ser | Ser | Asn | Ile | Glu | Lys | Ala | Arg | Met | Met | Val | Glu | Val | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ile | Lys | Asp | Gln | Gly | Phe | Arg | Val | Glu | Asp | Ile | Leu | Thr | Glu | Lys | Asn |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Gln | Val | Val | Asn | Xaa | Lys | Tyr | Asn | Phe | Xaa | Asn | Glu | Asp | Asp | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Ala | Ala | Val | Gly | Phe | Gly | Gly | Val | Thr | Ser | Leu | Gln | Ile | Val | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Leu | Thr | Glu | Arg | Gln | Arg | Ile | Leu | Asp | Lys | Gln | Arg | Ala | Leu | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Ala | Gln | Glu | Val | Thr | Lys | Ser | Leu | Pro | Ile | Lys | Asp | Asn | Ile | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Asp | Ser | Gly | Val | Tyr | Val | Glu | Gly | Leu | Glu | Asn | Val | Leu | Ile | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Xaa | Lys | Cys | Cys | Asn | Pro | Ile | Pro | Gly | Asp | Asp | Ile | Val | Gly | Tyr |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Thr | Lys | Gly | His | Gly | Thr | Lys | Val | His | Arg | Thr | Asp | Cys | Pro | Asn |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Lys | Asn | Glu | Thr | Glu | Arg | Leu | Ile | Asn | Val | Glu | Trp | Val | Lys | Xaa |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Lys | Asp | Ala | Thr | Gln | Lys | Tyr | Gln | Val | Asp | Leu | Glu | Val | Thr | Ala | Tyr |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Asp | Arg | Asn | Gly | Leu | Leu | Asn | Glu | Val | Leu | Gln | Ala | Val | Ser | Ser | Thr |
| 225 |     |     |     | 230 |     |     |     |     |     | 235 |     |     |     |     | 240 |
| Xaa | Gly | Asn | Leu | Ile | Lys | Val | Ser | Gly | Arg | Ser | Asp | Ile | Asp | Xaa | Asn |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Xaa | Ile | Ile | Asn | Ile | Ser | Val | Met | Val | Lys | Asn | Val | Asn | Asp | Val | Tyr |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Arg | Val | Val | Glu | Lys | Thr | Lys | Gln | Leu | Gly | Asp | Val | Tyr | Thr | Gly | Asn |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Lys | Ser | Leu | Gly | Thr | Arg | Gly | Ser | Lys | Asn | Ile | Glu | Ser | Arg | Trp | Tyr |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Lys | Arg | Gly |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 305 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Thr | Val | His | Pro | Ile | Arg | Ile | Pro | Pro | Gly | Asp | Pro | Val | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Val | Asp | Ile | Val | Ile | Gly | Arg | Val | Ala | Gln | Val | His | Ile | Ala | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Xaa | Val | Ile | Leu | Asp | Asn | Gly | Lys | Leu | Asp | Ile | Lys | Ser | Ile | Lys | Pro |
|     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ile | Ala | Arg | Leu | Gly | Tyr | Ser | Asp | Tyr | Thr | Val | Val | Asn | Glu | Ile | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Glu | Met | Lys | Ala | Pro | Xaa | Ala | Ser | Lys | Glu | Glu | Leu | Ala | Gly | Leu | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Arg | Asn | Phe | Asp | Asn | Gln | Ser | Asp | Glu | Lys | Arg |     |     |     |     |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Thr | Arg | Leu | Lys | Thr | Met | Gly | Lys | Leu | Ala | Met | Leu | Met | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Lys | Asp | Leu | Asp | Gln | Ala | Phe | Lys | Lys | Lys | Asp | Thr | Val | Leu | Ile | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Ile | Ile | Glu | Arg | Asp | Glu | Asp | Ile | Asp | Asp | Leu | Tyr | Ser | His | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Asn | Ala | Thr | Tyr | Leu | Ile | Asp | Asn | Asp | Pro | Phe | Val | Ala | Ala | Gln |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | His | Leu | Ala | Ala | Arg | His | Leu | Glu | Arg | Ile | Gly | Asp | His | Ile | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asn | Ile | Ala | Glu | Ser | Val | Tyr | Phe | Tyr | Leu | Thr | Gly | Thr | His | Tyr | Glu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | Ile | Thr |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Asn | Lys | Ile | Leu | Ser | Gln | Phe | Leu | Asn | Ile | Lys | Pro | Pro | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Val | Ser | Glu | Met | Val | Gly | Arg | Leu | Glu | Lys | Ala | Gly | Tyr | Val | Glu | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Pro | Tyr | Lys | Gly | Val | Arg | Leu | Thr | Glu | Asp | Gly | Leu | Thr | His | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Asp | Ile | Ile | Lys | Arg | His | Arg | Leu | Leu | Glu | Leu | Phe | Leu | Ile | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Leu | Lys | Tyr | Asn | Trp | Glu | Glu | Val | His | Gln | Glu | Ala | Glu | Ile | Leu |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Glu | His | Arg | Ile | Ser | Asp | Leu | Phe | Val | Glu | Arg | Leu | Asp | Ser | Cys |     |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Gly | Asn | Xaa | Xaa | Gln | Ala | Asp | Leu | Ile | Gly | Tyr | Ser | Phe | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Phe Asp Gly Ala Ile Xaa Arg Gln Glu Ala Ser Xaa Asp Val His Ala  
20 25 30  
Val Ile Leu Ser Asn Lys Thr Leu  
35 40

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

Val Val Ser Met Lys Tyr Asn Thr Asn Val Lys His Thr Thr Leu Glu  
1 5 10 15  
Ala Phe Val Thr Thr Val Asn Asp Leu Gly Ile Glu Leu Ile Ile Asn  
20 25 30  
Glu Ala Leu Arg Glu Val Arg Lys Arg Gln Leu Ile Glu Leu Ile Asp  
35 40 45  
Asp Ala Leu Val Asn Lys Asp Glu Ala Ala Phe Asn Gln Tyr Thr Ala  
50 55 60  
Glu Tyr Lys Asn Leu Glu Ala Phe Leu Gly Xaa  
65 70 75

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

Val Tyr Lys Val Lys Val Ala Val Ile Met Gly Ser Ser Ser Asp Trp  
1 5 10 15  
Lys Ile Met Gln Glu Ser Cys Asn Met Leu Asp Tyr Leu Glu Ile Pro  
20 25 30  
Tyr Glu Lys Gln Val Val Ser Ala His Arg Thr Pro Lys Met Met Val  
35 40 45  
Gln Phe Ala Ser Glu Ala Arg Glu Arg Gly Ile Asn Ile Ile Ile Ala  
50 55 60  
Gly Ala Gly Gly Ala Xaa His Leu Pro Gly Met Val Ala Ser Leu Thr  
65 70 75 80  
Thr Leu Pro Val Ile Gly Val Pro Ile Glu Thr Xaa Lys Phe Lys Gly  
85 90 95  
Tyr

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single



[illegible]

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Met | Ile | Met | Arg | Lys | Glu | Ile | Glu | Ala | Leu | Ile | Phe | Ser | Asp | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Ser | Tyr | Asp | Ile | Tyr | Val | Asn | Thr | Gly | Val | Asn | Gln | Gly | Leu | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Asp | Ile | Lys | Asp | Gly | Tyr | Leu | Thr | Ile | Asp | Ser | Met | Pro | Tyr | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Ala | Glu | Arg | Leu | Tyr | His | Phe | Ala | Tyr | Gly | Thr |     |     |     |     |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Cys | Ile | Val | Leu | Val | Lys | Val | Val | Glu | Asn | Ala | Glu | Ile | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Ile | Glu | Ile | Phe | Asn | Ser | Val | Asp | Asn | Asn | Asn | Lys | Lys | Ile | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Lys | Asp | Gly | Asn | Val | Val | Gly | Ala | Val | Ser | Cys | Gln | Tyr | Gly | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Asp | Asp | Gly | Ser | Arg | Phe | Tyr | Asn | Met | Met | Lys | Lys | Gly | Glu | Ser |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Glu | Asp | Tyr | Thr | Leu | Val | Ser | Leu | Leu | Thr | Lys | Gly | Gly | Glu | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ala | Ser | Leu | Ser | Ile | Ala | Asp | Met | Ala | Asp | Asp | Glu | Thr | Ile | Cys | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Cys | Asn | Gly | Val | Asp | Lys | Gly | Thr | Ile | Val | Asn | Ala | Ile | Thr | Glu | Asn |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Phe | Thr | Thr | Val | Glu | Glu | Val | Thr | Ala | Lys | Thr | Lys | Ala | Gly | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Cys | Gly | Lys | Cys | Lys | Pro | Gln | Ile | Ala | Gln | Ile | Leu | Gln | His | Thr |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Gly | Asp | Asp | Phe | Val | Ala | Ala | Lys | Pro | Ala | Gly | Ile | Cys | Gly | Cys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Thr | Asp | Leu | Thr | Arg | Asp | Gln | Ile | Val | Thr | Gln | Ile | Arg | Ala | Lys | Gly |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Leu | Lys | Thr | Ser | Lys | Glu | Val | Arg | His | Val | Leu | Asn | Phe | Lys | Asn | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Gly | Cys | Pro | Lys | Cys | Arg | Pro | Ala | Ile | Asn | Tyr | Tyr | Leu | Asn | Met |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Tyr | Pro | His | Asp | His | Glu | Asp | Glu | Arg | Glu | Ser | Arg | Phe | Ala | Asn |
| 210 |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Arg | Tyr | His | Ala | Asn | Ile | Gln | Asn | Asp | Gly | Thr | Phe | Ser | Val | Ile |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Pro | Gln | Met | Arg | Gly | Gly | Val | Thr | Asp | Ala | Asp | Gln | Leu | Ile | Arg | Leu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Glu | Val | Ala | Lys | Lys | Tyr | His | Val | Pro | Leu | Val | Lys | Val | Thr | Gly |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Gln | Arg | Val | Gly | Leu | Tyr | Gly | Gly |     |     |     |     |     |     |     |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Met | Thr | Pro | Leu | Val | Glu | Pro | Xaa | Pro | Xaa | Thr | Val | Ser | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Asn | Lys | Ser | Asn | Ser | Asn | Ser | Ser | Thr | Leu | Xaa | Tyr | Leu | Arg | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Glu | Asn | Arg | Gly | Trp | Asp | Phe | Asp | Gly | Ser | Tyr | Gly | Trp | Gln | Cys |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Phe | Asp | Leu | Xaa | Asn | Val | Phe | Trp | Xaa | Ser | Ser | Ser | Met | Gly | Met | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Lys | Gly | Phe | Trp | Arg |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Gln | Leu | Ile | Thr | Gln | Ile | Tyr | Gly | Ala | Glu | Lys | Arg | Val | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Trp | Val | Asn | Gln | Leu | Val | Ser | Xaa | Ser | Phe | Asn | Lys | Lys | Ile | Arg | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Arg | Thr | Xaa | Ser | Asp | Trp | Ile | Ser | Ser | Asn | Pro | Ile | Glu | Val | Asp |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Asn | Phe | Ile | Lys | Asp | Pro | Tyr | Ser | Gly | Phe | Asn | Val | Ser | Xaa | Gln | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Tyr | His | Thr | Ala | Tyr | Tyr | Met | Leu | His | Thr | Ser | Gln | Leu | Lys | Asn |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Met | Lys | Met | Leu | Asn | His | Ala | Met | Pro | Ile | Leu | Leu | Val | Ser | Gly | Tyr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Asp | Ser | Leu | Gly | Asp | Tyr | Gly | Lys | Gly | Ile | Leu | Lys | Leu | Ala | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Tyr | Arg | Glu | Ala | Gly | Ile | Lys | Asn | Cys |     |     |     |     |     |     |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

```
Val Thr Leu Glu Val Ala Glu Met Xaa Asn Ser Xaa Lys Asp Xaa Lys
 1 5 10 15
Lys Phe Glu Ile Ile Asp Arg Xaa Lys Ser Phe Tyr Asp Glu Glu Gln
 20 25 30
Xaa Ile Asp Leu Val Phe Val Val Asn Gln Ile Asn Gly Trp Asn Arg
 35 40 45
Leu Asn Ile Ile Ser Asp Arg Leu
50 55
```

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

```
Val Asp Ser Val Thr Ile Lys Val Leu Asn Glu Pro Ser Pro Lys Leu
 1 5 10 15
Leu Thr Thr Trp Tyr Ala Glu Gln Val Thr Gln Gly Lys Ile Lys Thr
 20 25 30
Ser Lys Tyr Val Lys Lys Glu Cys Glu Arg His Leu Arg Tyr Leu Glu
 35 40 45
Asn Gly Gly Lys Trp Val Phe Asp Glu Glu Leu Ala His Arg Pro Ile
 50 55 60
Arg Phe Ile Glu Lys Phe Cys Lys Xaa Ser Lys Gly Ser Lys Arg Gln
 65 70 75 80
Leu Ala Leu Gln Pro Trp Gln His Phe Ile Ile Gly Ser Leu Phe Gly
 85 90 95
Trp Val His Lys Glu Thr Lys Leu Arg Arg Phe Lys Glu Ala Leu Ile
 100 105 110
Phe Met Gly Ala Lys Lys Trp
 115
```

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Xaa | Xaa | Val | Ile | Lys | Glu | Lys | Pro | Xaa | Ala | Arg | Trp | Leu | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Pro | Xaa | Ser | Pro | Xaa | Xaa | Ala | Ile | Asp | Gly | Asp | Thr | Leu | Val | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Xaa | Xaa | Ala | Ser | Asn |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 35  |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Asn | Leu | Ser | Ile | Ser | Leu | Thr | Ser | Leu | Ala | Thr | Gly | Ile | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Val | Ala | Ala | Gly | Asp | Ile | Ala | Asp | Lys | Ile | Gly | Gln | Xaa | Arg | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Tyr | Met | Gly | Leu | Ile | Ile | Xaa | Met | Phe | Xaa | Ser | Leu | Leu | Leu | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Ser | Asp | Ile | Thr | Ala | Leu | Leu | Ile | Ile | Xaa | Arg | Asn | Phe | Thr | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Ile | Ser | Xaa | Tyr | Leu | Gly | Tyr | Pro | Pro | Thr | Val | Gly | Val | Leu | Asn |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asn | Gln | Phe | Lys | Gly | Glu | His | Leu | Arg | Arg | Ala | Ile | Ser | Tyr | Leu | Met |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Ile | Ser | Thr | Val | Gly | Gly | Ile | Gly | Leu | Ala | Gly | Val | Ile | Gly | Gly | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Ala | Thr | Asn | Phe | Gly | Trp | Gln | Met | Asn | Phe | Ile | Ile | Ser | Ile | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Xaa | Phe | Ile | Ala | Ile | Leu | Leu | Leu | Lys | Gly | Thr | Pro | Glu | Lys | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Gln | His | Xaa | His | Arg | His | Pro | Phe | Asp | Tyr | Lys | Gly | Met | Ser | Ile |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Phe | Ala | Val | Met | Ile | Gly | Ser | Phe | Thr | Leu | Leu | Leu | Thr | Gln | Gly | Phe |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Gln | Gly | Trp | Phe | Ser | Thr | Phe | Ser | Phe | Ile | Cys | Leu | Ser | Ile | Phe |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ile | Ile | Thr | Thr | Leu | Ile | Phe | Ile | Ile | Ile | Glu | Arg | Arg | His | Glu | Val |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Pro | Phe | Tyr |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     | 210 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

Val Ala Pro Phe Leu Tyr Leu Xaa Ile Asn Asp Glu Xaa Xaa Asp Met  
 1 5 10 15  
 Lys Ile Ala Gly Asp Leu Asn Ala Tyr Asn Ala Leu Xaa Ala Tyr Thr  
 20 25 30  
 Val Xaa Arg Glu Leu Gly Leu Asn Glu Gln Xaa Asn  
 35 40

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

Val Tyr Val Ile Ser Leu Asn Asp Asn Ala Ala Asp Gly Arg Asp Thr  
 1 5 10 15  
 Ser Trp Ile Tyr Asp Ala Asp Phe Gly Lys Ile Ile  
 20 25

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

Val Met Ser Lys Leu Arg Pro Leu Leu His Tyr Ala Arg Ala Lys Asp  
 1 5 10 15  
 Ile Asp Asn Tyr Arg Thr Val Glu Glu Ser Tyr Arg Gln Gly Gln Tyr  
 20 25 30  
 Tyr Arg Xaa Xaa Ile Val Asp Gly Lys Leu Asn Ile Gln Phe Asn Glu  
 35 40 45  
 Gly Glu Pro Tyr Phe Gly Arg His  
 50 55

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

Val His Pro Asp Val Leu Leu Thr Arg Tyr Val Glu Gly Lys Glu Asp  
 1 5 10 15  
 Gln Val Glu Lys Val Leu Tyr Gln Leu Ala Asp Ile Asp Ile Ser Glu  
 20 25 30

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Pro | Lys | Asp | Phe | Ile | Leu | Leu | Pro | Thr | His | Pro | Tyr | Gln | Xaa | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Leu | Xaa | Gln | Tyr | Pro | Gln | Tyr | Met | Gln | Tyr | Ser | Glu | Gln | Gly | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Lys | Asp | Leu | Gly | Val | Ser | Gly | Asp | Leu | Val | Ser | Pro | Thr | Ser | Xaa |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Xaa | Arg | Thr | Val | Phe | Ser | Lys | Ala | Leu | Asn | Ile | Tyr | Leu | Xaa | Xaa | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | His | Val | Xaa | Ile | Thr | Asn | Phe | Xaa | Arg | Thr | Asn | Asp | Leu | Glu | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Ile | Xaa | Arg | Thr | Ser | Cys | Met | Pro | Arg | Met | Ser | Ser | Ser | Ser | Asp | Gln |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

Arg

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gln | Asn | Lys | Glu | Leu | Ile | Gln | His | Ala | Ala | Tyr | Ala | Ala | Ile | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Ile | Leu | Asn | Glu | Tyr | Phe | Arg | Glu | Glu | Asn | Leu | Tyr | Gln | Val | Pro |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Gln | Asn | His | Gln | Trp | Ser | Ile | Gln | Leu | Ser | Glu | Leu | Glu | Thr | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Gly | Glu | Phe | Arg | Tyr | Trp | Ser | Ala | Met | Gly | His | His | Met | Tyr | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Glu | Val | Trp | Leu | Ile | Asp | Gly | Lys | Ser | Lys | Lys | Ile | Thr | Thr | Tyr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Glu | Ala | Ile | Ala | Arg | Ile | Leu | Pro | His | Met | Ala | Gln | Ser | Ala | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Gln | Thr | Ala | Val | Gln | Pro | Thr | Tyr | Gly | Xaa | Asn | Tyr | Val | Xaa | His |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

Arg

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ala | Val | Ser | Phe | Leu | Thr | Ser | Arg | Asp | Ile | Pro | Xaa | Asp | Lys | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Lys | Met | Asp | Val | Asp | Pro | Pro | Xaa | Tyr | Leu |     |     |     |     |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

```
Val Lys Asn Val Lys Thr Gln Ser Ile Gln Asn Ala Ser Ile Val Thr
 1 5 10 15
Val Glu Tyr Glu Asn Asn Thr Asp Met Asp Lys Ala Glu Glu Gln Leu
 20 25 30
Lys Lys Glu Ile Asp Lys Ile Lys Phe Lys Asp Glu Val Gly Gln Pro
 35 40 45
Glu Leu Arg Arg Asn Ser Met Asp Ala Phe Pro Val Leu Ala Tyr Ser
 50 55 60
Phe Gln Ile Lys Arg
65
```

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

```
Val Met His Xaa Ile Phe Pro Val Val Ser Xaa Thr Phe Ala Ser Phe
 1 5 10 15
Lys Ser Met Tyr Gly Gly Ile Pro Gln Asp Phe Ile Asp Tyr Leu Phe
 20 25 30
Ile Asp Glu Ala Gly Gln Ala Ile Pro Gln Ala Ala Val Gly Ala Leu
 35 40 45
Tyr Arg Ser Lys Lys Val Val Ala Val Gly Asp Pro Ile Gln Ile Glu
 50 55 60
Pro Val Val Thr Leu Glu Ser His Leu Ile Asp Asn Ile Arg Lys Asn
 65 70 75 80
Tyr His Val Pro Glu Tyr Leu Val Ser Lys Glu Ala Ser Val Gln Ser
 85 90 95
Val Ala Asp Asn Ala Asn Gln Tyr Gly Phe Trp Lys Ser Asp Ala Thr
100 105 110
Asp Ser Asn Gln Lys Thr Trp Ile Gly Ile Pro Leu Trp Val His Arg
115 120 125
Arg Cys Leu Lys Pro Met Phe Thr Ile Ala Asn Gln Ile Ala Tyr Asn
130 135 140
Asn Lys Met Val Leu Ala Ser Asn Ile Thr Lys Val Gly Lys Thr Gly
145 150 155 160
Trp Tyr Asp Val Lys Gly Asn Ala Val Gln Asn Ile Xaa Glu Arg Ala
165 170 175
Trp Val Lys Lys
180
```

(2) INFORMATION FOR SEQ ID NO:338:



- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 112 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Lys | Phe | Phe | Asp | Tyr | Thr | Phe | Ala | Ser | Val | Gly | Val | Lys | Pro | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Leu | Lys | Gln | Phe | Asp | Tyr | Lys | Met | Val | Glu | Val | Thr | Gln | Gly | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Ala | Asn | Tyr | Tyr | Pro | Gly | Asn | Ser | Pro | Leu | His | Leu | Arg | Val | Tyr |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Tyr | Asp | Thr | Ser | Asn | Arg | Gln | Ile | Leu | Arg | Ala | Ala | Ala | Val | Gly | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Gly | Ala | Asp | Lys | Arg | Ile | Asp | Val | Leu | Ser | Met | Ala | Met | Met | Asn |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gln | Leu | Thr | Val | Asp | Glu | Leu | Thr | Glu | Phe | Xaa | Val | Xaa | Tyr | Ala | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Tyr | Trp | His | Pro | Lys | Asp | Leu | Xaa | Asn | Met | Ile | Gly | Leu | Gln | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:339:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 97 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Met | Gln | Ser | Ser | Lys | Trp | Asn | Ala | Met | Ser | Leu | Leu | Met | Asp | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Thr | Lys | Gln | Ala | Glu | Val | Leu | Arg | Thr | Ala | Ile | Asp | Glu | Ala | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ile | Val | Ile | Gly | Ile | Gly | Ala | Gly | Met | Ser | Ala | Ser | Asp | Gly | Phe |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Thr | Tyr | Val | Gly | Glu | Arg | Phe | Thr | Glu | Asn | Phe | Pro | Asp | Phe | Ile | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Lys | Tyr | Arg | Phe | Phe | Asp | Met | Leu | Gln | Ala | Ser | Leu | His | Pro | Tyr | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ser | Trp | Gln | Glu | Tyr | Trp | Ala | Phe | Glu | Ser | Arg | Phe | Ile | Thr | Xaa | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

Tyr

(2) INFORMATION FOR SEQ ID NO:340:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 93 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

```
Val Tyr Pro Ile Lys Ala Ile Ile Asp Ser Leu Thr Thr Phe Ser Gly
 1 5 10 15
Ile Glu His Arg Leu Gln Tyr Val Gly Thr Asn Arg Thr Asn Lys Tyr
 20 25 30
Tyr Asn Asp Ser Xaa Ala Thr Asn Thr Leu Ala Thr Gln Phe Ala Leu
 35 40 45
Asn Ser Phe Asn Gln Pro Ile Ile Trp Leu Leu Trp Trp Tyr Trp Ile
 50 55 60
Glu Gly Asp Glu Phe Asp Glu Leu Ile Pro Tyr Met Glu Asn Val Xaa
65 70 75 80
His Asp Gly Cys Ile Arg Thr Asn Glu Ser Xaa Val Cys
 85 90
```

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

```
Val Met Gly Thr Asp Lys Arg Val Ser Pro Asp Leu Phe Ile Lys Arg
 1 5 10 15
Leu Asn Phe Tyr Asp Tyr Leu Leu Leu Asn Ser Asp Gly Leu Thr Asp
 20 25 30
Tyr Val Lys Asp Asn Glu Ile Lys Arg Leu Leu Val Lys Glu Gly Thr
 35 40 45
Ile Glu Asp His Gly Asp Gln Leu Met Gln Leu Ala Leu Asp Asn His
 50 55 60
Ser Lys Asp Asn Val Thr Phe Ile Leu Ala Ala Ile Xaa Gly Asp Lys
65 70 75 80
Val
```

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

```
Val Lys Leu Lys Gly Met Arg Lys Gln Tyr Glu Val Gly Glu Gln Ala
 1 5 10 15
Ser Pro Ile Glu Phe Val Thr Gly Arg Val Asn Pro His Arg
 20 25 30
```

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Glu | Val | Gln | Val | Met | Lys | Phe | Gly | Lys | Thr | Ile | Ala | Val | Val | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Ser | Ser | Val | Leu | Leu | Xaa | Gly | Cys | Thr | Thr | Asp | Lys | Lys | Glu | Ile |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Lys | Ala | Tyr | Leu | Lys | Gln | Val | Asp | Lys | Ile | Lys | Asp | Asp | Glu | Glu | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Xaa | Thr | Val | Xaa | Lys | Lys | Ile | Ala | Glu | Leu | Asp | Glu | Lys | Lys | Lys |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Lys | Leu | Thr | Glu | Asp | Val | Asn | Ser | Lys | Asp | Thr | Ala | Gly | Ser | Arg | Xaa |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Lys | Gln |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Gln | Ser | Ser | Ser | Leu | Leu | Asn | Xaa | Phe | Lys | Val | Phe | Ala | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Ser | Asp | Thr | Val | Ile | His | Gly | Ser | Asp | Val | Asp | Leu | Val | Asn | Trp |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Val | Glu | Asn | Ala | Leu | Gln | Ser | Gly | Leu | Ala | Ala | Lys | Glu | Arg | Lys | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Leu | Ala | Val | Ser | Pro | Lys | Ser | Gly | Leu | Glu | His | Met | Ser | Phe | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Asn | Gly | Ser | Val | Lys | Glu | Val | Xaa | Gly | Ala | Asp | Met | Tyr | Asp | Ala | Ile |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Asn | Ala | Leu | Ala | Asp | Leu | His | Glu | Asp | Tyr | Arg | Asp | Asn | Ala | Thr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ile | Tyr | Met | Arg | Tyr | Ala | Asp | Tyr | Val | Lys | Ile | Ile | Ser | Val | Leu | Ser |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Asn | Gly | Thr | Thr | Asn | Phe | Phe | Asp | Thr | Pro | Ala | Glu | Lys | Val | Xaa | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Xaa | Pro | Val | Gly | Ile | Tyr | Arg | Cys | Arg | Xaa | Leu | Pro | Leu | Leu | Trp | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Phe | Asn | Tyr | Cys | Gly | Xaa | Tyr | Leu | Leu | Met | Gly | Gln | Pro | Tyr | Asp |
| 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |     |
| Thr | Asp |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Tyr | Lys | Thr | Asp | Leu | Tyr | Xaa | Gln | Xaa | Xaa | Lys | Ile | Asp | Thr | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Lys | Val | Ile | Lys | Glu | Val | Glu | Leu | Lys | Lys | Pro | Ile | Thr | Tyr | Glu | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Ala | Thr | Ser | Asp | Ser | Lys | Leu | Xaa | Lys | Glu | Trp | Met | Asp | Ser |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Pro | Arg | Tyr | Lys | Xaa | Thr | Leu | Leu | His | Arg | Arg | Leu | His | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ile | Leu | Xaa | Lys | Met | Leu | Glu | Asp | Leu | Ser | Phe | Glu | Ala | Pro | Ser | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Asn | Ala | Val | Val | Asp | Ile | Thr | Pro | Gln | Tyr | Val | Asp | Asp | Lys | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Ser | Ile | Ser | Thr | Xaa | Lys | Asp | Leu | Ser | Ala | Phe | Ile | Leu |     |     |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Lys | Ile | Leu | Lys | Asp | Thr | Asn | Leu | Met | Tyr | Leu | Glu | Trp | Asn | Tyr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Leu | Val | Xaa | Arg | Val | Val | Ala | Val | Val | Glu | Xaa | Gln | Gly | Thr | Leu | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Ala | Val | Asn | Lys | Ala | Leu | Gln | Tyr | Trp | Val | Ser | His | Val | Asp | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | His | Tyr | Leu | Leu | Gly | Ser | Ala | Leu | Gly | Pro | Asp | Pro | Phe | Pro | Thr |
|     |     |     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |
| Ile | Val | Arg | Asp | Phe | Gln | Ser | Val | Ile | Gly | Lys | Glu | Xaa | Lys | Ser | Gln |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Leu | Lys | Lys | Glu | Gly | Arg | Leu | Pro | Asp | Ala | Ile | Val | Ala | Cys | Ile |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |

Gly Gly Gly Ser Asn Ala Ile Gly Leu Val Pro Phe Ile His Leu Leu  
100 105 110  
Lys Met Met Leu His  
115

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

Val Gly Arg Leu Pro Lys Lys Ile Gln Asn Ile Glu Gln Arg Pro Xaa  
1 5 10 15  
Gly Val Ser Xaa Thr Thr Phe Thr Ile Ala Val Asn Arg Thr Phe Thr  
20 25 30  
Asn Ala Gln Gly Glu Arg Glu Ala Asp Phe Ile Asn Cys Val Thr Phe  
35 40 45  
Arg Lys Gln Ala Glu Asn Val Asn Asn Tyr Leu Ser Lys Gly Ser Leu  
50 55 60  
Ala Gly Val Asp Gly Arg Leu Gln Ser Arg Ser Tyr Asp Asn Lys Glu  
65 70 75 80  
Gly Arg Arg Val Phe Val Thr Glu Val Val Ala Asp Ser Val Gln Phe  
85 90 95  
Leu Glu Pro Lys Asn Asn Asn Gln Xaa Gln Asn Asn Asn Tyr Gln Gln  
100 105 110  
Gln Gly Gln Ala Gln Thr Gly Asn Asn Pro Phe Asp Asn Ser Glu Glu  
115 120 125  
Asp Phe Ser Asp Leu Pro Phe  
130 135

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

Val Val Ser Gln Ser Ile Leu Leu Thr Leu Ser Thr Xaa Leu Thr Asn  
1 5 10 15  
Val Thr Xaa Leu Thr Ser Xaa Ala Gln Xaa Pro Ala Asp Tyr Val Lys  
20 25 30  
Asn Met Ile Thr Gly Ala Ala Gln Met Asp Gly Gly Ile Leu Val Val  
35 40 45  
Ser Ala Ala Asp Gly Pro Met Pro Gln Thr Arg Glu His Ile Leu Leu  
50 55 60  
Ser Arg Asn Val Gly Val Pro Ala Leu Val Val Phe Leu Asn Lys Val  
65 70 75 80  
Asp Met Val Asp Asp Glu Glu Leu Leu Glu Leu Val Glu Met Glu Val  
85 90 95  
Arg Asp Leu Leu Ser Glu Tyr Asp Phe Pro Gly Asp Asp Val Pro Val

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Ile | Ala | Gly | Ser | Ala | Leu | Lys | Ala | Leu | Glu | Gly | Asp | Ala | Gln | Tyr | Glu |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Glu | Lys | Ile | Leu | Glu | Leu | Met | Glu | Ala | Val | Asp | Thr | Tyr | Ile | Pro | Leu |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Gln | Thr |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Val | Lys | Val | Ser | Gly | Cys | Ser | Asp | Leu | Val | Gln | Cys | Ala | Ile | His | Asp |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Cys | Gln | Tyr | Tyr | Glu | Val | Gln | Met | Pro | Gln | Ala | His | Arg | Val | Val | Pro |  |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |  |
| Thr | Thr | Ile | Asn | Met | Gly | Asn | His | Ser | Trp | Lys | Ala | Leu | Glu | Ile | Ile |  |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |  |
| Tyr | Glu | Thr | Tyr | Cys | Thr | Leu | Cys | Asp | Ser | Xaa | Leu | Asn | Lys | Xaa | Thr |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Thr |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Val | Xaa | Val | Asn | Ile | Asn | Cys | Ala | Asn | Pro | Glu | Cys | Asn | Lys | Gln | Ile |  |  |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Leu | Val | Ser | Glu | Glu | Xaa | Glu | Thr | Lys | Tyr | Leu | Gly | Ala | Cys | Ser | Tyr |  |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |  |  |
| Glu | Cys | Ala | Lys | His | Glu | Arg | Asn | Arg | Tyr | Val | Gln | Ala | Asn | Asn | Ile |  |  |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |  |
| Ser | Asp | Asn | Glu | Trp | Gln | Gln | Arg | Leu | Thr | Asn | Phe | Asp | Asp | Leu | His |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Gln | His | Ala |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

```
Val Thr Arg Ser Lys Met Ile Val Val Glu Ser Tyr Asp Val Asn Gly
 1 5 10 15
Asn Lys Val Glu Leu Thr Ala His Glu Asp Val Ala Arg Met Ile Leu
 20 25 30
His Ile Ile Asp Gln Met Asn Gly Leu Pro Phe Xaa Glu Arg Ala Asp
 35 40 45
Arg Ile Leu Thr Asp Lys Glu Val Glu Ala Tyr Phe Ile Asn Asp
 50 55 60
```

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

```
Val Thr Lys Asn Ala Gly Asn His Glu Ile Glu Ile Asp Arg Pro Ile
 1 5 10 15
Val Asn Pro Ile Lys Lys Leu Pro Thr Arg Phe Thr Ile Asn Val Ala
 20 25 30
Ile Gly Asn Phe Glu Val Asn Leu
 35 40
```

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

```
Val Lys Gly Gln Asn Leu Thr His Gly Thr Asn Ala Ile Asp Tyr Ile
 1 5 10 15
Thr Phe Asp Pro Asn Thr Asn Thr Asn Gly Ile Thr Ala Ala Trp Ala
 20 25 30
Asn Arg Gln Gln Pro Asn Asn Gln Ala Gly Val Gln His Leu Asn
 35 40 45
Val Asp Val Thr Tyr Pro Gly Ile Ser Ala Ala Lys Arg Val Pro Val
 50 55 60
Thr Val Asn Val Tyr Gln Phe Gly Ile Pro Ser Asn Tyr Leu Tyr Asn
 65 70 75 80
Asn Ser Trp Trp His Phe Ser Lys Trp Tyr Ala Ser Ile Arg Ile Cys
 85 90 95
Thr Tyr Ala Lys Arg Phe Arg Phe Thr Asn Arg Trp Ile Tyr Val
 100 105 110
```

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Val | Thr | Thr | Gln | Asn | Gln | Ala | Ile | Asp | Asn | Thr | Thr | Gly | Ala | Thr | Thr |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Glu | Glu | Lys | Asn | Ala | Ala | Lys | Asp | Leu | Val | Leu | Xaa | Ala | Lys | Glu | Lys |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Ala | Xaa | Gln | Asp | Ile | Leu | Xaa | Ala | Gln | Xaa | Thr | Asn | Asp | Val | Thr | Gln |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Ile | Asn | Asp | Gln | Ala | Val | Ala | Asp | Ile | Gln | Gly | Ile | Thr | Gly | Asp | Thr |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Thr | Ile | Xaa | Asp | Val | Ala | Ile | Asp | Xaa | Xaa | Ala | Thr | Pro | Ala | Thr | Xaa |  |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |  |
| Xaa | Xaa | Ala | Leu | Xaa | Gly | His | Xaa | Ala | Xaa | Ala | Thr | Xaa | Glu | Xaa | Xaa |  |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |  |
| Xaa | Gln | Xaa | Xaa | Xaa | Thr | Lys | Xaa | Xaa | Ala | Gln | Xaa | Xaa | Thr | Xaa | Val |  |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |  |
| Phe | Thr | Xaa | Leu | Xaa | Xaa | Cys | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Val | Xaa |  |  |
|     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |  |  |
| Xaa | Leu | Ala | Xaa | Xaa | Xaa | Arg | Thr | Leu | Xaa | Ser | Arg | Xaa | Xaa | Xaa | His |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Xaa | Xaa | Xaa | Xaa | Xaa | Asn | Arg | Phe |     |     |     |     |     |     |     |     |  |  |
| 145 |     |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Val | Val | Ser | Leu | Ile | Asp | Asp | Glu | Asp | Asp | Asn | Xaa | Asn | Asp | Arg | Gln |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Leu | Val | Val | Ser | Ala | Pro | Ser | Lys | Lys | Pro | Thr | Thr | Pro | Thr | Thr | Tyr |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Thr | Glu | Thr | Thr | Thr | Gln | Val | Xaa | Met | Pro | Thr | Val | Glu | Arg | Gln | Thr |  |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |  |
| Gln | Gln | Gln | Ile | Val | Tyr | Lys | Thr | Pro | Lys | Thr | Ile | Ser | Trp | Ile | Lys |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Trp |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

```
Val Lys Ile Met Glu Met Ser Val Thr Glu Val Ile Phe Ser Phe Leu
 1 5 10 15
Gly Gly Leu Gly Ile Phe Leu Tyr Gly Leu Lys Ile Met Gly Asp Gly
 20 25 30
Leu Gln Ala Ser Ala Gly Asp Arg Leu Arg Asp Ile Leu Asn Lys Phe
 35 40 45
Thr Ser Asn Pro Val Leu Gly Val Ile Ala Gly Ile Val Val Thr Ile
 50 55 60
Leu Ile Gln Ser Ser Ser Gly Thr Thr Val Ile Thr Ile Gly Leu Val
65 70 75 80
Thr Ala Gly Phe Met Thr Leu Lys Gln Ala Ile Gly Val Ile Met Gly
 85 90 95
Ala Asn Ile Gly Thr Thr Val Thr Ala Phe Ile Ile Xaa Ile Arg Phe
 100 105 110
Arg Arg Ile Cys Lys Cys Gln Phe
 115 120
```

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

```
Val Leu Cys Asp Ala Asp Val Leu Ala Leu Ile Asp Ile Asp Val Asp
 1 5 10 15
Ile Asp Val Leu Lys Glu Pro Asp Ala Leu Val Leu Val Asp Cys Leu
 20 25 30
Val Thr Leu Asn His Xaa Met Met
 35 40
```

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

```
Val Leu Val Glu Leu Glu Ser Leu Thr Leu Val Glu Pro Asp Ile Glu
 1 5 10 15
Ser Leu Lys Leu Val Asp Val Glu Thr Asp Thr Leu Pro Leu Ile Glu
 20 25 30
Ser Asp Val Glu Ser Asp Val Leu Val Glu Phe Asp Pro Leu Met Leu
 35 40 45
Asp Glu Ser Leu Val Asp Ile Glu Ser Leu Ser Asp Ala Leu Met Leu
```

50  
Ile Glu Ser Asn  
65

55

60

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Ile | Ser | Lys | Xaa | Gln | Trp | Val | Val | Val | His | Phe | Tyr | Pro | Ser | Trp |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Lys | Asp | Ala | Glu | Gly | His | Phe | Glu | Asn | Asn | Gly | Arg | Cys | Asn | Leu | Gly |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Val | Xaa | Thr | Leu | Asn | Leu | Pro | Arg | Met | Ala | Leu | Glu | Ser | Ala | Gly | Asn |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Met | Thr | Lys | Phe | Trp | Glu | Ile | Phe | Tyr | Glu | Arg | Ile | Asp | Val | Leu | His |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Asp | Ala | Leu | Leu | Tyr | Arg | Ile | Asn | Arg | Leu | Lys | Asp | Xaa | Val | Pro | Asn |  |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Asn | Ala | Pro | Ile | Leu | Tyr | Lys | Ser | Gly | Ala | Phe | Asn | Tyr | Lys | Leu | Lys |  |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Glu | Thr | Asp | Asp | Val | Ala | Glu | Leu | Phe | Lys | Asn | Lys | Arg | Ala | Thr | Ile |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ser | Met | Gly |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Xaa | Ser | Thr | Lys | Thr | Ala | Leu | Xaa | Gly | Asp | Ala | Lys | Leu | Asn | Glu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ala | Lys | Ala | Ala | Ala | Lys | Gln | Thr | Leu | Gly | Thr | Leu | Thr | His | Ile | Asn |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asn | Ala | Gln | Arg | Asn | Ala | Leu | Asp | Asn | Glu | Ile | Thr | Xaa | Ala | Thr | Asn |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |
| Val | Glu | Val | Leu | Ile | Gln | Leu | Lys | Pro | Lys | Arg | Asn | Asn |     |     |     |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Glu | Met | Ala | Lys | Lys | Ala | Pro | Asp | Val | Gly | Asp | Tyr | Lys | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Phe | Pro | Ala | Asp | Asp | Val | Ser | Ile | Phe | Arg | Ser | Glu | Arg | Gly | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Glu | Asn | Ile | Val | Arg | Glu | Ile | Ser | Asn | Met | Lys | Asn | Glu | Pro | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Trp | Met | Leu | Asp | Phe | Arg | Leu | Lys | Ser | Leu | Lys | Leu | Phe | Tyr | Lys | Met |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Met | Pro | Gln | Trp | Gly | Gly | Asp | Leu | Ser | Glu | Leu | Asn | Phe | Asp | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ile | Thr | Tyr | Tyr | Val | Lys | Pro | Ser | Glu | Gln | Ala | Glu | Arg | Ser | Trp | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Val | Pro | Glu | Glu | Ile | Lys | Arg | Thr | Phe | Asp | Lys | Leu | Gly | Ile | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Ala | Glu | Gln | Lys | Tyr | Leu | Ala | Gly | Val | Ser | Ala | Gln | Tyr | Glu | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Val | Val | Tyr | His | Asn | Met | Glu | Lys | Glu | Leu | Glu | Glu | Lys | Gly | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Phe | Lys | Asp | Thr | Asp | Ser | Ala | Leu | Gln | Glu | Asn | Glu | Glu | Leu | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Lys | Tyr | Phe | Ala | Ser | Val | Val | Pro | Ala | Ala | Asp | Asn | Lys | Phe | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Leu | Asn | Ser | Ala | Val | Trp | Ser | Gly | Xaa | Ser | Leu | Ile | Tyr | Val | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Asn | Ile | Lys | Leu | Asp | Thr | Pro | Leu | Gln | Ala | Tyr | Phe | Arg | Ile | Asn |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Glu | Asn | Met | Gly | Gln | Phe | Glu | Arg | Thr | Leu | Ile | Ile | Ala | Asp | Glu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gly | Ala | Ser | Val | His | Tyr | Val | Glu | Gly | Trp | Tyr | Cys | Thr | Ser | Leu | Tyr |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Asn |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Lys | Gln | His | Lys | Ala | Trp | Val | Asn | Ile | Met | Tyr | Gly | Cys | Asp | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Cys | Thr | Tyr | Cys | Ile | Val | Pro | Xaa | Thr | Arg | Ser | Lys | Asp | Arg | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Arg | Pro | Glu | Asp | Ile | Ile | Asp | Glu | Val | Arg | Glu | Leu | Ala | Arg | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Tyr | Lys | Glu | Ile | Thr | Leu | Leu | Gly | His | Asn | Val | Asn | Ser | Tyr | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Asp | Leu | Gln | Asp | Ile | Glu | Tyr | Asp | Leu | Gly | Asp | Leu | Leu | Gln | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ile | Ser | Lys | Ile | Ala | Ile | Pro | Arg | Val | Arg | Phe | Thr | Thr | Ser | His | Pro |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Trp | Asp | Phe | Thr | Asp | His | Met | Ile | Asp | Val | Ile | Ser | Glu | Gly | Gly | Asn |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Ile | Val | Pro | His | Ile | His | Leu | Pro | Val | Gln | Ser | Gly | Asn | Asn | Ala | Val |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Leu | Lys | Ile | Met | Gly | Arg | Lys | Tyr | Thr | Arg | Glu | Ser | Tyr | Leu | Asp | Leu |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Val | Lys | Arg | Ile | Lys | Asp | Arg | Leu | Pro | Asn | Val | Ala | Leu | Thr | Thr | Asp |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |
| Ile | Ile | Val | Gly | Tyr | Pro | Asn | Glu | Ser | Glu | Glu | Gln | Phe | Glu | Glu | Thr |  |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |
| Leu | Thr | Leu | Tyr | Asp | Glu | Val | Gly | Phe | Glu | His | Ala | Tyr | Thr | Tyr | Leu |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |
| Tyr | Ser | Gln | Arg | Asp | Gly | Thr | Pro | Ala | Ala | Lys | Met | Lys | Asp | Asn | Val |  |  |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |  |  |
| Pro | Leu | Asn | Val | Lys | Lys | Glu | Arg | Leu | Gln | Arg | Leu | Asn | Lys | Lys | Val |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |
| Gly | His | Tyr | Ser | Gln | Ile | Ala | Met | Ser | Lys | Tyr | Glu | Gly | Gln | Thr | Val |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |
| Thr | Val | Leu | Cys | Glu | Gly | Ser | Ser | Lys | Lys | Asp | Asp | Gln | Val | Leu | Ala |  |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |
| Gly | Tyr | Thr | Asp | Lys | Asn | Lys | Leu | Val | Asn | Phe | Lys | Ala | Pro | Lys | Glu |  |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |
| Met | Ile | Gly |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|     |     | 275 |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Gln | Tyr | Leu | Val | Thr | Thr | Phe | Lys | Asp | Ser | Thr | Gly | Arg | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| His | Glu | His | Ile | Thr | Val | Ala | Arg | Asp | Asn | Gln | Thr | Phe | Thr | Val | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Ala | Glu | Ser | Lys | Glu | Glu | Ala | Glu | Arg | Lys | Tyr | Glu | Ala | Gln | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Ile | Arg | Arg | Asp | Gly | Asp | Ala | Lys | Glu | Asn | Xaa | Asn | Asp |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Tyr | Lys | Lys | Ala | Gln | Ala | Phe | Asp | Glu | Ile | Leu | Glu | Gly | Met | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ala | Ile | Gln | His | Ser | Val | Lys | Xaa | Gly | Ile | Glu | Leu | Asp | Glu | Ala |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Gly | Ile | Met | Ala | Gly | Gln | Val | Val | Tyr | Lys | Tyr | Glu | Glu | Glu |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Asp | Met | Lys | Phe | Lys | Lys | Val | Leu | Val | Ala | Thr | Ala | Met | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Val | Leu | Ala | Thr | Gly | Val | Val | Gly | Tyr | Gly | Asn | Gln | Ala | Asp | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Val | Tyr | Ser | Gln | Asn | Gly | Leu | Val | Leu | His | Asp | Asp | Ala | Asn | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Glu | His | Glu | Leu | Ser | Tyr | Ile | Asp | Val | Leu | Leu | Asp | Lys | Asn | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Gln | Ala | Thr | Lys | Asp | Asn | Leu | Arg | Ser | Tyr | Phe | Ala | Asp | Lys | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | His | Ser | Ile | Lys | Asp | Ile | Ile | Asn | Lys | Ala | Lys | Gln | Asp | Gly | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Val | Ser | Lys | Tyr | Glu | His | Val | Lys |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Asn | Lys | Glu | Tyr | Glu | Ile | Glu | Pro | Gly | Lys | Arg | Glu | Cys | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Met | Met | Lys | Arg | Leu | Asn | Lys | Leu | Val | Leu | Gly | Ile | Ser | Phe | Leu | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Val | Ile | Ser | Ile | Thr | Ala | Gly | Cys | Gly | Ile | Gly | Lys | Glu | Ala | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Lys | Lys | Ser | Phe | Glu | Lys | Thr | Leu | Ser | Met | Tyr | Pro | Ile | Lys | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Glu | Asp | Leu | Tyr | Asp | Lys | Glu | Gly | Tyr | Arg | Asp | Asp | Gln | Phe | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Asn | Asp | Lys | Gly | Thr | Trp | Ile | Ile | Asn | Ser | Glu | Met | Val | Ile | Gln |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Asn | Asn | Glu | Asp | Met | Val | Ala | Lys | Gly | Met | Val | Leu | Tyr | Ile | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Asn | Ile | Pro | Lys | Met | Leu | Lys | Tyr | Asp | Gln | Ile | Leu | Val | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Asn | Pro | Pro | Ile | Leu | Pro | Leu | Ile | Pro | Asp | Val | Leu | His | Arg | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Lys | Lys | Lys | Tyr | Ser | Phe | Val | Val | Tyr | Asp | Ile | Ala | Pro | Asp | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Ile | Lys | Thr | Gly | Ala | Thr | Arg | Pro | Gly | Ser | Met | Ile | Asp | Lys | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Met | Arg | Tyr | Ile | Asn | Arg | His | Val | Tyr | Lys | Asn | Ala | Glu | Asn | Val | Ile |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Val | Leu | Gly | Tyr | Gly | Asn | Glu | Lys | Leu | Leu | Thr | Lys | Ser | Ser | Asn | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Lys | Met | Leu | Thr | Ile | Ser | Met |     |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Lys | Tyr | Ile | Glu | Ala | Pro | Tyr | Glu | Pro | His | Lys | Phe | Val | Lys | Met |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Lys | Asp | Lys | Glu | Leu | Ala | Asp | Glu | Lys | Glu | Gly | Gly | Leu | Arg | Xaa |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Ala | Cys | Phe | Glu | Met | Arg | Leu | Asp | Ile | Val | Ala | Lys | Ala | Ala | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | His | Gly | Tyr | Asp | Tyr | Phe | Gly | Ser | Ala | Ile | Thr | Leu | Ser | Pro | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Asn | Ala | Gln | Leu | Ile | Asn | Glu | Leu | Gly | Met | Asp | Cys | Pro | Lys | Asn |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Arg | Cys | Glu | Leu | Ile | Cys | Lys |     |     |     |     |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:



(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Leu | Ala | Asp | Ile | Thr | Val | Asn | Ala | Met | Lys | Gly | Ile | Tyr | Leu | Arg |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Tyr | Asp | Glu | Asn | Gly | Ala | Ile | Thr | Ser | His | Thr | Ile | Asp | Lys | Asp | Gly |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Val | Lys | Ile | Ser | Gly | Asp | Lys | Val | Asp | Ile | Thr | Ala | Asn | Arg | Glu | Phe |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Asn | Val | Phe | Ala | Asn | Asn | Ile | Asn | Asn | Lys | Val | Gly | Lys | Asn | Asp | Ile |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Val | Asn | Ser | Leu | Asn | Leu | Ser | Asn | Glu | Gly | Leu | Asp | Ile | Asn | Val | Asn |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Arg | Ile | Gly | Ile | Lys | Gly | Gly | Asn | Ala | Asn | Arg | Tyr | Val | Gln | Val | Gln |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Asn | Asp | Phe | Ile | Glu | Leu | Gly | Gly | Ile | Val | Gln | Arg | Thr | Trp | Lys | Gly |  |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Lys | Arg | Ser | Thr | Asp | Asp | Ile | Phe | Thr | Arg | Leu | Lys | Asp | Gly | His | Leu |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Arg | Phe | Arg | Asn | Asn | Thr | Ala | Gly | Gly | Ser | Leu | Tyr | Met | Ser | His | Phe |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Gly | Ile | Ser | Thr | Tyr | Ile | Asp | Gly | Glu | Gly | Glu | Asp | Gly | Gly | Ser | Ser |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Gly | Thr | Ile | Gln | Trp | Trp | Asp | Lys | Thr | Tyr | Ser | Asp | Ser | Gly | Met | Asn |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Gly | Ile | Thr | Ile | Asn | Ser | Tyr | Gly | Gly | Val | Val | Ala | Leu | Thr | Ser | Asp |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Tyr | Asn | Arg | Ile | Ile | Ile | Asp | Ser | Tyr | Ala | Ser | Ala | Asn | Ile | Glu | Ser |  |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Arg | Glu | Ala | Pro | Ile | Tyr | Leu | Ser | Pro | Asn | Thr | Gln | Lys | Leu | Asn | Leu |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Xaa | Leu | Xaa | Arg | Phe | Ala | Phe | Thr | Leu | Ser | Asn | Ala | Asp | Arg | Xaa | Ile |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Thr | Lys | Leu | Ala | Val | Ile | Ser | Cys | Trp | Val | Gln | Asp | Xaa | Xaa | Tyr | Lys |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Xaa | Gly | Ala | Gly | Leu | Arg | Phe | Ser | Lys | Arg | Thr | Asn | Lys | Gly | Leu | Val |  |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Gln | Val | Val | Asn | Gly | Asp | Tyr | Ala | Thr | Gly | Gly | Asp | Thr | Thr | Ile | Glu |  |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Ser | Gly | Met | Ala | Lys | Phe | Asn | Leu | Val | Xaa | Arg | Lys | Arg | Trp | Lys |     |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Asn | Pro | Thr | His | Val | Lys | Tyr | Ala | Ala | Glu | Arg | Leu | Ala | Asp | Ser |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Glu | Val | Leu | Val | Cys | Thr | Val | Ile | Gly | Phe | Pro | Leu | Gly | Ala | Ser | Thr |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Thr | Ala | Thr | Lys | Ala | Phe | Glu | Thr | Glu | Asp | Ala | Ile | Gln | Asn | Gly | Ala |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |



Asp Glu Ile Asp Met Val Ile Asn Ile Gly Ala Leu Lys Asp Gly Arg  
50 55 60  
Phe Asp Asp Val Gln Gln Asp Ile Glu Ala Val Val Lys Ala Ala Lys  
65 70 75 80  
Gly His Thr Val Lys Val Ile Ile Glu Thr Val Leu Leu Glu Pro  
85 90 95

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

Val Lys Ile Tyr Glu Asp Thr Asn Ile Asp Thr Leu Xaa Leu Leu Asn  
1 5 10 15  
Glu Ala Xaa Ile Phe Lys Xaa Thr Leu Phe Trp Cys Xaa Xaa Ser Asn  
20 25 30

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

Val Ala His Asp Asn His Ile Gly Thr Tyr Cys Ile Val Met Ser Gly  
1 5 10 15  
Arg Gly Pro Ser Asp Lys Glu Val Asp His Ile Ser Asn Pro Val Arg  
20 25 30  
Thr Ile Lys Ser Gln His Pro Gln Leu Lys Ile Cys Ala Cys Leu Gly  
35 40 45  
Leu Thr Asp Cys Arg Pro Ser  
50 55

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

Val Ile Asp Asp Leu Val Ser Asp His Ile Ala Thr Gly Gln Leu Leu  
1 5 10 15  
Val Lys Met Ser Asp Leu Thr Ser Ser Tyr Glu Pro Pro Ile Glu Ala  
20 25 30

Cys Gly Thr Trp Arg Leu Val Tyr Gln Arg Leu Lys Ala Leu Glu Val  
35 40 45  
Leu Thr His Glu His Val His Leu Glu Asn His Val Leu Phe Lys Lys  
50 55 60  
Val Ser  
65

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

Val Leu Met Ile Phe Gly Pro Glu Gly Gly Leu Ser Glu Ile Glu Ile  
1 5 10 15  
Ser Leu Phe Ser Asn Thr Ser Thr Val Val Gly Leu Gly Pro Arg Ile  
20 25 30  
Leu Arg Ala Glu Thr Ala Pro Leu Tyr Ala Leu Ser Ala Ile Ser Tyr  
35 40 45  
Glu Lys Glu Leu Met Gly  
50

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

Val Ser Ser Ile Trp Lys Glu Lys Glu Phe Glu Pro Ser Asp Ile Val  
1 5 10 15  
Asp Ala Tyr Leu Val Ile Ala Ala Thr Asn Glu Pro Arg Val Asn Glu  
20 25 30  
Ala Val Lys Gln Ala Leu Pro Glu His Ala Leu Phe Asn Asn Val Gly  
35 40 45  
Asp Ala Ser Asn Ala Asn Val Val Phe Pro Ser Ala Leu His Arg Asp  
50 55 60  
Lys Leu Thr Ile Ser Val Ser Thr Asp Gly Ala Ser Pro Lys Leu Thr  
65 70 75 80  
Lys Ser Ile Met Ala Glu Leu Glu Ala Leu Tyr Pro Pro Ser Tyr Ser  
85 90 95  
Ser Tyr Ile Asp Phe Leu Tyr Thr Cys Arg Gln Lys Ile Lys Val Leu  
100 105 110  
Asp Ile Thr Tyr Ile Arg Lys Ala Thr Val Thr Val Thr Asn Cys Val  
115 120 125  
Thr Arg Ile Phe Lys Ser  
130

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Asn | His | Leu | Cys | His | Gly | Glu | Asp | Gln | Asp | Val | Xaa | Ala | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Ile | Thr | Asp | Leu | Glu | Asn | Lys | Gly | Ile | Ala | Leu | His | Thr | Asn | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Thr | Thr | Glu | Leu | Ser | Ser | Asp | Asp | His | His | Thr | Thr | Val | Arg | Xaa |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Val | Gly | Asn | Xaa | Glu | Ala | Asp | Ala | Val | Leu | Leu | Ala | Ile | Gly | Arg |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Lys | Pro | Asn | Thr | Ala | Leu | Ala | Leu | Glu | Asn | Thr | Asp | Ile | Glu | Leu | Gly |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Arg | Gly | Glu | Ile | Lys | Val | Asn | Ala | Gln | Leu | Gln | Thr | Ser | Val | Pro |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| His | Ile | Tyr | Ala | Ala | Gly | Asp | Val | Lys | Gly | Gly | Leu | Gln | Phe | Thr | Tyr |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| Ile | Ser | Leu | Asp | Asp | Tyr | Arg | Ile | Ile | Lys | Ser | Ala | Leu | Tyr | Gly | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Ser | Arg | Thr | Thr | Asp | Asn | Arg | Gly | Ser | Val | Pro | Tyr | Thr | Val | Phe |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Asp | Pro | Pro | Leu | Ser | Arg | Val | Gly | Leu | Thr | Ser | Lys | Glu | Ala | Ala |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Ala | Gln | His | Tyr | Asp | Tyr | Thr | Glu | His | Gln | Leu | Leu | Val | Ser | Ala | Ile |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Pro | Arg | His | Lys | Ile | Asn | Asn | Asp | Pro | Arg | Gly | Leu | Phe | Lys | Val | Val |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| Ile | Asn | Asn | Glu | Asn | Asn | Met | Ile | Leu | Gly | Ala | Thr | Leu | Tyr | Gly | Lys |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Gln | Ser | Glu | Glu | Leu | Ile | Asn | Ile | Ile | Lys | Leu | Ala | Ile | Asp | Gln | Asn |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Ile | Pro | Tyr | Thr | Val | Leu | Arg | Asp | Ser | Ile | Tyr | Ser | His | Pro | Thr | Met |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Gly | Arg | Ile | Ile |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Glu | Trp | Ala | Leu | Tyr | Ile | Ala | Lys | Asn | Lys | Ile | Ala | Ile | Asp |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Val | Pro | Gly | Ser | Gly | Met | Gly | Ala | Gln | Cys | Trp | Glu | Phe | Thr |     |     |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Glu | Leu | Arg | Glu | Glu | His | Lys | Gln | His | His | Asn | Glu | Leu | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Ser | His | Lys | Glu | Leu | Lys | Asp | Lys | Gln | Asp | Lys | Val | Val | Asp | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Leu | Glu | Gln | Thr | Lys | Ile | Leu | Asn | Arg | Ile | Glu | Glu | Arg | Tyr | Xaa |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Gln | Val | Xaa | Val | Xaa | Gln | Lys | Asn | Glu | Glu | Lys | Thr | Leu | Ala | Gln |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Lys | Trp | Leu | Val | Gly | Ala | Ile | Trp | Ala | Leu | Val | Thr | Ile | Val | Met |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Ile | Ala | Val | Ile | Thr | Ala | Ser | Ile | Xaa | Ala | Leu | Leu | Pro |     |     |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Ser | Thr | Leu | Ile | Arg | Ile | Gly | Asp | Ile | Ile | Gln | Ser | Ser | Thr |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Asn | Thr | Asn | Pro | Ile | Ile | Met | Gly | Ile | Ile | Leu | Gly | Gly | Ile | Ile | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Val | Gly | Thr | Ala | Pro | Leu | Ser | Met | Ala | Leu | Thr | Ala | Leu | Leu |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Gly | Leu | Thr | Gly | Val | Pro | Met | Ala | Ile | Gly | Ala | Met | Ala | Ala | Phe | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ser | Ala | Phe | Met | Asn | Gly | Thr | Leu | Phe | His | Arg | Leu | Lys | Leu | Gly | Asp |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |
| Arg | Lys | Ser | Thr | Ile | Ala | Val | Ser | Ile | Glu | Pro | Leu | Ser | Gln | Ala | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Val | Ser | Ala | Asn | Pro | Ile | Pro | Ile | Tyr | Ile | Thr | Asn | Phe | Phe | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Ala | Ile | Ala | Gly | Leu | Ile | Ile | Ala | Met | Ser | Gly | Leu | Ile | Asn | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Thr | Gly | Thr | Ala | Thr | Pro | Ile | Xaa | Gly | Phe | Leu | Val | Met | Xaa | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Asn | His | Pro | Met | Thr | Ile | Val | Ile | Tyr | Gly | Val | Val | Met | Ala | Ile |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |
| Val | Gly | Cys | Ala | Cys | Arg | Val | Ile | Leu | Gly | Ser | Ile | Arg | Ile |     |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

```
Val Gly Lys Thr Gly Phe Ala Leu Asn Met Met Leu Asn Ile Ala Arg
 1 5 10 15
Asn Gly Tyr Lys Thr Ser Phe Phe Ser Leu Glu Thr Thr Gly Thr Ser
 20 25 30
Val Leu Lys Arg Met Leu Ser Thr Ile Thr Gly Ile Glu Leu Thr Lys
 35 40 45
Ile Lys Glu Ile Arg Asn Leu Thr Pro Asp Asp Leu Thr Lys Leu Thr
 50 55 60
Asn Ala Met Gly Ser Lys Ser Leu Lys Leu Gly Ile
65 70 75
```

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

```
Val Pro Asn Glu Thr Glu Ala Glu Leu Leu Ser Gly Ile Lys Val Thr
 1 5 10 15
Asn Glu Gln Ser Met Lys Asp Asn Ala Asn Tyr Phe Leu Ser Leu Gly
 20 25 30
Ile Lys Thr Val Leu Ile Thr Leu Gly Lys Gln Gly Thr Tyr Phe Ala
 35 40 45
Thr Lys Asn Gln Ser Gln His Ile Glu Ala Tyr Lys Val Asn Ala Ile
 50 55 60
Asp Thr Thr Ala Ala Gly Asp Thr Phe Ile Gly Ala Phe Val Ser Arg
65 70 75 80
Leu Asn Lys Ser Gln Asp Asn Leu Ala Asp Ala Ile Asp Phe Gly Asn
 85 90 95
Lys Ala Ser Ser Leu Thr Val Gln Lys Thr Arg Arg Ala Ser Ile Tyr
100 105 110
Ser Ser Thr Arg Arg Ser Lys Ser Ser Leu Asn Glu Ser Asn Thr Ala
115 120 125
Met Ile
130
```

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Tyr | Lys | Met | Arg | Lys | Ile | Gly | Tyr | Ala | Arg | Val | Ala | Tyr | Pro | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Asn | Leu | Asp | Thr | Gln | Leu | Thr | Lys | Leu | Leu | Ile | Asn | Gly | Cys | Asp |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Val | Tyr | Ser | Glu | Gln | Val | Asn | Val | Tyr | Tyr | Lys | Glu | Gln | Leu | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Glu | His | Cys | Leu | Asp | Glu | Leu | Lys | Thr | Asp | Asp | Thr | Leu | Val | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Glu | Lys | Leu | Lys | Val | Leu | Gly | Phe | Thr | Pro | Lys | Lys | Leu | Met | Glu | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Phe | Glu | Ser | Arg | Ile | Leu | Pro | Tyr | Asp | Ile | His | Leu | Glu | Val | Leu | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Leu | Gly | Ile | Asn | Thr | Asn | Ser | Glu | Glu | Gly | Gln | Ser | Phe | Ile | Glu | Val |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Phe | Lys | Met | Leu | Ala | Asp | Ser | Glu | Asn | Ile | Leu | Leu | Lys | Glu | Arg | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Asn | Gly | Leu | Glu | Ser | Ala | Lys | Glu | Arg | Gly | Arg | Tyr | Gly | Gly | Arg |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Gln | Leu | Ser | Glu | Asp | Lys | Arg | Lys | Tyr | Ile | Lys | Gln | Leu | Phe | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Arg | Met | Tyr | Thr | Pro | Asn | Glu | Ile | Ser | Lys | Trp |     |     |     |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Ile | Met | Ile | Asn | Glu | Met | Leu | Asn | Pro | Lys | Gln | Gln | Glu | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Trp | Thr | Cys | Phe | Ile | Asn | Asp | Lys | Pro | Lys | Val | Leu | Ile | Ala | Ser | Gly |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Lys | Arg | Ala | Gly | Lys | Thr | Tyr | Val | Phe | Ile | Leu | Leu | Phe | Leu | Met |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Ile | Ala | Thr | Tyr | Lys | Asp | Lys | Gly | Leu | Asn | Phe | Ile | Ile | Gly | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ala | Thr | Gln | Ala | Ser | Ile | Arg | Arg | Asn | Ile | Leu | Asp | Asp | Met | Glu | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Leu | Gly | Arg | Glu | Leu | Thr | Leu | Asp | Lys | Ser | Asn | Ala | Val | Lys | Ile |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Phe | Gly | Asn | Lys | Val | Tyr | Val | Phe | Asp | Gly | Gln | Asn | Ser | Asp | Ala | Trp |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Lys | Lys | Ala | Arg | Gly | Phe | Thr | Ser | Ala | Gly | Ala | Phe | Leu | Asn | Glu | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Ala | Leu | His | Asn | Met | Phe | Ile | Lys | Glu | Val | Phe | Ser | Arg | Cys | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Tyr | Lys | Gly | Ala | Arg | Ile | Leu | Ile | Asp | Thr | Asn | Pro | Glu | Asn | Pro | Met |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| His | Pro | Val | Lys | Lys | Asp | Tyr | Ile | Asp | Lys | Ser | Gly | Gln | Arg | Leu | Ser |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Asn | Gly | Arg | Leu | Asn | Ile | Lys | Ala | Phe | Gln | Phe | Thr | Leu | Phe | Asp | Asn |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |
| Thr | Phe | Leu | Asp | Glu | Glu | Tyr | Ile | Glu | Ser | Ile | Ile | Ala | Ser | Thr | Pro |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |
| Thr | Gly | Met | Phe | Thr | Asp | Arg | Asp | Ile | Tyr | Gly | Lys | Trp | Val | Ser | Ala |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |
| Glu | Gly | Val | Val | Tyr | Lys | Asp | Phe | Lys | Glu | Lys | Val | His | Tyr | Ile | Thr |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |
| Glu | Glu | Glu | Phe | Lys | Thr | Lys | Gln | Ile | Lys | Arg | Lys | Tyr | Ala | Gly | Val |  |  |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |  |  |
| Asp | Trp | Gly | Tyr | Glu | His | Tyr | Gly | Ser | Ile | Met | Val | Val | Ala | Glu | Asp |  |  |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |  |  |
| Phe | Asp | Gly | Asn | Lys | Tyr | Val | Ile | Glu | Glu | His | Ala | His | Arg | His | Lys |  |  |
|     | 275 |     |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |  |
| Glu | Ile | Asp | Asp | Trp | Val | Ala | Ile | Ala | Lys | Glu | Leu |     |     |     |     |  |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Leu | Ile | Arg | Ser | His | Ala | Cys | Gly | Leu | Gly | Glu | Pro | Phe | Pro |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Lys | Glu | Val | Ala | Leu | Val | Met | Met | Ile | Xaa | Arg | Leu | Asn | Thr | Leu | Leu |
|     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |     |
| Lys | Gly | His | Ser | Gly | Ala | Thr | Leu | Val | Ile | Ser | Glu | Thr | Ile | Thr | Ile |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Phe | Tyr | Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     | 50  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | His | Val | Leu | Asp | Phe | Asn | Asp | Lys | Ile | Ile | Asp | Phe | Leu | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Thr | Asp | Asp | Pro | Ser | Leu | Val | Arg | Ala | Ile | His | Lys | Arg | Asn | Val | Asn |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Asp | Asn | Ser | Glu | Met | Leu | Glu | Leu | Leu | Ile | Ser | Ser | Glu | Arg | Ala | Glu |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Xaa | Phe | Arg | Glu | Arg | His | Arg | Val | Ile | Ile | Arg | Asp | Ser | Asn | Lys | Gln |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Trp | Arg | Glu | Phe | Ile | Ile | Asn | Trp | Val | Gln | Asp | Thr | Met | Asp | Gly | Tyr |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Thr | Glu | Ile | Glu | Cys | Ile | Ala | Ser | Tyr | Leu | Ala | Asp | Ile | Thr | Thr | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |

Lys Pro Tyr Ala Pro Gly Lys Phe Glu Lys Lys Thr Thr Ser Glu Ala  
                   100                  105                  110  
 Leu Lys Asp Val Leu Ser Asp Thr Gly Trp Glu Val Ser Glu Xaa Thr  
                   115                  120                  125  
 Glu Tyr Asp Gly Leu Arg Thr Thr Ser Trp Thr Ser Tyr Xaa Thr Arg  
                   130                  135                  140  
 Tyr Glu Val Leu Lys Gln Leu Cys Thr Thr Tyr Lys Met Ala Leu Asp  
                   145                  150                  155                  160  
 Phe Tyr Ile Glu Leu Ser Ser Asn Thr Val Lys Gly Arg Tyr Val Val  
                                   165                  170                  175  
 Leu Asn Lys Lys Asn Ser Leu Phe Gln Gly Lys Glu Ile Glu Tyr Gly  
                   180                  185                  190  
 Lys Asp Leu Ala Trp Val Asn  
                   195

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

Val Leu Val Gln Gly Gln Val Cys Ser His Leu Ser Thr Xaa Leu Gly  
   1                  5                  10                  15  
 Leu Ile Ile Ile Asp Glu Glu His Glu Ser Thr Tyr Lys Gln Glu Asp  
                   20                  25                  30  
 Tyr Pro Arg Tyr His Ala Arg Glu Ile Ala Gln Trp Arg Ser Glu Tyr  
                   35                  40                  45  
 His His Cys Pro Val Ile Leu Gly Ser Ala Thr Pro Cys Leu Glu Ser  
                   50                  55                  60  
 Tyr Ala Arg Ala Glu Lys Asp Val Tyr His Leu Leu Ser Leu Pro Asn  
                   65                  70                  75                  80  
 Arg Val Asn Gln Gln Ala Leu Pro Glu Ile Asp Ile Val Asp Met Arg  
                   85                  90                  95  
 Glu Glu Leu Ser Glu Gly Asn Arg Ser Met Phe Ser Lys Asp Leu Arg  
                   100                  105                  110  
 Glu Ala Ile Gln Leu Arg Xaa Arg Ser Thr Gly Thr Ser Cys Phe Ile  
                   115                  120                  125  
 Phe Lys Ser Asp Val Val Met His Arg Leu Cys Tyr Val Gly Ile Val  
                   130                  135                  140  
 Asp Met Tyr Arg Asn Val Gln Xaa Val Ile Phe His  
                   145                  150                  155

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

Val Lys Tyr Leu Asn Asp Asp Ile Ala Lys Gly Ser Ile Phe Asp Tyr



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Leu | Glu | Ser | Asn | Met | Lys | Leu | Arg | Ile | Gly | Phe | Ser | Asp | Ile | Phe | Phe |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asn | Val | Asp | Lys | Leu | Thr | Ser | Ser | Glu | Ala | Ser | Leu | Leu | Gln | Leu | Ser |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Thr | Gly | Glu | Pro | Cys | Leu | Arg | Tyr | His | Gln | Thr | Phe | Tyr | Thr | Met | Thr |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Gly | Lys | Pro | Phe | Asp | Ser | Ser | Asp | Ile | Val | Phe | His | Tyr | Xaa | His | Ala |  |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Gln | Phe | Tyr | Ile | Pro | Ser | Lys | Lys |     |     |     |     |     |     |     |     |  |
|     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Arg | His | Leu | His | Ile | Pro | Leu | Gln | Ser | Gly | Ser | Asp | Thr | Val | Leu |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Lys | Arg | Met | Arg | Arg | Lys | Tyr | Thr | Met | Asp | Arg | Phe | Ser | Glu | Arg | Leu |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Thr | Lys | Leu | His | Lys | Ala | Leu | Pro | Asp | Leu | Ala | Val | Thr | Ser | Asp | Val |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Ile | Val | Gly | Phe | Pro | Gly | Glu | Thr | Glu | Ala | Glu | Phe | Gln | Glu | Thr | Tyr |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |
| Asp | Phe | Ile | Val | Lys | His | Lys | Phe | Ser | Glu | Leu | His | Val | Phe | Pro | Tyr |  |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     |     | 80  |  |
| Ser | Pro | Arg | Ile | Gly | Thr | Pro | Ala | Ala | Arg | Met | Asp | Asp | Gln | Ile | Asp |  |
|     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |  |
| Glu | Glu | Ile | Lys | Asn | Glu | Arg | Val | His | Lys | Val | Asn | Tyr | Ala |     |     |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Phe | Val | Val | Glu | Ala | Leu | Val | Lys | Thr | Arg | Glu | Gly | His | Gly | Asn |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
| Leu | Glu | Leu | Leu | Asp | Lys | Glu | Val | Ala | Thr | Pro | Leu | Asp | Asp | Lys | Val |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Lys | Ile | Lys | Val | His | Tyr | Ala | Gly | Ile | Cys | Gly | Thr | Asp | Leu | His | Thr |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Tyr | Glu | Gly | His | Tyr | Xaa | Val | Asn | Phe | Pro | Val | Thr | Leu | Gly | His | Glu |  |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |
| Phe | Ser | Gly | Xaa | Ile | Val | Glu | Val | Gly | Ser | Arg | Arg |     |     |     |     |  |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Thr | Ser | His | Val | Asn | Ser | Ile | Lys | Ile | His | Ile | Gly | Arg | Xaa | Lys |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Gln | Gly | Lys | Thr | Ile | Leu | Lys | Asn | Ile | Ser | Cys | His | Ile | Pro | Lys | Gly |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asp | Lys | Trp | Ile | Leu | Tyr | Gly | Leu | Xaa | Gly | Ala | Gly | Lys | Thr | Thr | Leu |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Leu | Asn | Ile | Leu | Asn | Ala | Tyr | Glu | Pro | Ala | Thr | Thr | Gly | Gly | Val | Asn |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Leu | Phe | Gly | Lys | Met | Pro | Gly | Lys | Val | Gly | Tyr | Ser | Ala | Glu | Thr | Xaa |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Arg | Gln | His | Ile | Gly | Phe | Val | Ser | His | Ser | Leu | Leu | Glu | Lys | Xaa | Pro |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Arg | Gly |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Val | Ile | Ser | Gly | Ala | Phe | Lys | Ser | Thr | Gly | Val | Tyr | Gln | Asp | Ile |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Asp | Asp | Glu | Val | Arg | Asn | Glu | Ala | His | His | Leu | Leu | Lys | Leu | Val | Gly |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ile | Ser | Ala | Lys | Ala | Gln | Gln | Tyr | Ile | Gly | Tyr | Leu | Ser | Thr | Gly | Glu |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Lys | Gln | Arg | Val | Met | Ile | Ala | Arg | Ala | Leu | Met | Gly | Gln | Pro | Gln | Val |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Phe | Asn | Phe | Arg |     |     |     |     |     |     |     |     |     |     |     |     |  |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Xaa | Gly | Val | Xaa | Pro | Lys | Pro | Leu | His | Ala | Asn | Leu | Met | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Thr | Leu | Ser | Gly | His | Ile | Gln | His | Ile | Ala | Phe | Gly | Pro | Ile | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Leu | Glu | Ser | Ile | Lys | His | Leu | Gly | Thr | Asn | Gly | Gly | Gly | Phe | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Gly | Asn | Ser | Ala | Thr | Pro | Phe | Glu | Asn | Pro | Asn | Ile | Trp | Ser | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Ile | Glu | Met | Gly | Ser | Met | Met | Leu | Leu | Pro | Met | Ser | Met | Leu | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Phe | Gly | Arg | Met | Leu | Ser | Arg | His | Gly | Lys | Arg | Val | His | Arg | His |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Leu | Ile | Leu | Phe | Val | Ala | Met | Phe | Phe | Ile | Phe | Ile | Ala | Ile | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Leu | Thr | Met | Trp | Ser | Glu | Tyr | Arg | Gly | Asn | Pro | Ile | Leu | Ala | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| Leu | Gly | Ile | Tyr | Gly | Pro | Asn | Met | Glu | Gly | Lys | Glu | Val | Arg | Phe | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Gly | Leu | Ser | Ala | Leu | Phe | Thr | Val | Ile | Thr | Thr | Ala | Phe | Thr | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gly | Ser | Val | Asn | Asn | Met | His | Asp | Ser | Leu | Thr | Pro | Ile | Gly | Gly | Leu |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | Pro | Met | Val | Leu | Met | Met | Leu | Asn | Val | Val | Phe | Gly | Gly | Glu | Gly |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Val | Gly | Leu | Met | Asn | Leu | Leu | Ile | Xaa | Xaa | Leu | Leu | Thr | Val | Phe | Ile |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Cys | Ser | Leu | Met | Val | Gly | Lys | Thr | Pro | Glu | Tyr | Leu | Asn | Met | Pro | Ile |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gly | Ala | Arg | Glu | Met | Lys | Cys | Ile | Val | Leu | Val | Phe | Leu | Ile | His | Pro |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Ile | Leu | Ile | Leu | Val | Phe | Ser | Ala | Leu | Ala | Phe | Met | Ile | Pro | Gly | Ala |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ser | Glu | Ser | Ile | Thr | Asn | Pro | Ser | Phe | His | Gly | Ile | Ser | Gln | Val | Met |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Cys | Glu | Phe | Ile | Lys | Pro | Pro | Thr | His | Val | Xaa | Gly | Ile | Ile | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Val | Val | Gly | Gly | Tyr | Val | Xaa | Ala | Arg | Asn | Xaa | Xaa | Leu | Gln | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Ser | Gln | Ala | Arg | Gln | Thr | Ala | Xaa | Asp | Ile | Val | Xaa | Gln | Ala | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Glu | Ala | Asp | Xaa | Ile | Lys | Lys | Glu | Lys | Leu | Leu | Xaa | Ala | Lys | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Xaa | Gln | Leu | Xaa | Arg | Glu | Xaa | Thr | Glu | Ala | Glu | Xaa | Arg | Glu | Arg |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |

Arg Xaa Asp Leu Xaa Arg Gln Gly Asn Pro Thr Ser Ser Lys Arg Arg  
85 90 95  
Lys Leu Arg Ala His Ser  
100

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

Val Arg Leu His Leu Cys Leu His Gln Arg Lys Ala Phe Leu Thr Asp  
1 5 10 15  
Trp Ser Tyr Ile Ala Gly Asn Ile Ala Ile Val Ala Ile Ile Pro Leu  
20 25 30  
Leu Ile Tyr Phe Tyr Val Pro Phe Phe Lys Lys Leu Lys Val Thr Ser  
35 40 45  
Ala Tyr Glu Tyr Leu Glu Ala Arg Phe Gly Pro Ser Ile Arg Val Xaa  
50 55 60  
Gly Ser Leu Leu Phe Val Val Tyr His Leu Gly Arg Val Ala Ile Val  
65 70 75 80  
Ile Tyr Leu Pro Thr Leu Ala Ile Thr Ser Val Ser Asp Met Asn Pro  
85 90 95  
Tyr Ile Xaa Gly Ser Leu Val Gly Leu Leu Cys Ile Xaa Xaa Thr Ser  
100 105 110  
Xaa Gly Xaa Phe Xaa Gly Val Arg Leu Glu  
115 120

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

Val Tyr Lys Ile Thr Ile Asn Glu Val Phe Asn Met Thr Glu Thr Thr  
1 5 10 15  
Phe Asn Pro Ile Thr Ser Leu Thr Ile Asn Asn Glu Glu Val Lys Ala  
20 25 30  
Lys Ala Thr Phe Met Phe Asp Lys Thr Ala Lys Lys Phe Ala Thr Glu  
35 40 45  
Gln Glu Asp Asn Lys Gly Arg Lys Gln Thr Ile Ser Gly Phe Thr Asn  
50 55 60  
Val Tyr Xaa Ala Leu Leu Glu Arg Asp Thr Val Ala Ile Val Asp Phe  
65 70 75 80  
Trp Glu Cys Ala Thr Ala Tyr Leu Gly Lys Ser Ala Pro Lys Arg Glu  
85 90 95  
Asp Ile Glu Ala Glu Ile Met Glu Ile Ile Glu Arg Glu Asn Asp Thr  
100 105 110  
Leu Ile Phe Tyr Lys Val Arg Trp Thr

115

120

## (2) INFORMATION FOR SEQ ID NO:399:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

```

Val Pro Ser Asn Lys Val Ala Phe Ile Pro Ser Glu Ala Gln Phe Ile
 1 5 10 15
Gln Leu Cys Gln Asp Asp Asn Asp Val Lys Gln Ala Ser His Asn Leu
 20 25 30
Tyr Asp Gly Val Thr Phe Thr
 35

```

## (2) INFORMATION FOR SEQ ID NO:400:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

```

Val Asn Gly Val Gln Asp Asn Ser Ile Gly Ser Thr Asn Glu Ser Gln
 1 5 10 15
Phe Leu Gly Asn Tyr Ile Val Ile Lys His Ala Glu Asn Glu Tyr Ser
 20 25 30
Leu Ile Ala His Leu Gln Gln Tyr Ser Ile Ile Val Asn Glu Gly Gln
 35 40 45
Asn Val Lys Tyr Gly Asp Phe Leu Gly Lys Val Gly Asn Ser Gly Asn
 50 55 60
Ser Thr Glu Pro His Ile His Phe Gln Val Met Asn Asp Lys Asn Ile
 65 70 75 80
Glu Ala Cys Thr Ser Leu Lys Ile Arg Phe Leu Asn Asn Leu Glu Leu
 85 90 95
Ile Lys Gly Asp Val Val Cys Gly Leu Gln Gly Glu
 100 105

```

## (2) INFORMATION FOR SEQ ID NO:401:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

```

Val His Lys Glu Asn Ile Met Leu Asn Xaa Ser Ala Thr Asp Lys Glu

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Ser | Val | Leu | Xaa | Gln | Met | Ser | Asp | Val | Leu | Phe | Gln | Asn | Gly | Phe | Val |  |  |
|     |     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |  |  |
| Lys | Ser | Thr | Phe | Lys | Asp | Ala | Val | Ile | Asp | Arg | Glu | Lys | Glu | Xaa | Xaa |  |  |
|     |     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |  |  |
| Thr | Gly | Leu | Pro | Thr | His | Leu | Cys | Ser | Val | Ala | Ile | Pro | His | Thr | Asp |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Val | Glu | His | Ile | Asn | His | Arg | Thr | Ile | Gly | Val | Gly | Val | Leu | Glu | Lys |  |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |  |  |
| Glu | Val | Ala | Val | Ile | Gly | Met | Gly | Thr | Ile | Gly | Ser | Thr | Gly | Arg | Arg |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Arg | Ala | Ala | Phe | Gly | Lys | Asn | Gly | Gly | Asn | Met | Gly | Val | Ser | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Ser | Val | Ala | Tyr | Met | Phe | Asp | His | Val | Ala | Thr | Phe | Gly | Ile | Glu | Gly |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Lys | Ser | Val | Asp | Glu | Ile | Leu | Glu | Thr | Leu | Met | Glu | Pro | Arg | Cys | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |
| Met | Xaa | Met | Met |     |     |     |     |     |     |     |     |     |     |     |     |
|     | 50  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Met | Phe | Asn | Thr | Thr | Val | Asn | Ser | Asp | Thr | Asp | Val | Ile | Lys | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |
| Gly | Arg | Leu | Leu | Val | Asp | Lys | Gly | Ala | Gln | Ser | Val | Ile | Val | Ser | Leu |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Gly | Gly | Asp | Gly | Ala | Ile | Tyr | Ile | Asp | Lys | Glu | Ile | Ser | Ile | Lys | Ala |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Val | Asn | Pro | Gln | Gly | Lys | Val | Val | Asn | Thr | Val | Gly | Ser | Gly | Asp | Ser |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Thr | Val | Ala | Gly | Met | Val | Ala | Gly | Ile | Ala | Ser | Arg | Phe | Asn | Asp |     |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Ile | Ser | Asn | Asp | Ala | Ile | Val | Glu | Leu | Val | Ser | Arg | Ile | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Val | Ser | Glu | Met | Met | Glu | Arg | Glu | Thr | Asp | Leu | Gly | Val | Ala | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Phe | Glu | Ile | Ile | Thr | Ala | Met | Met | Phe | Leu | Tyr | Phe | Gly | Glu | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| His | Pro | Val | Asp | Phe | Val | Ile | Val | Glu | Ala | Gly | Leu | Gly | Ile | Lys | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Ser | Thr | Asn | Val | Phe | Thr | Pro | Val | Leu | Ser | Ile | Leu | Thr | Ser | Ile |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Leu | Asp | His | Thr | Asp | Ile | Leu | Gly | Gly | Thr | Tyr | Leu | Asp | Ile | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Arg | Asp | Lys | Gly | Ala | Ile | Ile | Lys | Pro | Asn | Val | Pro | Val | Ile | Tyr | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Lys | Asn | Glu | Asp | Ala | Leu | Lys | Tyr | Val | Arg |     |     |     |     |     |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Phe | Ile | Gly | Thr | Tyr | Met | Ile | Leu | Ser | Ile | Arg | Lys | Glu | Ser | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Val | Ile | Thr | Asp | Thr | Asp | Glu | Ala | Leu | Lys | Gln | Val | Leu | Lys | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Xaa | Glu | Asn | Lys | Val | Ile | Ser | Gln | Asn | Asn | Lys | Glu | Val | Thr | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Ala | Asp | Thr | Ile | Cys | Val | His | Gly | Asp | Gly | Glu | His | Ala | Leu | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Val | Ser | Gln | Ile | Arg | Glu | Ile | Leu | Met | Xaa | Glu | Gly | Ile | Asp | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gln | Ser | Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Phe | Ala | Asp | Arg | Arg | Tyr | Glu | Asp | Asp | Gly | Gln | Leu | Val | Ser | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Glu | Ser | Asp | Ala | Val | Ile | Thr | Asp | Thr | Asp | Glu | Ala | Leu | Lys | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Leu | Lys | Met | Val | Xaa | Glu | Asn | Lys | Val | Ile | Ser | Lys | Asn | Asn | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Val | Thr | Leu | Gln | Ala | Asp | Thr | Ile | Cys | Val | His | Gly | Asp | Gly | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| His | Ala | Leu | Leu | Phe | Val | Ser | Gln | Ile | Arg | Glu | Ile | Leu | Met | Lys | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Ile | Asp | Ile | Gln | Ser | Leu |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Tyr | Asp | Ile | Glu | Val | Ser | Asp | Tyr | Lys | Gly | Leu | Thr | Tyr | Lys | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Ala | Phe | Arg | Gly | Lys | Val | Ile | Leu | Val | Val | Asn | Thr | Ala | Thr | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Ile | Tyr | Ser | Glu | Gln | Leu | Lys | Lys | Leu | Glu | Thr | Leu | Xaa | Gln | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Lys | Asp | Arg | Gly | Phe | Val | Val | Leu | Ser | Ser | Pro | Asn | Asn | Asn | Cys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Asn | Arg | Gln | Pro | Xaa | Ser | Asn | Glu | Glu | Ile | Leu | Lys | Ile | Xaa | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Xaa | Glu | Ile | Trp | Val | Leu | His | Phe | Gln | Cys |     |     |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Glu | Ile | Glu | Asn | Glu | Pro | Tyr | Phe | Val | Gly | Lys | Asp | Ile | Ala | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Leu | Gly | Tyr | Ala | Arg | Ala | Asp | Asn | Ala | Ile | Arg | Asn | His | Val | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Glu | Asp | Lys | Leu | Thr | His | Gln | Phe | Ser | Asp | Ser | Arg | Ser | Lys | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Cys | Asn | Asp | Gln | Ser | Thr | Asn | Gln | Asp | Tyr | Thr | Val |     |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:409:



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Arg | Xaa | Leu | Ile | Xaa | Glu | Ser | Xaa | Ile | Asp | Leu | Ala | Ser | Pro | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Asn | Arg | Pro | Phe | Ile | Asp | Val | Phe | Leu | Glu | Pro | Thr | Lys | Leu | Tyr |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Xaa | Pro | Val | Leu | Ala | Leu | Lys | Lys | Glu | Val | Ser | Ile | Lys | Ala | Met |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | His | Ile | Thr | Gly | Gly | Gly | Phe | Tyr | Glu | Asn | Ile | Pro | Arg | Ala | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | Ala | Gly | Tyr | Ala | Ala | Arg | Ile | Asp | Thr | Thr | Ser | Phe | Pro | Thr | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Ile | Phe | Asp | Trp | Leu | Gln | Gln | Gln | Gly | Asn | Ile | Asp | Thr | Asn | Glu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Met | Tyr | Asn | Ile | Phe | Asn | Met | Gly | Ile | Gly | Tyr | Thr | Val | Ile | Val | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Lys | Asp | Ala | Ser | Thr | Arg | Phe | Glu | Asp | Phe | Ser | Arg | Thr | Lys | Cys |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Gly | Ser | Leu | Ser | Asn | Trp | Ser | Tyr | Cys | Glu | Lys |     |     |     |     |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Ile | Phe | Pro | Asn | Lys | Ala | Leu | Ile | Glu | Ser | Ala | Val | Ala | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Glu | Leu | Asp | Glu | Ser | Val | Phe | Asn | Gln | Leu | Val | Thr | Asp | Met | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Glu | His | His | Tyr | Asn | Ile | Pro | Gln | His | Tyr | Ile | Asn | Leu | Tyr | Ile |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Asp | Asn | Ile | Lys | Thr | Leu | Lys | Asp | Val | Pro | Ala | Ser | Tyr | Met | Asn | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Asn | Val | Asp | Val | Val | Ala | Asp | Leu | Leu | Leu | Glu | Lys | Ser | Lys | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Xaa | Tyr | Gly |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

```
Val Leu Phe Ile Gly Phe Phe Val Val Ile Ile Asn Thr Ile Ala Asp
 1 5 10 15
Leu Leu Thr Leu Leu Asp Pro Lys Gln Arg Leu Gln Leu Gly Asn
 20 25 30
Pro Thr Lys His Asn Gln Tyr Thr Ile Asp Ile Arg Lys
 35 40 45
```

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

```
Val Leu Ile Glu Val His Asp Pro His Glu Leu Glu Arg Ala Xaa Xaa
 1 5 10 15
Val Asn Ala Lys Leu Ile Gly Val Asn Asn Arg Asp Leu Lys Arg Phe
 20 25 30
Val Thr Asn Val Glu His Xaa Asn Thr Ile Leu Glu Asn Lys Lys Pro
 35 40 45
Asn His His Tyr Ile Ser Glu Ser Gly Ile His Asp Ala Ser Asp Val
 50 55 60
Arg Lys Ile Leu His Ser Gly Ile Asp Gly Leu Leu Ile Gly Glu Ala
 65 70 75 80
Leu Met Arg Cys Asp Asn Leu Ser Glu Phe Leu Arg Gln Leu Lys Xaa
 85 90 95
Xaa Lys Val Lys Ser
 100
```

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

```
Val Ser Asp Glu Pro Xaa Ile Tyr Lys Phe Ile Gln His Asn Xaa Glu
 1 5 10 15
Asn Phe Ile Xaa Thr Ala Ser Xaa Ile Met Asp Gly His Thr Xaa Val
 20 25 30
Ala Pro Leu Lys Xaa Thr His Lys Leu Pro Cys Ala Phe Cys Ser Tyr
 35 40 45
Gln Ser Val Cys His Val Asp Xaa Met Ile Asp Ser Lys Arg Tyr Xaa
 50 55 60
Xaa Val Asp Glu Thr Ile Asn Pro Ile Glu Ala Ile His Asn Ile Asn
 65 70 75 80
```

Ile Asn Asp Val Phe Gly Gly Glu  
85

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asp | His | Leu | Xaa | Val | Thr | Leu | Arg | Ile | Asp | Arg | Glu | Asn | His | Met |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Gly | Arg | Leu | Ala | Ser | Glu | Ser | Val | Val | Glu | Asn | Met | Phe | Thr | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | His | Asp | Asp | Asn | Leu | Lys | Asn | Glu | Val | Ile | Glu | Ala | Lys | Pro | Trp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Xaa | Glu | Arg | Ile | Thr | Asn | Trp |     |     |     |     |     |     |     |     |     |
| 50  |     |     |     |     |     | 55  |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Xaa | Tyr | Met | Asp | Lys | Gly | Leu | Thr | Gly | His | Ile | Met | Arg | Arg | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Thr | Glu | Ala | Asp | Ala | Ser | Ile | Asn | Trp | Ala | Leu | Gly | Leu | Met | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Gly | Ser | Gln | Ile | Ile | Asp | Asn | Thr | Thr | Asn | Leu | Cys | Gly | Asp | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Thr | Xaa | Xaa | Leu | Lys | Ser | Gly | Gly | Xaa | Gly | Thr | Gly | Glu | Gln | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Asn | Leu | Thr | Ser | Lys | Xaa | Ala | Gln | Ile | Trp |     |     |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Tyr | Lys | Gln | Gly | Glu | Pro | Asn | Leu | Trp | Thr | Gly | Arg | Leu | Asp | Ser |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Thr | Asp | Pro | Lys | Lys | Phe | Arg | His | Phe | Gln | Thr | Val | Thr | Phe | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Leu | Ser | Lys | Leu | Glu | Lys | Ser | Ser | Met | Pro | Ser | Gly | Val | Gly | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Gly | Tyr | Ala | Val | Gly | Gln | Arg | Cys | Cys | Phe | Xaa | Gln | Gly | Ala | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Trp | Cys | Lys | Arg | Arg | Thr | Arg | Cys | Asp |     |     |     |     |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | His | His | Ile | Thr | His | Tyr | Ile | Asp | Gln | Leu | Asp | Arg | Phe | Ser | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Gly | Asp | Val | Ile | Lys | Xaa | His | Ser | Gly | Gly | Tyr | His | His | Lys | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Thr | Phe | Asn | Lys | Leu | Gly | Tyr | Ile | Asn | Glu | Asn | Tyr | Ile | Glu | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Asp | Val | Glu | Asn | Asn | Glu | Lys | Leu | Lys | Lys | Met | Ala | Xaa | Thr | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Gly | Gly | Val | Ala | Cys | Ala | Thr | Gln | Ile | Ala | Gln | Glu | Lys | Tyr | Glu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gln | Gly | Phe | Lys | Asn | Met | Cys | Val | Xaa | Thr | Asn | Asp | Ile | Glu | Ala | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Lys | Asn | Asn | Leu | Gln | Xaa | Glu | Gln | Val | Xaa | Val | Val | Ala | Pro | Thr | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Met | Glu | Arg | Asp | Thr | His | Lys | Asp | Gly | Lys | Val | Lys | Trp | Gln | Leu | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     | 130 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Arg | Gly | Ser | Lys | Ile | Gln | Thr | Ile | Gly | Val | Ile | Leu | Pro | Ser | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Asn | Pro | Phe | Phe | Ser | Ala | Leu | Met | Gln | Ser | Ile | His | Asp | His | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Ser | Asp | Val | Asp | Leu | Cys | Phe | Leu | Thr | Ser | Thr | Ala | Thr | Asp | Xaa |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Asp | Asn | Ile | Lys | His | Leu | Ile | Asp | Arg | Gly | Ile | Asp | Gly | Leu | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Ala | Gln | Tyr | Ile | Ser | Ser | Pro | Asp | Ala | Leu | Asn | Asn | Tyr | Leu | Lys |

|     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     | 70  |     | 75  |     | 80  |     |     |     |     |     |
| Lys | His | His | Val | Pro | Tyr | Val | Val | Leu | Asp | Gln | Lys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Xaa | Asp | Glu | Xaa | Xaa | Val | Asp | Lys | Asp | Ala | Leu | Arg | Asn | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Leu | Val | Lys | Gly | Gln | Phe | Lys | Ala | Asp | His | Gln | Tyr | Gln | Ile | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Gly | Pro | Gly | Xaa | Val | Asp | Glu | Val | Tyr | Lys | Gln | Phe | Ile | Asp | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Gly | Ala | Gln | Glu | Ala | Ser | Lys | Asp | Glu | Ala | Lys | Gln | Ala | Ala | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Lys | Gly | Asn | Pro | Val | Gln | Arg | Leu | Ile | Lys | Leu | Leu | Gly | Glu | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Phe | Ile | Pro | Ile | Leu | Pro | Ala | Ile | Val | Thr | Thr | Gly | Leu | Leu | Met | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Gln |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Gln | Leu | Leu | Met | His | Met | Ile | His | Tyr | Gly | Thr | Ser | Val | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Ile | Arg | Thr | Gln | Ser | Ile | Leu | Asn | Asp | Asp | Lys | Val | Asn | Gln | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Asp | Tyr | Ile | Glu | Leu | His | Phe | His | Glu | Asp | Leu | Ser | Leu | Ser | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Ser | Glu | Tyr | Val | Gly | Trp | Ser | Glu | Ser | His | Leu | Ser | Lys | Lys | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Glu | Ser | Leu | Gly | Val | Gly | Phe | Gln | His | Phe | Leu | Asn | Thr | Thr | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ile | Glu | His | Ala | Lys | Leu | Asp | Leu | Thr | Tyr | Thr | Asp | Glu | Thr | Ile | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Ile | Ala | Leu | Gln | Asn | Gly | Phe | Ser | Ala | Ala | Ser | Phe | Ala | Arg |     |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |     |     |
| Thr | Phe | Lys | His | Phe | Thr | His | Gln | Thr | Pro | Lys | Gln | Tyr | Arg | Gly | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Pro | Ala | Ile | Thr | Glu | Asn | Gln | Gln | Ser | Ala | Gln | His | Asn | Tyr | His |
|     | 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |

Asp Arg Glu Leu Ile Leu Leu Asn Asp Tyr Ile Glu Glu Met Asn  
 145 150 155 160  
 Gln Phe Asn

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Leu | Gly | Gly | Ser | Val | Thr | Ser | Ile | Gln | Pro | Leu | Arg | Ile | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Thr | Ser | Asn | Glu | Asn | Phe | Thr | Asp | Lys | Asp | Trp | Gln | Ile | Thr | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Pro | Arg | Thr | Leu | His | Ile | Glu | Asn | Ser | Thr | Asn | Arg | Thr | Asn | Asn |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Arg | Glu | Arg | Asn | Ile | Glu | Leu | Val | Gly | Asn | Leu | Leu | Pro | Gly | Asp |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Tyr | Phe | Gly | Thr | Ile | Arg | Phe | Gly | Arg | Lys | Glu | Gln | Leu | Phe | Glu | Ile |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Arg | Val | Xaa | Pro | His | Xaa | Pro | Gln | Leu | Gln | Arg | Gln | Leu | Ser | Asn | Xaa |
|     |     |     |     | 85  |     |     | 90  |     |     |     |     |     |     | 95  |     |
| Glu | Val | Arg | Asn | Tyr | Lys | Ser | Ala | Cys |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Lys | Arg | Leu | Ile | Asn | Glu | Thr | Phe | Asp | Ala | Asn | Tyr | Ile | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ile | Glu | Gly | Gly | Ile | Glu | Glu | Thr | Gln | Thr | Leu | Ile | His | Leu | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Asp | Tyr | Val | Ser | Tyr | Arg | Ser | Glu | Ile | Val | Gly | Lys | Ser | Phe | Ile |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Lys | Leu | Gln | Arg | Asn | Leu | Val | Leu |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     | 55  |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

```
Val Ile Thr Phe Val Leu Val Pro Val Leu Ile Pro Thr Leu Lys Arg
 1 5 10 15
Met Lys Phe Gly Gln Ser Ile Arg Glu Gly Pro Gln Ser His Met
 20 25 30
Lys Lys Thr Gly Thr Pro Thr Met Gly Gly Leu Thr Ile Ser Ile Lys
 35 40 45
Val Phe Val Ile Thr Val Phe Gly Gly Tyr Tyr Ile Cys Lys Ile Lys
 50 55 60
Leu Ile Gln Ser Tyr Leu Leu Leu Phe Val Thr Asp Trp Phe Trp Val
65 70 75 80
Asn Trp Phe Tyr Arg
 85
```

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

```
Val Met Xaa Asn Gly Xaa Leu Ile Glu His Gly Thr Arg Glu Ser Val
 1 5 10 15
Leu His His Pro Glu His Val Tyr Thr Lys Tyr Leu Leu Ser Xaa Xaa
 20 25 30
Lys Lys Xaa Asn Asp His Phe Lys His Val Met Arg Gly Asp Val His
 35 40 45
Xaa
```

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

```
Val Pro Thr Ile Asp Ser Val Lys Thr Tyr Gly Leu Val Ser Ile Pro
 1 5 10 15
Gly Met Met Thr Gly Leu Ile Ile Gly Gly Val Pro Pro Leu Gln Ala
 20 25 30
Ile Lys Phe Gln Leu Leu Val Val Phe Ile His Thr Thr Ala Xaa Ile
 35 40 45
Met Ser Ala Leu Ile Ala Thr Tyr Leu Ser Tyr Gly Gln Phe Phe Asn
 50 55 60
Ala Arg His Gln Leu Val Ala Arg Asn Thr Asp Val Lys Ser Glu Ser
65 70 75 80
```

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

```
Val Met Pro Xaa Val Phe Trp Xaa Pro Phe Pro Xaa Ile Phe Ile Gly
 1 5 10 15
Thr Ala Leu Pro Leu Ala Gly Thr Val Ala Thr Gly Ala Ile His Phe
 20 25 30
Thr Ala Asn Glu Val Ile Pro Ile Gly Xaa Met Leu Xaa Asn Asn Gly
 35 40 45
Leu Ile Ala Ile Asn Leu Ala Tyr Gln Asn Leu Asp Arg Ala Phe Val
 50 55 60
Gln Asp Gly Thr Asn Ile Glu Ser Lys Leu Ser Leu Ala Ala Thr Pro
 65 70 75 80
Lys Leu Ala Ser Lys Gly Ala Ile Arg Glu Ser Ile Arg Leu Ala Ile
 85 90 95
Gly Ala Asn Asn
 100
```

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

```
Val Lys Val Gly Lys Ser Met Glu Gly Leu Asn His Arg Arg Asn Thr
 1 5 10 15
Glu Lys Glu Glu Thr Thr Gln Thr Gln Ser Val Ala Pro Asn Thr Gly
 20 25 30
Glu Glu Gly Met Ser Ser Gly Lys
 35 40
```

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

```
Val Gln Phe Leu Asn Gln Trp Leu Gly Asp Thr Leu Ala Phe Lys Val
 1 5 10 15
Lys His Met Leu Arg Gln Arg Val Ile Tyr Lys Asn Asn Gly His Pro
```





(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Tyr | Ala | Gly | Glu | Asn | Phe | Met | Ile | Leu | Leu | Ala | Ser | Arg | Leu | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Val | Val | Tyr | Ser | Leu | Gly | Leu | Ala | Arg | Thr | Arg | Arg | Gln | Ala | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Leu | Val | Asn | His | Gly | His | Ile | Leu | Val | Asp | Gly | Lys | Arg | Val | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Pro | Ser | Tyr | Ser | Val | Lys | Pro | Gly | Gln | Thr | Ile | Ser | Val | Arg | Glu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Ser | Gln | Lys | Leu | Asn | Ile | Ile | Val | Glu | Ser | Val | Glu | Ile | Asn | Asn |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Phe | Val | Pro | Glu | Tyr | Leu | Asn | Phe | Asp | Ala | Asp | Ser | Leu | Thr | Gly | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Val | Arg | Leu | Pro | Glu | Arg | Ser | Glu | Leu | Pro | Ala | Glu | Ile | Asn | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Leu | Ile | Val | Glu | Tyr | Ser | Cys | Gln | Asp | Asn | Thr | Phe | Ile | Thr | Ile |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | His | Asn | Cys | Gly | Cys | Phe | Phe | Tyr |     |     |     |     |     |     |     |
|     |     |     | 130 |     |     |     | 135 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | His | Leu | Val | Arg | Met | Val | Tyr | Lys | Gly | Lys | Ile | Ser | Asp | His | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ser | Val | Trp | Glu | Lys | Ala | Thr | Thr | Tyr | Gln | Met | Tyr | His | Gly | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Leu | Leu | Ile | Ile | Gly | Val | Ile | Ser | Gly | Thr | Thr | Ser | Ile | Asn | Val |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Trp | Ala | Gly | Trp | Leu | Ile | Phe | Ala | Gly | Ile | Ile | Phe | Phe | Ser | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Leu | Tyr | Ile | Leu | Val | Leu | Thr | Gln | Ile | Lys | Val | Leu | Gly | Ala | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Pro | Ile | Gly | Gly | Val | Leu | Phe | Ile | Ile | Gly | Trp | Ile | Met | Leu | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Ala | Thr | Phe | Lys | Phe | Ala | Gly |     |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

```
Val Leu Lys Leu Phe Gln Met Arg Ser Pro Ile Phe Arg Glu Pro Ser
 1 5 10 15
Ala Asn Asn Ala Val Lys Thr Leu Ile Ala Met Gly Ser Ile Leu Ala
 20 25 30
Phe Leu Leu Val Gly Ile Gly Gly Leu Ala Tyr Val Tyr Gly Ile Met
 35 40 45
Pro Gln Thr Glu Thr Thr Val Leu Ser Gln Leu Ala Met Gln Ile Phe
 50 55 60
Gly
65
```

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

```
Val Met Arg Gly Thr Ile Ile Ile Pro Thr Thr Lys Pro Gly Leu Ile
 1 5 10 15
Ala Leu Asn Ser Pro Arg Pro Asp Met Lys Asp Leu Asn Thr Gly Val
 20 25 30
Thr Lys Val Asn Ala Lys Lys Pro Asn Thr Ile Val Gly Ile Pro Ala
 35 40 45
Lys Ile Ser Asn Ile Gly Leu Ile Met Arg Arg Ala Arg Ala Leu Ala
 50 55 60
Tyr Ser Leu Lys
65
```

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

```
Val Ser Asp Thr Ala Val Met Ile Ala Trp Leu Val Lys Ile Pro His
 1 5 10 15
Ser Thr Met Pro Ile Leu Gly Thr Ser Gln Leu Lys Arg Xaa Asp Gln
 20 25 30
Ala Ile Glu Gly Leu Gln Leu Asn Leu Asp Asp Gln Val Val Gly
```

## (2) INFORMATION FOR SEQ ID NO:436:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

```

Val Asp Ile Pro Leu Leu Phe Glu Asn Glu Leu Glu Asn Thr Val Asp
 1 5 10 15
Glu Val Trp Val Val Tyr Thr Ser Glu Ser Ile Gln Met Asp Arg Leu
 20 25 30
Met Xaa Arg Xaa Asp Leu Ser Leu Glu Asp Ala Lys Ala Arg Val Tyr
 35 40 45
Xaa Pro Asn Phe Tyr
 50

```

## (2) INFORMATION FOR SEQ ID NO:437:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

```

Val Met Gln Val Phe Thr Trp Gln Gln Tyr Val Glu Ile Val Val Asn
 1 5 10 15
Glu Gly Arg Asp Ala Ala Asn Ala Ala Gln Glu Lys Ala Val Lys Glu
 20 25 30
Gly Lys Ile Ile Ile Lys Asp Ser Ile Ala Asp Ile Phe Leu Gln Gln
 35 40 45
Ile Leu Thr Arg Pro Ala Glu His Asp Val Val Ala Thr Met Asn Leu
 50 55 60
Asn Gly Asp Tyr Ile Ser Asp Ala Leu Ala Ala Gln Val Gly Xaa Ile
 65 70 75 80
Gly Ile Ala Pro Gly Ala Asn Ile Asn Tyr Glu Thr Gly His Ala Ile
 85 90 95
Phe Glu Ala Thr His Gly Leu Xaa Ser Lys Ile Cys Arg Phe Lys
 100 105 110

```

## (2) INFORMATION FOR SEQ ID NO:438:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Met | Phe | Ile | Thr | Gly | Met | Gln | Tyr | Gly | Asp | Lys | Val | Ala | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| His | Val | Ser | Arg | Gly | Ala | Val | Phe | Gly | Met | Thr | Gly | Val | Leu | Val | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Thr | Asp | Gln | Leu | Leu | Ala | Phe | Phe | Asn | Asn | Arg | Tyr | Trp | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Gln | Phe | Asn | Pro | Arg | Gly | Gly | Trp | Ser | Pro | Ser | Gly | Pro | Arg | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Ala | Asn | Gly | Gly | Leu | Ile | Thr | Lys | His | Gln | Leu | Xaa | Glu | Val | Gly |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Glu | Gly | Asp | Lys | Gln | Glu | Met | Val | Ile | Pro | Leu | Thr | Arg | Arg | Lys | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Ile | Gln | Leu | Thr | Glu | Gln | Val | Met | Arg | Ile | Ile | Gly | Met | Asp | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Xaa | Pro | Asn | Asn | Ile | Thr | Val | Asn | Asn | Asp | Thr | Ser | Thr | Val | Glu | Lys |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Phe | Glu | Thr | Asn | Cys | Tyr | Val | Lys |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ala | Gly | Ala | Leu | Asp | Val | Asn | Gln | Val | Asn | Val | Ser | Glu | Asn | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Ala | Asn | Gln | Pro | His | Ser | Val | Leu | Leu | Ile | Asp | Thr | Gln | Ala | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Glu | Asn | Asn | Ser | Glu | Leu | Asn | Gln | Val | Gly | Thr | Ser | Thr | Lys | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Ile | Ala | Phe | Cys | Ile | Asp | Val | Arg | Ser | Glu | Pro | Phe | Arg | Arg | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Glu | Ala | Ala | Gly | Pro | Phe | Glu | Thr | Ile | Gly | Ile | Ala | Gly | Phe | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gly | Leu | Pro | Ile | Gln | Lys | Asp | Ala | Val | Asp | Glu | Gln | Phe | Lys | His | Asp |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Leu | Pro | Val | Met | Ser | Arg | Ala | Ala | Gly | Ile | Ser | His |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Phe | Gly | Val | Thr | Gly | Thr | Asn | Gly | Lys | Thr | Ser | Ile | Ala | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Asp | Ser | Phe | Asn | Ser | Xaa | Lys | Val | Thr | Lys | Lys |     |     |     |     |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asp | Gly | Thr | Ala | Asn | Gly | Val | Gly | Ser | Thr | Leu | Xaa | Leu | Asn | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Leu | Asp | Gln | Phe | Ile | Leu | Leu | Ile | Phe | Tyr | Gly | Thr | Phe | Pro | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Asp | Phe | Thr | Glu | Phe | Gly | Ser | Pro | Phe | Gly | Gly | Gly | Lys | Ile | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Asn | Pro | Ser | Asn | Leu | Pro | Asp | Gly | Asp | Gly | Asn | Gly | Gly | Gly | Val |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Glu | Phe | Gly | Leu | Thr | Lys | Ser | Ser | Arg | Thr | Ser | Leu | Thr | Ile | Ser |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asn | Asp | Val | Tyr | Phe | Asp | Leu | Gly | Ser | Gln | Arg | Gly | Ser | Gly | Ala | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Asn | Arg | Gly | Thr | Ile | Asn | Lys | Ile | Ile | Gly | Val | Arg | Lys |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Asp | Asn | Asp | Leu | Asn | Gln | Val | Thr | Leu | Ala | Asp | Tyr | Ala | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Lys | Lys | Leu | Ile | Ser | Val | Val | Pro | Ser | Ile | Asp | Thr | Gly | Val | Cys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Gln | Gln | Thr | Arg | Lys | Phe | Asn | Ser | Glu | Ala | Ser | Lys | Glu | Glu | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Val | Leu | Thr | Ile | Ser | Ala | Asp | Leu | Pro | Phe | Ala | Gln | Lys | Arg | Trp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Cys | Ala | Ser | Ala | Gly | Leu | Asp | Asn | Val | Ile | Thr | Leu | Ser | Asp | His | Arg |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Asp | Leu | Ser | Phe | Gly | Glu | Asn | Tyr | Gly | Val | Val | Met | Glu | Arg | Thr | Ser |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Cys | Arg | Ile | Arg | His | Glu | Leu | Val | Gln | Tyr | Leu | Tyr |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Gln | Glu | Arg | Tyr | Ser | Arg | Gln | Ile | Leu | Phe | Lys | Gln | Ile | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Ile | Gly | Gln | Ser | Lys | Ile | Asn | Gln | Lys | Cys | Ala | Leu | Ile | Ile | Gly |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Gly | Ala | Leu | Gly | Thr | His | Val | Ala | Glu | Gly | Leu | Val | Arg | Ala | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Ala | Lys | Leu | Ile | Ile | Val | Asp | Arg | Asp | Tyr | Ile | Glu | Phe | Ser | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Leu | Gln | Arg | Gln | Thr | Leu | Phe | Thr | Glu | Glu | Asp | Ala | Leu | Lys | Met | Met |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Lys | Val | Val | Ala | Lys | Lys | His | Leu | Leu | Ala | Leu | Arg | Ser | Asp |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Val | Asp | Ile | Asp | Gly | Cys | Ile | Ala | His | Val | Asp | Tyr | Tyr | Phe | Leu | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Thr | Trp | Thr | Gly | Arg | Trp | Thr | Leu | Leu | Leu | Met | Gln | Pro | Ile | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Lys | His | Asp | Asn |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 130 |

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Leu | Met | Lys | Leu | Val | Phe | Val | Ala | Arg | Ala | Gly | Asn | Met | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Ala | Ile | Phe | Thr | Gly | Ile | Ile | Asn | Ser | Ser | Asn | Leu | Asp | Ala | Asn |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Ile | Tyr | Leu | Thr | Asn | Lys | Ser | Asn | Glu | Gln | Ala | Leu | Lys | Ala | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ala | Glu | Lys | Leu | Gly | Val | Asn | Tyr | Ser | Tyr | Asp | Asp | Ala | Thr | Leu | Leu |





(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

```
Val Lys Glu Ile Thr Lys Leu Asn Gly Leu Cys Leu Lys Trp Val Ala
 1 5 10 15
Pro Gly Thr Arg Gly Val Pro Asp Arg Ile Ile Ile Met Pro Glu Gly
 20 25 30
Lys Thr Tyr Phe Val Glu Met Lys Gln Glu Lys Gly Lys Leu His Pro
 35 40 45
Leu Gln Lys Tyr Val His Arg Gln Phe Glu Asn Arg Asp His Lys Val
 50 55 60
Tyr Val Leu Trp Asn Lys Glu Gln Val Asn Thr Phe Ile Arg Met Val
65 70 75 80
Gly Gly Thr Phe Gly Asp
 85
```

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

```
Val Trp Gly Ile Val Ile Leu Gly Gly Tyr Glu Gln Phe Ile Lys Ser
 1 5 10 15
His Leu Arg Lys Ile Tyr Ile Asp Gly Val Ser Asn Met Gln Glu His
 20 25 30
Val Val Val Thr Leu Asp Gly Lys Asp Tyr Leu Val Glu Pro Gly Thr
 35 40 45
Asn Leu Leu Glu Phe Ile Lys Ser Gln Asp Thr Phe Val Pro Ser Ile
 50 55 60
Cys Tyr Asn Glu Ser Met Gly Pro Ile Gln Thr Cys Asp Thr Cys Thr
65 70 75 80
Val Glu Ile Asp Gly Lys Ile Glu Arg Ser Cys Ser Thr Val Ile Asp
 85 90 95
Arg Pro Met Thr Val Asn Thr Val Asn Asp Val Lys Asp Ala Gln
 100 105 110
Lys Glu Pro
 115
```

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

```
Val Leu Thr Met Ile Ser Tyr Leu Leu Phe Leu Leu Ser Gly Leu Ala
 1 5 10 15
Asn Gly Leu Ile Asn Met Asn Lys Glu Gly Ile Asp Lys Trp Gln Ala
 20 25 30
```

Asp Ala Ile Xaa Leu Asn Lys Asp Ala Asn Gln Thr Val Gln Xaa Ser  
 35 40 45  
 Cys Phe  
 50

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

Val Lys Lys Val Val Lys Tyr Leu Ile Ser Leu Ile Leu Ala Ile Ile  
 1 5 10 15  
 Ile Val Leu Phe Val Gln Thr Phe Val Ile Val Gly His Val Ile Pro  
 20 25 30  
 Asn Asn Asp Met Ser Pro Thr Leu Asn Lys Gly Asp Arg Val Ile Val  
 35 40 45  
 Asn Lys Ile Lys Val Thr Phe Asn Gln Leu Asn Asn Gly Asp Ile Ile  
 50 55 60  
 Thr Tyr Arg Arg Gly Asn Glu Ile Tyr Thr Ser Arg Ile Ile Ala Lys  
 65 70 75 80  
 Pro Gly Gln Ser Met Ala Phe Arg Gln Gly Gln Leu Tyr Arg Asp Asp  
 85 90 95  
 Arg Pro Val Asp Ala Ser Tyr Ala Lys Asn Arg Lys Ile Lys Asp Phe  
 100 105 110  
 Ser Leu Arg Asn Phe Lys Glu Leu Asp Gly Asp Ile Ile Pro Pro Asn  
 115 120 125  
 Asn Phe Val Val Leu Asn Asp His Asp Asn Asn Gln His Asp Ser Arg  
 130 135 140  
 Gln Phe Gly Leu Ile Asp Lys Lys Asp Ile Ile Gly Asn Ile Ser Leu  
 145 150 155 160  
 Arg Tyr Tyr Pro Phe Ser Lys Trp Thr Ile Gln Phe Lys Ser  
 165 170

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

Val Ser Lys Leu Lys Lys Glu Leu Leu Glu Trp Ile Ile Ser Ile Ala  
 1 5 10 15  
 Val Ala Phe Val Ile Leu Phe Ile Val Gly Lys Phe Ile Val Thr Pro  
 20 25 30  
 Tyr Thr Ile Lys Gly Glu Ser Met Asp Pro Thr Leu Lys Asp Gly Glu  
 35 40 45  
 Arg Val Ala Val Asn Ile Ile Gly Tyr Lys Thr Gly Gly Leu Glu Lys  
 50 55 60  
 Gly Asn Val Val Val Phe His Ala Asn Lys Asn Asp Asp Tyr Val Lys

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Arg | Val | Ile | Gly | Val | Pro | Gly | Asp | Lys | Val | Glu | Tyr | Lys | Asn | Asp | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Tyr | Val | Asn | Gly | Lys | Lys | Gln | Asp | Glu | Pro | Tyr | Leu | Asn | Tyr | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Lys | His | Lys | Gln | Gly | Asp | Tyr | Ile | Thr | Gly | Thr | Phe | Gln | Val | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Leu | Pro | Glu | Cys | Glu | Ser | Gln | Ile | Lys | Cys | Gln | Ser | Lys | Arg | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asn | Ile |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Glu | Arg | Asn | Gln | Lys | Val | Pro | Xaa | Gly | Pro | Glu | Asn | Pro | Glu | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Ser | Arg | Pro | Thr | His | Pro | Xaa | Gly | Pro | Val | Asn | Pro | Asn | Asn | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Gly | Leu | Ser | Xaa | Asp | Arg | Ala | Lys | Pro | Asn | Gly | Pro | Gly | Pro | Phe | Asn |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Trp | Ile | Lys | Met | Ile | Lys | Val | Lys | Lys | Ser | Lys | Ile | Ala | Lys | Glu | Ser |
| 50  |     |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Val | Ala | Asn | Gln | Glu | Lys | Arg | Ala | Glu | Leu | Pro | Lys | Thr | Gly | Leu |     |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| Glu | Ser | Thr | Gln | Lys | Gly | Leu | Ile | Phe | Ser | Ser | Ile | Ile | Gly | Ile | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Gly | Leu | Met | Leu | Leu | Ala | Arg | Arg | Arg | Lys | Asn |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | His | Val | Asp | Val | Asp | Glu | Arg | Leu | Ile | Asp | Phe | Gln | Ile | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Met | Pro | Leu | Pro | Lys | Asn | Asp | Arg | Ser | Gln | Arg | Pro | Ala | Arg | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Lys | Thr | Ile | Gln | Ala | Lys | Thr | Arg | Gly | Lys | Ser | Leu | Asp | Lys | Ser | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Asp | Asp | Lys | Gly | Arg |     |     |     |     |     |     |     |     |     |     |
| 50  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Phe | His | Ile | Leu | Gln | Asn | Ile | Gly | Met | Thr | Ile | Gln | Leu | Leu | Pro |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ile | Thr | Gly | Ile | Pro | Leu | Pro | Phe | Ile | Ser | Tyr | Gly | Gly | Ser | Ala | Leu |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Trp | Ser | Met | Met | Thr | Gly | Ile | Gly | Ile | Val | Leu | Ser | Ile | Tyr | Tyr | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Pro | Lys | Arg | Tyr | Val | Asp | Leu | Tyr | His | Pro | Lys | Ser | Asn |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Xaa | Arg | Glu | Val | Val | Asn | His | Ile | Glu | Gln | Thr | Ile | Xaa | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Gly | Val | Asn | Glu | Met | Ser | Phe | Asp | Thr | Met | Val | Leu | Phe | Gly | Asp |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Xaa | Ala | Ser | Pro | His | Gly | Thr | Pro | Gly | Asp | Arg | Arg | Leu | Lys | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Glu | Tyr | Val | Leu | Phe | Asp | Leu | Gly | Val | Ile | Tyr | Glu | His | Tyr | Cys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Asp | Met | Thr | Arg | Thr | Ile | Lys | Phe | Trp |     |     |     |     |     |     |
| 65  |     |     |     |     |     | 70  |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gln | Val | Gly | Asp | Gly | Pro | Xaa | Gln | Arg | Glu | Ile | Val | Phe | Pro | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Thr | Asp | Xaa | Xaa | Ser | Trp | Gly | Gly | Xaa | Thr | Lys |     |     |     |     |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Gly | Pro | Asn | Thr | Glu | Ala | Glu | Phe | Arg | Lys | Glu | Ile | Gln | Leu | Pro |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Gly | Asn | Ala | Ser | Trp | Gly | Val | Gly | Pro | Asn | Thr | Glu | Xaa | Ile | Gly | Phe |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Pro | Ile | Ser | Ser | Asp | Asn | Ala | Ser | Trp | Gly | Val | Gly | Pro | Asn | Lys | Glu |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Asn | Phe | Glu | Lys | Lys | Phe | Tyr | Arg | Gln | Cys | Glu | Leu | Gly | Cys | Gly | Pro |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Gln | His | Arg | Ser | Leu | Arg |     |     |     |     |     |     |     |     |     |     |  |
| 65  |     |     |     |     | 70  |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Thr | Arg | Leu | Phe | Tyr | Met | Phe | Asp | Lys | Glu | Thr | Met | Ile | Ala | Ser |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Met | Gly | Ile | Gly | Gly | Gly | Leu | Gly | Asn | Ala | Ala | Leu | Phe | Thr | Arg | Phe |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Ser | Ala | Ile | Val | Xaa | Tyr | Xaa | Ser | Phe | Asp | Cys | Xaa | Ile | Arg | Lys |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Phe | Lys | Leu | Lys | Thr | Pro | Gly | Arg | Glu | Asp | Glu | Glu | Thr | Glu | Ile | Arg |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asn | Ser | Ser | Val | Ala | Lys | Leu | Pro | Xaa | Asp | Val | Leu | Asp | Xaa | Met | Gly |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Trp | Lys | Arg | Lys | His |     |     |     |     |     |     |     |     |     |     |     |  |
| 50  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Arg | Met | Thr | Glu | Gln | Pro | Ser | Tyr | Tyr | Ser | Ile | Ile | Thr | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Val | Arg | Tyr | Asp | Asn | Arg | Leu | Thr | Asp | Ser | Glu | Lys | Leu | Leu | Phe |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Glu | Ile | Thr | Ser | Leu | Ser | Asn | Lys | Tyr | Gly | Tyr | Cys | Thr | Ala | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Gly | Tyr | Phe | Ala | Lys | Leu | Tyr | Glu | Val | Thr | Lys | Val | Thr | Val | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Arg | Ile | Ala | Asn | Leu | Lys | Glu | Cys | Gly | Tyr | Leu | His | Val | Glu | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ile | Arg | Asn | Gly | Asn | Glu | Ile | Lys | Gln | Arg | Lys | Leu | Tyr | Pro | Leu | Thr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Met | Ile | Arg | Pro | Ile | Asn | Thr | Asn | Asp | Asn | Thr | Pro | Ile | Asn | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Val | Asn | Thr | Pro | Ile | Ile | Thr | Asn | Val | Lys | Glu | Thr | Ile | Gln | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Ile | Ile | Gln | Val | Ile | Thr | Ile |     |     |     |     |     |     |     |     |
|     | 130 |     |     |     |     |     | 135 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Phe | Xaa | Ala | Ala | Ile | Arg | Met | Asp | Lys | Ser | Gly | Tyr | Ser | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Leu | Tyr | Glu | Gln | Asn | Thr | His | Ile | Gly | Gly | Lys | Val | Asn | Xaa | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Ser | Asp | Gly | Phe | Gly | Phe | Asp | Leu | Gly | Pro | Ser | Ile | Leu | Thr | Met |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Tyr | Ile | Cys | Glu | Lys | Leu | Phe | Glu | Tyr | Ser | Lys | Lys | Gln | Met | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Tyr | Val | Thr | Ile | Lys | Arg | Leu | Xaa | His | Gln | Trp | Arg | Ser | Phe | Phe |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Asp | Gly | Thr | Thr | Ile | Asp | Leu | Tyr | Glu | Gly | Ile | Lys | Glu | Thr | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | His | Asn | Ala | Ile | Leu | Ser | Lys | Gln | Asp | Ile | Glu | Glu | Leu | Gln | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Leu | Asn | Tyr | Thr | Arg | Arg | Ile | Asp | Arg | Ile | Thr | Glu | Lys | Gly | Tyr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Asn | Tyr | Gly | Leu | Asp | Thr | Leu | Ser | Gln | Ile | Ile | Lys | Phe | His | Gly |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Leu | Asn | Ala | Leu | Ile | Asn | Tyr | Asp | Tyr | Val | His | Thr | Met | Gln | Gln |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |
| Ala | Ile | Asp | Lys | Arg | Ile | Ser | Asn | Pro | Tyr | Leu | Arg | Gln | Met | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |
| Tyr | Phe | Ile | Lys | Tyr | Val | Gly | Ser | Ser | Ser | Tyr | Asp | Ala | Xaa | Ala |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |
| Leu | Ser | Met | Leu | Phe | His | Met | Gln | Gln | Glu | Gln | Gly | Xaa | Xaa | Tyr |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |
| Glu | Gly | Gly | Ile | His | His | Xaa | Ala | Asn | Ala | Leu | Glu | Lys | Leu | Ala |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| Glu | Glu | Gly | Val | Thr | Ile | His | Thr | Gly | Ala | Arg | Val | Asp | Asn | Ile |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |
| Thr | Tyr | Gln | Arg | Arg | Val | Thr | Gly | Val | Arg | Leu | Asp | Thr | Gly | Glu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |
| Val | Lys | Ala | Asp | Tyr | Ile | Ile | Ser | Asn | Met | Glu | Val | Ile | Pro | Thr |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |
| Lys | Tyr | Leu | Ile | His | Leu | Gly | Tyr | Ser | Thr | Ile | Lys | Gln | Ile | Arg |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |
| Gly | Ile |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     | 290 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Arg | Thr | Ser | Arg | Gln | Ser | Pro | Phe | Ala | Gln | Arg | Ile | Glu | Gln | Gln |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Gln | Lys | Arg | Leu | Asn | Leu | Pro | Asp | Leu | Pro | Thr | Thr | Thr | Ile | Gly | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Pro | Gln | Ser | Arg | Glu | Val | Arg | Lys | Tyr | Arg | Ala | Asp | Trp | Lys | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Arg | Ile | Thr | Asp | Glu | Ala | Tyr | Glu | Thr | Phe | Leu | Lys | Asn | Glu | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Arg | Trp | Ile | Lys | Ile | Gln | Glu | Asp | Ile | Gly | Leu | Asp | Val | Leu | Val |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| His | Gly | Glu | Phe | Glu | Arg | Asn | Asp | Met | Val | Glu | Phe | Phe | Gly | Glu | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Leu | Gln | Gly | Phe | Leu | Val | Thr | Lys | Phe | Gly | Trp | Val | Gln | Ser | Tyr | Gly |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Arg | Ala | Val | Lys | Pro | Pro | Ile | Ile | Tyr | Gly | Asp | Val | Lys | Trp | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Pro | Leu | Thr | Val | Asp | Glu | Thr | Val | Tyr | Ala | Gln | Ser | Leu | Thr | Asp |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Lys | Pro | Val | Lys | Gly | Met | Leu | Thr | Gly | Pro | Val | Thr | Ile | Leu | Asn | Trp |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |
| Ser | Phe | Glu | Arg | Val | Asp | Leu | Pro | Arg | Lys | Val | Ala | Gln | Asp | Gln | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Leu | Ala | Ile | Asn | Glu | Glu | Val | Leu | Ala | Leu | Glu | Ala | Ala | Gly | Ile |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Lys | Val | Ile | Gln | Val | Asp | Glu | Pro | Ala | Leu | Arg | Glu | Gly | Leu | Pro | Leu |
|     | 195 |     |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Arg | Ser | Glu | Tyr | His | Glu | Gln | Tyr | Leu | Lys | Asp | Ala | Gly | Phe | Ile | Ile |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Lys | Met | Met | Pro | Arg | Lys | Phe | Arg | Val | Leu | Gln | Ile | Gly | Gly | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Leu | Glu | Pro | Ile | Phe | Gln | His | Lys | Lys | Gly | Val | Ser | Trp | Asp | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Asp | Ile | Gly | Leu | Phe | Glu | Phe | Asp | Ser | Gly | Tyr | Val | Glu | Ala | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Ala | Ile | Val | Glu | Ala | Glu | Gly | Arg | Phe | Asp | Phe | Ile | Tyr | Ile | Gln |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Pro | Tyr | Ser | Glu | Thr | Leu | Thr | Asn | Leu | Leu | Gln | Met | Ile | Ser | Glu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Pro | Tyr | Asn | Thr | Tyr | Val | Asp | Glu | Ser | Phe | Trp | Ser | Val | Glu | Tyr | Glu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gln | Asp | Glu | Asn | Cys | Pro | Lys | Ile | Arg | Cys | Ser | Thr | Asn | Tyr | Ile | Thr |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Ile | Leu | Glu | Gly | Thr |     |     |     |     |     |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 115 |

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Arg | Lys | Gly | Tyr | Tyr | Pro | Ile | Lys | Arg | Ala | Ile | Asp | Leu | Val | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Ile | Val | Leu | Leu | Phe | Leu | Thr | Phe | Pro | Ile | Met | Phe | Ile | Phe | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |     |     |
| Ile | Ala | Ile | Val | Ile | Asp | Ser | Pro | Gly | Asn | Pro | Ile | Tyr | Ser | Gln | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Val | Gly | Lys | Met | Gly | Lys | Leu | Ile | Lys | Ile | Tyr | Lys | Leu | Arg | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Met | Cys | Lys | Asn | Ala | Glu | Lys | Asn | Gly | Ala | Gln | Trp | Ala | Asp | Lys | Asp |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asp | Asp | Arg | Ile | Thr | Asn | Val | Gly | Lys | Phe | Ile | Arg | Lys | Thr | Arg | Ile |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     | 95  |     |     |
| Asp | Glu | Leu | Pro | His | Leu | Ile | Asn | Val | Val | Lys | Gly | Glu | Met | Ser | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Gly | Pro | Arg | Pro | Glu | Arg | Pro | Glu | Phe | Val | Glu | Leu | Phe | Ser | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Glu | Val | Ile | Gly | Phe | Glu | Gln | Arg | Cys | Leu | Val | Thr | Pro | Gly | Leu | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Leu | Ala | Gln | Ile | Gln | Gly | Gly | Tyr | Asp | Leu | Thr | Pro | Gln | His | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |



Leu Lys Tyr Asp Met Lys Tyr Ile His Lys Gly Ser Leu Met Met Glu  
                           165                          170                          175  
 Leu Tyr Ile Ser Ile Arg Thr Leu Met Val Val Ile Thr Gly Glu Gly  
                           180                          185                          190  
 Ser Arg

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

Val Lys Ala Leu Lys Leu Tyr Gly Val Glu Asp Leu Arg Tyr Glu Asp  
 1                          5                          10                          15  
 Asn Glu Lys Pro Val Ile Glu Ser Ala Asn Asp Val Ile Val Lys Val  
                           20                          25                          30  
 Arg Ala Thr Gly Ile Cys Gly Ser Asp Thr Ser Arg Asn Xaa Xaa Met  
                           35                          40                          45  
 Gly Pro Tyr Ile Lys Gly Met Pro Phe Gly His Glu Phe Ser Gly Val  
                           50                          55                          60  
 Val Asp Ala Ile Gly Ser Asp Val Thr His Val Asn Val Gly Asp Lys  
 65                          70                          75                          80  
 Val Thr Gly Cys Pro Ala Ile Pro Cys Tyr Gln Cys Glu  
                           85                          90

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

Val Gly Glu Ala Glu Ser Ser Leu Ser Phe Ile Gly Glu Leu Asp Asn  
 1                          5                          10                          15  
 Ile Asp Asp Lys Thr Tyr Gln Asp Ala Leu Val Ile Val Cys Asp Thr  
                           20                          25                          30  
 Ala Asn Ala Pro Arg Ile Asp Asp Glu Arg Tyr Ser Thr Gly Ser Lys  
                           35                          40                          45  
 Leu Ile Lys Ile Asp His His Pro Ala Val Asp Gln Tyr Gly Asp Ile  
                           50                          55                          60  
 Asn Leu Val Asn Thr Asn Ala Ser Ser Thr Ser Glu Ile Ile Tyr Asp  
 65                          70                          75                          80  
 Leu Ile Ser His Phe Asn Asp Glu Ala Ile Val Asn Lys Gly Thr Ser  
                           85                          90                          95  
 Glu Cys Phe Ile Pro Trp Tyr Arg Arg  
                           100                          105

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Met | Ser | Leu | Val | Ile | Val | Leu | Ile | Lys | Asp | Gly | Cys | Val | Ser | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Ser | Leu | Ile | Arg | Gln | Gly | Asn | Met | Ile | Lys | Arg | Asp | Xaa | Pro | Met |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Ile | Pro | Leu | His | Gln | Thr | Glu | Glu | Glu | Phe | Tyr | Thr | Phe | Ile | Gly |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Gln | Phe | Tyr | Ser | Leu | Asn | Gln | His | Ile | Leu | Pro | Lys | Glu | Val | His | Val |
|     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |
| Pro | Arg | Asn | Leu | Asp | Lys | Glu | Met | Ile | Gln | Ser | Val | Val | Asp | Thr | Lys |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Val | Gln | Pro | Ala | Arg | Gly | Pro | Lys | Lys | Asp | Met | Val | Asp | Leu | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ala | His | Asn | Ala | Lys | Val | Ser | Leu | Asn | Asn | Lys | Phe | Glu | Leu | Ile | Ser |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Arg | Asp | Glu | Ser | Arg | Thr | Ile | Lys | Ala | Ile | Glu | Glu | Leu | Gly | Thr | Gln |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Met | Gly | Ile | Gln | Thr | Pro | Ile | Arg | Ile | Glu | Ala | Phe | Asp | Asn | Ser | Asn |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| Ile | Gln | Gly | Val | Asp | Pro | Val | Ser | Ala | Met | Val | Thr | Phe | Val | Asp | Gly |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Lys | Pro | Asp | Lys | Lys | Asn | Tyr | Arg | Lys | Tyr | Lys | Ile | Lys | Thr | Val | Lys |
|     |     | 165 |     |     |     | 170 |     |     |     |     |     |     | 175 |     |     |
| Gly | Pro | Asp | Asp | Tyr | Lys | Ser | Met | Arg | Glu | Val | Val | Arg | Arg | Arg | Tyr |
|     |     | 180 |     |     |     | 185 |     |     |     |     |     |     | 190 |     |     |
| Ser | Arg | Val | Leu | Asn | Glu | Gly | Leu | Pro | Leu | Pro | Asp | Leu | Ile | Ile | Val |
|     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |
| Asp | Gly | Gly | Lys | Gly | His | Met | Asn | Gly | Val | Ile | Asp | Val | Leu | Gln | Asn |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Glu | Leu | Gly | Leu | Asp | Ile | Pro | Val | Ala | Gly | Leu | Gln | Lys | Asn | Asp | Lys |
| 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| His | Gln | Thr | Ser | Glu | Leu | Leu | Leu | Trp | Arg |     |     |     |     |     |     |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Gln | Xaa | Thr | Arg | Phe | His | Asn | Ile | Cys | Pro | His | Lys | Gln | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Leu | Ser | Glu | Gly | Thr | Val | Ser | Gly | Glu | Tyr | Val | Phe | Cys | Pro | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Asp | Gln | Lys | Ile | Asp | Leu | Asn | Thr | Gly | Ile | Val | Gln | Glu | Pro | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

Glu Gly Cys Val Asp Val Tyr Glu Val Glu Val Thr Asp Gly Asn Val  
 50 55 60  
 Tyr Ile Cys Leu  
 65

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

Val His Val Leu Ala Phe Leu Thr Lys His His Ser Glu Lys Phe Asn  
 1 5 10 15  
 Ser Ser Ser Leu Ala Glu Leu Thr Cys Leu Xaa Pro Val Gln Leu Arg  
 20 25 30  
 Arg Val Thr Thr Gln Leu Val Asp Leu Xaa Met Ile Asp Thr Ile Arg  
 35 40 45  
 Gly Lys Asp Gly Gly Tyr Leu Ala Asn Asp Gln Ser Ala Asp Val Ser  
 50 55 60  
 Leu Ala Thr Leu Tyr Lys His Phe Val Leu Glu Lys Glu Gln His Thr  
 65 70 75 80  
 Arg Leu Phe Thr Trp Arg Arg Arg Gln Ser Leu Ser Asn Cys Ser  
 85 90 95

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

Val Gly Phe Leu Asn His Met Leu Thr Leu Phe Thr Phe His Ser Gly  
 1 5 10 15  
 Leu Ser Leu Asn Ile Glu Ala Gln Gly Asp Ile Asp Val Asp Asp His  
 20 25 30  
 His Val Thr Glu Asp Ile Gly Ile Val Ile Gly Gln Leu Leu Leu Glu  
 35 40 45  
 Met Ile Lys Asp Lys Lys His Phe Val Arg Tyr Gly Thr Met Tyr Ile  
 50 55 60  
 Pro Met Asp Glu Thr Leu Ala Arg Val Val Val Asp Ile Ser Gly Arg  
 65 70 75 80  
 Pro Tyr Leu Ser Phe Asn Ala Ser Leu Ser Lys Glu Lys Val Gly Thr  
 85 90 95  
 Phe Asp Thr Glu Leu Val Glu Glu Phe Phe Arg Ala Val Val Ile Asn  
 100 105 110  
 Ala Arg Leu Thr Thr His Ile Asp Leu Ile Arg Gly Gly Asn Thr His  
 115 120 125  
 His Glu Ile Glu Ala Ile Phe Lys Ala Phe Ser Arg Ala Leu Gly Ile  
 130 135 140  
 Ala Leu Thr Ala Thr Asp Asp Gln Arg Val Pro Ser Ser Lys Gly Val

145  
Ile Glu

150

155

160

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Thr | Ala | Met | Gly | Asn | Leu | Lys | Gln | Gly | Ile | Ala | Asn | Lys | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | Val | Lys | Ala | Ser | Glu | Asn | Tyr | His | Asp | Ala | Asp | Val | Asp | Lys | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Ala | Tyr | Thr | Asn | Ala | Val | Ser | Gln | Ala | Glu | Gly | Ile | Ile | Asn | Gln |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Thr | Asn | Pro | Thr | Leu | Asn | Pro | Asp | Asp | Ile | Thr | Pro | Cys | Ile | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Ser | Asp |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Glu | Ala | Gln | Lys | Asp | Val | Ala | Asn | Val | Leu | Glu | Asn | Val | Glu | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Asp | Ala | Xaa | Val | Gly | Ala | Thr | Asp | Thr | Ile | Ala | Leu | Ala | Ala | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Tyr | Tyr | Ser | Asp | Lys | Asn | Asp | Val | Met | Lys | Pro | His | Gln | Ile | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Xaa | Gly | Gly | Asp | Pro | Met | Thr | Gln | Leu | Val | Ser | Pro | Ser | Ile | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Thr | Ile | His | Tyr | Asn | Tyr | Cys | Glu | Ala | Gly | Gln | Cys | Ala | Arg | Trp | Gln |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Arg | Tyr | Asn | Arg | Cys | Leu | Lys | Ser | Lys | Ile | Cys | His | Ile | Ala | Ser | Gln |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Xaa | Asp | Cys |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asp | His | Glu | Val | Phe | Gln | Gln | Phe | Gly | Glu | Ser | Leu | Pro | Val | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Pro | Thr | Leu | Pro | Pro | Met | Val | Phe | Gly | Asn | Arg | Asp | Lys | Lys | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Xaa | Gly | Gly | Thr | Asp | Ala | Leu | Val | Leu | Arg | Tyr | Leu | Thr | Pro | His | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Xaa | Trp | Asn | Ile | His | Ser | Met | Tyr | Gln | Asp | Asn | Lys | His | Met | Leu | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Phe | Arg | Gly | Val | His | Arg | Phe | Gly | Tyr | Xaa | Met | Lys | Met | Leu | Xaa |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asn | Thr | Ile | Ser | Lys | Ile | Met | Ile | Gly |     |     |     |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Tyr | Xaa | Arg | Asn | Gly | Val | Val | Thr | Ala | Arg | Ala | Val | Ile | Ser | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Met | Pro | Lys | Gly | Thr | Met | Phe | Met | Tyr | His | Ala | Gln | Asp | Lys | His |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Gln | Thr | Pro | Gly | Ser | Glu | Ile | Thr | Asp | Thr | Arg | Gly | Gly | Ser | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Ala | Pro | Thr | Arg | Ile | His | Leu | Lys | Pro | Thr | Gln | Leu | Val | Gly | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Ala | Gln | Ile | Ser | Tyr | His | Phe | Asn | Tyr | Tyr | Gly | Pro | Ile | Gly | Asn |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gln | Arg | Asp | Leu | Tyr | Val | Ala | Val | Arg | Lys | Met | Lys | Glu | Val | Asn | Trp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Glu | Asp |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Trp | Gly | Thr | Asn | Pro | Glu | Met | Gly | Val | Asn | Phe | Ser | Glu | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Pro | Glu | Ile | Asn | Asp | Ile | Asn | Asp | Gln | Arg | Ala | Tyr | Asp | Tyr | Met |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Leu | Glu | Pro | Gly | Gln | Lys | Ala | Glu | Asp | Ile | Asp | Leu | Gly | Tyr | Val |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Leu | Gly | Ser | Cys | Thr | Asn | Ala | Arg | Leu | Ser | Asp | Leu | Ile | Glu | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | His | Ile | Val | Lys | Gly | Asn | Lys | Val | His | Pro | Asn | Ile | Thr | Ala | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Val | Pro | Gly | Ser | Arg | Thr | Val | Lys | Lys | Glu | Ala | Glu | Lys | Leu | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Asp | Thr | Ile | Phe | Lys | Asn | Ala | Gly | Phe | Glu | Trp | Arg | Glu | Pro | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Cys | Ser | Met | Cys | Leu | Gly | Met | Asn | Pro | Asp | Gln | Val | Pro | Glu | Gly | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| His | Cys | Ala | Ser | Thr | Ser | Asn | Arg | Asn | Phe | Glu | Gly | Arg | Gln | Gly | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Ala | Arg | Thr | His | Leu | Val | Ser | Pro | Ala | Met | Ala | Ala | Ala | Ala | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ile | His | Gly | Lys | Phe | Val | Asp | Val | Arg | Lys | Val | Val | Val |     |     |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Trp | Asn | Arg | His | Val | Leu | Xaa | Gly | Lys | Xaa | Gly | Asp | Pro | Gln | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Tyr | Ile | Asp | Leu | His | Leu | Ile | His | Glu | Val | Thr | Ser | Pro | Gln | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Glu | Gly | Leu | Arg | Leu | Gln | Asn | Arg | Lys | Leu | Arg | Arg | Pro | Asp | Leu |
|     | 35  |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Thr | Phe | Ala | Thr | Leu | Asp | His | Asn | Val | Pro | Thr | Ile | Asp | Ile | Phe | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Lys | Asp | Glu | Ile | Ala | Asn | Lys | Gln | Ile | Thr | Leu | Gln | Lys | Asn |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Ala | Ile | Asp | Phe | Gly | Val | His | Ile | Phe | Asp | Met | Gly | Ser | Asp | Glu | Gln |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Ile | Val | His | Met | Val | Gly | Pro | Glu | Thr | Gly | Leu | Thr | Gln | Pro | Gly |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Lys | Thr | Ile | Val | Cys | Gly | Asp | Ser | His | Thr | Ala | Thr | His | Gly | Ala | Phe |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Gly | Ala | Ile | Ala | Phe | Gly | Ile | Gly | Thr | Ser | Glu | Val | Glu | His | Val | Phe |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ala | Thr | Gln | Thr | Leu | Trp | Gln | Thr | Lys | Pro | Lys | Asn | Leu | Lys | Ile | Asp |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ile | Asn | Gly | Thr | Leu | Pro | Thr | Gly | Val | Tyr | Ala | Lys | Asp | Ile | Ile | Leu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| His | Leu | Ile | Lys | Thr | Tyr | Gly | Val | Asp | Phe | Gly | Thr | Gly | Tyr | Ala | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Phe | Thr | Gly | Glu | Thr | Ile | Lys | Asn | Leu | Ser | Met | Asp | Gly | Arg | Met |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Thr | Ile | Cys | Asn | Met | Ala | Ile | Glu | Gly | Gly | Ala | Lys | Tyr | Gly | Ile | Ile |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Gln | Pro | Asp | Asp | Ile | Thr | Phe | Glu | Tyr | Val | Lys | Gly | Arg | Pro | Phe | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |

Asp Asn Phe Ala Lys Ser Val Asp Lys Trp Arg Glu Leu Tyr Ser Asp  
245 250 255  
Gly Thr Thr Arg Tyr Leu Ile Val  
260

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

Val Ile Ile Asn Lys Val Met Thr Ser Asp Thr Pro Val Thr Ile Val  
1 5 10 15  
Ala Thr Gly Pro Leu Thr Asn Val Ala Thr Ala Leu Ile Arg Asp Pro  
20 25 30  
Arg Ile Ala Glu His Ile Glu Ser Ile Thr Leu Met Gly Gly Gly Thr  
35 40 45  
Phe Gly Asn Trp Thr Ala Tyr Ser Arg Ile Leu Ser Ile Pro Thr Ser  
50 55 60  
Phe Leu Thr Lys Ser Xaa Cys Gly Phe Val Asn Met Pro Leu Gly Val  
65 70 75 80  
Ile

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

Val Ala His Xaa His Val Val Asn Gly Thr Tyr Tyr Leu His Xaa His  
1 5 10 15  
Ile Val Xaa Gly Trp Gln Gly Val Lys Lys Thr Cys Asp Thr Ala Glu  
20 25 30  
Glu Leu Asp Thr Tyr Ile Lys Xaa Ser Asp Val Val Tyr Glu Glu Gln  
35 40 45  
Lys His Leu Xaa Leu Phe  
50

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ala | His | Ile | His | Val | Val | Asn | Gly | Thr | Tyr | Tyr | Phe | His | Gly | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Val | Pro | Gly | Trp | Gln | Gly | Val | Lys | Lys | Thr | Phe | Asp | Thr | Ala | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Leu | Glu | Thr | Tyr | Ile | Lys | Gln | Ser | Asp | Ser | Gly | Ile |     |     |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Cys | Thr | Tyr | Cys | Gly | Val | Gly | Cys | Ser | Phe | Glu | Val | Trp | Thr | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Arg | Glu | Ile | Leu | Lys | Val | Gln | Pro | Ser | His | Asp | Ser | Pro | Ala | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Ile | Ala | Thr | Cys | Val | Lys | Gly | Lys | Phe | Ser | Trp | Gly | His | Ile | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Asp | Gln | Arg | Leu | Thr | Lys | Pro | Leu | Val | Arg | Lys | Asn | Gly | Glu | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| His | Glu | Val | Glu | Trp | Asp | Glu | Ala | Leu | Asn | Val | Ile | Ala | Asp | Asn | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Thr | Ser | Ile | Lys | Glu | Lys | Tyr | Gly | Pro | Asp | Ala | Leu | Ser | Phe | Ile | Ser |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Ser | Lys | Ala | Thr | Asn | Glu | Glu | Ser | Xaa | Leu | Xaa | Gln | Lys | Leu | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Arg | Gln | Val | Ile | Gly | Thr | Asn | Asn | Val | Asp | Ser | Leu | Xaa | Lys | Asp | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Xaa | Lys | His | Leu | Gln | Gln | Lys | Ala | Tyr | Leu | Glu | Arg | Leu | Asp | Thr | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gly | Asp | Ser | Arg |     |     |     |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Lys | Ala | Val | Gly | Glu | Arg | Ile | Pro | Ile | Thr | Ile | Ile | Val | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Leu | Ala | Leu | Ile | Val | Ala | Leu | Ile | Ile | Ala | Ile | Pro | Ile | Gly | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Ser | Ala | Met | Lys | Arg | Asn | Ser | Trp | Leu | Asp | Ile | Thr | Leu | Met | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Ala | Leu | Ile | Gly | Leu | Ser | Ile | Pro | Ser | Phe | Trp | Gln | Gly | Leu | Leu |



|     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|
| 50  |     | 55  |     | 60  |     |
| Phe | Ile | Leu | Ala | Xaa | Ser |
| 65  |     | 70  |     | 75  |     |
| Met | Pro | Glu | His | Pro | Ile |
|     |     | 85  |     | 90  |     |
| Asn | Lys | Tyr | Cys | Cys | Phe |
|     |     | 100 |     | 105 |     |

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ala | Glu | Leu | Leu | Gly | Gly | Ser | Ala | Val | Thr | Glu | Gln | Val | Phe | Asn |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Asn | Gly | Ile | Gly | Arg | Tyr | Ile | Val | Gln | Lys | Gln | Leu | Ile | Pro | Asp |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ile | Pro | Ala | Val | Met | Gly | Gly | Val | Val | Tyr | Ile | Tyr | Gln | Leu |     |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | His | Ile | Ile | Ile | Asp | Gly | Asp | Ala | Cys | Pro | Val | Xaa | Asp | Ser |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Ile | Asp | Leu | Thr | Thr | Glu | Thr | Gly | Ile | Phe | Val | Thr | Ile | Ile | Arg |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Ser | Phe | Ser | His | Phe | Ser | Asn | Gln | Leu | Tyr | Pro | Pro | His | Val | Ser | Thr |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Leu | Tyr | Val | Asp | Asp | Gly | Pro | Asp | Ala | Val | Asp | Tyr | Lys | Ile | Val | Gln |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| Leu | Ser | Thr | Lys | Asp | Asp | Ile | Val | Val | Thr | Gln | Asp | Tyr | Gly | Leu | Ala |
| 65  |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Leu | Leu | Val | Asp | Lys | Val | Leu | Ile | Val | Met | His | His | Asn | Gly | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Ile | Tyr | Asn | Ser | Lys | Asn | Ile | Gln | Gln | Leu | Leu | Asp | Lys | Arg | Tyr | Met |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Asn | Ala | Gln | Ile | Arg | Lys | Gln | Gly | Gly | Arg | His | Lys | Gly | Pro | Pro | Pro |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Phe | Thr | Lys | Gln | Asp | Gln | Lys | Val | Phe | Glu | Gln | Ser | Leu | Leu | Lys | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | His | Arg | Ile | Lys | Glu | Leu | Asp |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Glu | Ser | Leu | Pro | Glu | His | Val | Asp | Thr | Ile | Ile | Asp | Ile | Lys |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |
| Ser | Arg | Thr | Glu | Gly | Glu | Leu | Ile | Thr | Lys | Glu | Lys | Glu | Leu | Val | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Lys | Phe | Thr | Pro | Glu | Asn | Ile | Asp | Asn | Val | Asp | Lys | Glu | Tyr | His |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Glu | Thr | Phe | Gly | Glu | Phe | Asp | Thr | Arg | Arg | Thr | Phe | Glu | Lys | Cys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asp | Ser | Ile | Ile | Leu | Asp | Ala | Ala | Gln | Thr | Pro | Leu | Val | Ile | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Ala | Pro | Arg | Leu | Gln | Ser | Asn | Leu | Phe | His | Ile | Val | Lys | Glu | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Asp | Thr | Leu | Ile | Glu | Asp | Val | His | Phe | Lys | Met | Lys | Lys | Thr | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Glu | Ile | Trp | Leu | Leu | Asn | Gln | Gly | Ile | Glu | Ala | Ala | Gln | Ser | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Asn | Val | Xaa | Asp | Leu | Tyr | Ser | Glu | Gln | Ala | Met | Val | Leu | Val | Arg |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Asn | Ile | Asn | Leu | Ala | Leu | Arg | Ser | Cys | Arg | Met | Phe | Leu | Gly | Ser | Tyr |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Ser | Tyr | Arg | Cys | Lys | Asn | Val | Leu | Lys | Phe | Gly | Cys | Met | Ile | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Gln | Pro | Gly | Gly |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Ser | Leu | Ala | Xaa | Val | Leu | Ile | Ile | Gly | Ile | Gly | Ala | Leu | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Ser | Ile | Ser | Xaa | Asn | Leu | Gly | Arg | Asn | Thr | Val | Leu | Val | Leu | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Ala | Leu | Pro | Xaa | Ile | Tyr | Phe | Thr | Leu | Ile | Ile | Arg | Ser | Xaa | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Xaa | Asp | Thr | Xaa | Arg | Ser | Arg | Val | Lys | Ala | Phe | Ile | Pro | Leu | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Leu | Gly | Met | Val | Phe | Trp | Ala | Ile | Gln | Glu | Gln | Gly | Ser | Asn | Val |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Leu | Asn | Ile | Tyr | Gly | Xaa | Xaa | His | Ser | Asp | Met | Lys | Leu | Asn | Leu | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Trp | Lys | Thr | Xaa | Phe | Gly | Glu | Ala | Ile | Phe | Gln | Ser | Ile | Asn | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Phe | Ile | Leu | Leu | Leu | Ala | Pro | Ile | Ile | Ser | Leu | Leu | Trp | Gln | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Xaa | Gly | Thr | Lys | Gln | Pro | Ser | Leu | Pro | Val | Lys | Phe | Ala | Ile | Gly | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Phe | Leu | Ala | Gly | Ala | Ser | Tyr | Ile | Leu | Ile | Gly | Ile | Val | Gly | Tyr | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ser | Gly | Ser | Ser | Asn | Phe | Ser | Val | Asn | Trp | Val | Ile | Leu | Ser | Tyr | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Cys | Val | Ile | Gly | Glu | Leu | Cys | Leu | Ser | Pro | Thr | Gly | Asn | Ser | Ala |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Ala | Val | Lys | Leu | Ala | Pro | Lys | Ala | Phe | Asn | Ala | Gln | Met | Met | Ser | Ile |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Trp | Tyr | Leu | Thr | Asn | Ala | Ser | Ala | Gln | Ala | Ile | Asn | Gly | Thr | Leu | Val |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Leu | Ile | Glu | Pro | Leu | Gly | Gln | Thr | Asn | Tyr | Phe | Ile | Phe | Leu | Gly |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |     |
| Val | Val | Ala | Ile | Ile | Val | Thr | Thr | Ile | Cys | Ile | Ser | Ile | Leu | Thr | Phe |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Asn | His | Gln | Ser | Asp | Glu | Arg | Tyr | Thr | Leu | Ile | Leu | Leu | Ala |     |     |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Pro | Pro | His | Pro | Asn | Gly | Val | Ser | Gln | Glu | Val | Leu | Ala | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Cys | Tyr | Leu | Thr | Gln | Xaa | Thr | Gln | Val | Xaa | Xaa | Xaa | Gly | Gly | Ala | Xaa |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Ile | Ala | Xaa | Leu | Thr | Tyr | Xaa | Ala | Xaa | Thr | Ile | Pro | Lys | Val | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Ile | Xaa | Gly | Pro | Gly | Thr | Gln | Phe | Val | Ala | Ser | Xaa | Xaa | Lys | Xaa |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Phe | Gly | Gln | Val | Ala | Tyr | Cys | Ser | His | Xaa | Arg | Xaa | Thr | Xaa | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Phe | Gln | Val | Gly | Gly | Ala | Gln | Ser | Ile | Ala | Ala | Leu | Thr | Tyr | Gly |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Thr | Glu | Thr | Ile | Pro | Lys | Val | Asp | Lys | Ile | Val | Gly | Pro | Gly | Asn | Gln |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Phe | Gly | Xaa | Ile | Cys | Pro | Lys | Asn | Ile | Tyr | Leu | Asp | Arg |     |     |     |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Gly | Met | Ser | Ile | Val | Leu | Ala | Gly | Gly | Met | Glu | Asn | Met | Ser | Gln |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Xaa | Pro | Met | Leu | Xaa | Asn | Asn | Ser | Arg | Phe | Gly | Phe | Lys | Met | Gly | His |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| His | Ser | Met | Val | Asp | Ser | Met | Val | Tyr | Asp | Gly | Leu | Thr | Asp | Val | Phe |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Thr | Gln | Tyr | His | Met | Gly | Ile | Thr | Ala | Glu | Asn | Leu | Val | Gly | Ala | Ile |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Trp | Tyr | Phe | Lys | Arg | Arg | Thr | Lys | Ile | His | Val | Ala | Gly | Asn | Leu | Thr |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Thr | Ile | Lys | Gln | Tyr | Val | His | Ser | Lys | Met | Val | Asn | Leu | Ile | Val | Lys |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |

(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Ile | Ser | Met | Lys | Trp | Leu | Ser | Arg | Ile | Leu | Thr | Val | Ile | Val | Thr |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Met | Ser | Met | Ala | Cys | Gly | Ala | Leu | Ile | Phe | Asn | Arg | Arg | His | Gln | Leu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Lys | Thr | Lys | Thr | Leu | Asn | Phe | Asn | His | Lys | Ala | Leu | Thr | Ile | Ile | Ile |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ala | Arg | Asn | Glu | Glu | Lys | Arg | Ile | Gly | His | Leu | Leu | His | Ser | Ile |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Gln | Gln | Gln | Val | Pro | Val | Asp | Val | Ile | Val | Met | Asn | Asp | Gly | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Asp | Glu | Thr | Ala | Arg | Val | Ala | Arg | Ser | Tyr | Gly | Ala | Thr | Val | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Val | Val | Asp | Asp | Thr | Asp | Gly | Lys | Trp | Tyr | Gly | Glu | Ile | Thr | Cys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Leu | Ser | Arg | Cys | Asp | Ala | Cys | Met | Tyr | Glu | Ser | Tyr | Cys | Leu | Cys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Cys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 130 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Ile | Leu | Gly | Thr | Val | Phe | Thr | Ala | Leu | Thr | Gly | Pro | Ile | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Val | Leu | Gly | Val | Leu | Ala | Gly | Leu | Ala | Val | Ala | Phe | Thr | Ile | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Lys | Lys | Ser | Glu | Thr | Phe | Arg | Asn | Cys | Val | Asn | Gly | Ala | Ile | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Val | Lys | Gln | Thr | Phe | Ser | Asn | Phe | Ile | Gln | Phe | Ile | Gln | Pro | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Asp | Ser | Val | Lys | Asn | Val | Phe | Lys | Gln | Ala | Val | Ser | Ala | Ile | Gly |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Asp | Phe | Ala | Lys | Asp | Ile | Trp | Ser | Gln | Ile | Asn | Gly | Phe | Phe | Asn | Glu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Gly | Ile | Ser | Ile | Ala | Gln | Ala | Leu | Gln | Asn | Ile | Cys | Asn | Phe | Ile |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |     |
| Lys | Ala | Ile | Phe | Glu | Phe | Ile | Leu | Lys | Phe | Cys | Asn |     |     |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Lys | Ser | Leu | Lys | Thr | Val | Ile | Gly | Met | Asn | Asn | Lys | Glu | His | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Ser | Val | Ile | Leu | Ala | Leu | Leu | Val | Leu | Met | Ser | Val | Val | Leu | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Met | Val | Trp | Asn | Phe | Ser | Pro | Asp | Ile | Ala | Asn | Val | Asp | Asn | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Ser | Lys | Lys | Ser | Glu | Thr | Lys | Pro | Leu | Thr | Thr | Pro | Met | Thr | Ala |

|                         |                                             |                         |     |    |  |
|-------------------------|---------------------------------------------|-------------------------|-----|----|--|
| 50                      |                                             | 55                      |     | 60 |  |
| Lys Met Asp Thr Thr     | Ile Thr Pro Phe Gln                         | Ile Ile His Ser Lys Asn |     |    |  |
| 65                      | 70                                          | 75                      | 80  |    |  |
| Asp His Pro Glu Gly     | Thr Ile Ala Thr Val Ser Asn Val Asn Lys Leu |                         |     |    |  |
|                         | 85                                          | 90                      | 95  |    |  |
| Thr Lys Pro Leu Lys     | Asn Lys Glu Val Xaa Ser Val Glu His Val Arg |                         |     |    |  |
|                         | 100                                         | 105                     | 110 |    |  |
| Arg Asp His Asn Leu Met | Ile Pro Asp Leu Ser Ser Asp Phe Thr Leu     |                         |     |    |  |
|                         | 115                                         | 120                     | 125 |    |  |
| Phe Asp Phe Thr Phe Asp | Leu Pro Leu Ser Thr Tyr Leu Gly Gln Val     |                         |     |    |  |
|                         | 130                                         | 135                     | 140 |    |  |
| Xaa Glu His             |                                             |                         |     |    |  |
| 145                     |                                             |                         |     |    |  |

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Val Ile Leu Pro Lys Leu Val Thr Tyr Gln Val Gln Pro Met Ser Met |  |
| 1 5 10 15                                                       |  |
| Met Leu Ile Pro Lys Gly Xaa Xaa Glu Leu Ala Leu Arg Phe Asn Gln |  |
| 20 25 30                                                        |  |
| Gly Ile Asn Xaa Gly Gly Asp Ala Leu Lys Lys Arg Thr His Phe Asn |  |
| 35 40 45                                                        |  |
| Ile Ala Gly Ala Phe Asn Pro Asp Val Arg Lys Leu Asp Gly Ala Val |  |
| 50 55 60                                                        |  |
| Xaa Arg Leu Glu Xaa Lys Asp Xaa Lys Arg Asn Val Leu Phe Xaa Asn |  |
| 65 70 75 80                                                     |  |
| Thr Thr Arg Val Gln Gln Arg Glu Asn His                         |  |
| 85 90                                                           |  |

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Val Leu Val Gln Pro His Ile Val Ile Lys Pro Glu Ala Gln Gln Ala |  |
| 1 5 10 15                                                       |  |
| Ile Lys Ala Thr Ala Glu Asn Gln Val Glu Ser Ile Lys Asp Thr Pro |  |
| 20 25 30                                                        |  |
| His Ala Thr Val Asp Glu Leu Asp Glu Ala Asn Gln Leu Ile Ser Asp |  |
| 35 40 45                                                        |  |
| Thr Leu Lys Gln Ala Gln Gln Glu Ile Glu Asn Thr Asn Gln Asp Ala |  |
| 50 55 60                                                        |  |
| Ala Val Thr Asp Val Arg Asn Gln Thr Ile Lys Ala Ile Glu Gln Ile |  |
| 65 70 75 80                                                     |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Pro | Lys | Val | Arg | Arg | Lys | Arg | Ala | Ala | Leu | Asp | Ser | Ile | Glu | Glu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Xaa | Lys | Asn | Gln | Leu | Gly | Cys | Asn | Pro | Glu | Ile | Arg | Gly | Ile | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Lys | Asp | Glu | Arg | Asp | Cys | Trp | Leu | Leu | Asp | Thr | Phe | Lys |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Leu | Leu | Pro | Leu | Ile | Ser | Asp | Asn | Met | Tyr | Leu | Gly | Tyr | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Gly | Leu | Leu | Ala | Ala | Tyr | Ala | Gly | Gly | Phe | Val | Cys | Thr | Tyr | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Gly | Pro | Thr | Lys | Ala | Met | Arg | Gln | Asp | Arg | Phe | Val | Gly |     |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Xaa | Xaa | Ile | Met | Lys | Phe | Lys | Ala | Ile | Ala | Lys | Xaa | Ser | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Leu | Gly | Met | Leu | Ala | Thr | Gly | Val | Ile | Thr | Ser | Asn | Val | Gln | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Gln | Ala | Xaa | Thr | Glu | Val | Xaa | Gln | Gln | Ser | Glu | Ser | Glu | Leu | Xaa |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Tyr | Tyr | Asn | Lys | Pro | Val | Leu | Glu | Arg | Lys | Asn | Val | Thr | Gly | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Xaa | Tyr | Thr | Glu | Lys | Gly | Lys | Asp | Tyr | Ile | Asp | Val | Ile | Val | Asp | Asn |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Gln | Tyr | Ser | Gln | Ile | Ser | Leu | Val | Arg | Ile |     |     |     |     |     |     |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Asn | Ile | Glu | Leu | Val | Leu | His | Gln | Arg | Xaa | Ala | Asn | Pro | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Ile | Ala | Asn | Ile | Ser | Asn | Asn | Ala | Thr | Val | Ser | Gln | Ala | Asp | Gln |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Thr | Ile | Ile | Asn | Ser | Leu | Thr | Phe | Thr | Ser | Asn | Ala | Pro | Asn | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Tyr | Ala | Thr | Ala | Ser | Ala | Asn | Glu | Ile | Thr | Ser | Lys | Thr | Val | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Val | Ser | Arg | Thr | Gly | Asn | Asn | Ala | Asn | Val | Thr | Val | Thr | Val | Thr |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| His | Gln | Asp | Gly | Thr | Thr | Ser | Thr | Val | Thr | Val | Pro | Val | Lys | His | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Pro | Glu | Ile | Val | Ala | His | Ser | His | Tyr | Thr | Val | Gln | Gly | Gln | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Pro | Ala | Gly | Asn | Gly | Ser | Ser | Ala | Ala | Asp | Tyr | Phe | Lys | Leu | Ser |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Gly | Ser | Ala | Ile | Pro | Asp | Ala | Thr | Ile | Thr | Trp | Val | Ser | Gly | Gln |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Xaa | Pro | Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Met | Glu | Asn | Ser | Arg | Pro | Glu | Arg | Asn | Glu | Ala | Thr | Met | His | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Glu | Met | Thr | Val | Glu | Glu | Ala | Leu | Ile | Thr | Met | Asn | Lys | Glu | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Gln | Val | Pro | Leu | Ala | Val | Arg | Lys | Ala | Ile | Pro | Gln | Leu | Thr | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Ile | Lys | Lys | Thr | Ile | Ala | Gln | Tyr | Lys | Lys | Gly | Gly | Arg | Leu | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Ile | Gly | Ala | Gly | Thr | Ser | Gly | Arg | Leu | Gly | Val | Leu | Asp | Ala | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Cys | Val | Pro | Thr | Phe | Asn | Thr | Asp | Pro | His | Glu | Ile | Ile | Gly | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Ala | Gly | Gly | Gln | His | Ala | Met | Thr | Met | Ala | Val | Glu | Gly | Ala | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | His | Lys | Lys | Leu | Ala | Glu | Glu | Asp | Leu | Lys | Asn | Ile | Asp | Leu | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Lys | Asp | Val | Val | Ile | Gly | Ile | Ala | Ala | Ser | Gly | Lys | Thr | Pro | Tyr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Ile | Gly | Gly | Leu | Thr | Phe | Ala | Asn | Thr | Ile | Gly | Ala | Thr | Thr | Val |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Ile | Ser | Cys | Asn | Glu | His | Ala | Val | Ile | Ser | Glu | Ile | Ala | Gln | Tyr |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Pro | Val | Glu | Val | Lys | Val | Gly | Pro | Glu | Val | Leu | Thr | Gly | Ser | Xaa | Arg |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Leu | Lys | Ser | Gly | Thr | Ala | Gln | Lys | Leu | Ile | Leu | Asn | Met | Ile | Ser | Thr |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Thr | Met | Val | Gly | Val | Gly | Lys | Val | Tyr | Asp | Asn | Leu | Met | Ile | Asp |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Lys | Ala | Thr | Asn | Gln | Lys | Leu | Ile | Asp | Arg | Ser | Val | Arg | Ile | Ile |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gln | Glu | Ile | Cys | Ala | Ile | Thr | Tyr | Asp | Glu | Ala | Met | Ala | Leu | Tyr | Gln |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Ser | Glu | His | Asp | Val | Glu | Ser | Cys | Asp | Ser | Tyr | Gly | Tyr | Val | Trp |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| His | Phe |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Xaa | Xaa | Ile | His | Ser | Gln | Gln | Ile | Val | Ile | Ala | Pro | Asp | Ser | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Glu | Ser | Met | Xaa | Xaa | His | Gln | Val | Xaa | Asn | Ile | Ile | Lys | Gln | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Phe | Thr | Asn | Val | Tyr | Gly | Asn | Thr | Leu | His | Tyr | Asp | Ile | Ile | Pro | Met |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Pro | Asp | Gly | Gly | Glu | Gly | Thr | Xaa | Asp | Xaa | Leu | Ile | His | Ala | Xaa | Xaa |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Ala | Thr | Lys | Tyr | Thr | Val | Ile | Val | Asn | Asp | Pro | Leu | Met | Arg | Pro | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Ala | Cys | Tyr | Ala | Arg | Ala | Asp | Glu | Gln | Gln | Ile | Ala | Ile | Ile | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Met | Ala | Ala | Ala | Ser | Gly | Leu | Asp | Leu | Leu | Glu | Lys | Glu | Glu | Arg | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Leu | Tyr | Thr | Ser | Ser | Tyr | Gly | Thr | Gly | Glu | Leu | Ile | Lys | Asp | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Asn | His | Gly | Ala | Lys | Thr | Ile | Ile | Leu | Gly | Ile | Gly | Gly | Ser | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Asn | Asp | Gly | Gly | Thr | Gly | Met | Leu | Ser | Ala | Leu | Gly | Val | Lys | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Thr | Asp | Val | Asn | Gly | Asp | Leu | Leu | Gln | Met | Asn | Gly | Ala | Asn | Leu | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| His | Ile | Ala | Gln | Ile | Asp | Ile | Thr | Asn | Leu | Ala | Asp | Ser | Arg | Xaa | Lys |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Val | Thr | Phe | Lys | Val | Ala | Cys | Asp | Val | Ser | Asn | Pro | Leu | Leu | Gly |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Glu | Asn | Gly | Ala | Thr | Tyr | Ile | Tyr | Gly | Pro | Gln | Lys | Cys | Ala | Asp | Ala |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Lys | Met | His | Thr |     |     |     |     |     |     |     |     |     |     |     |     |
| 225 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Lys | Gln | Cys | Ile | Asn | Asn | Asp | Glu | Trp | Phe | Val | Thr | Asn | Asp | Asn |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Gly | Tyr | Val | Lys | Glu | Gln | Tyr | Leu | Tyr | Xaa | Ala | Gly | Arg | Gln | Gln | Asp |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Met | Leu | Ile | Ile | Gly | Gly | Arg | Asn | Ile | Tyr | Pro | Ala | His | Val | Xaa | Arg |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Leu | Leu | Thr | Gln | Ser | Ser | Ser | Ile | Asp | Glu | Ala | Ile | Ile | Ile | Gly | Ile |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Pro | His | Glu | Arg | Phe | Gly | Xaa | Ile | Gly | Val | Leu | Leu | Tyr | Ser | Gly | Asp |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Val | Thr | Leu | Thr | His | Lys | Asn | Xaa | Lys | Gln | Phe | Xaa | Lys | Lys | Lys | Val |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Lys | Arg | His | Glu | Ile | Pro | Phe | Asp | Asp | Ser | Ser | Cys | Arg | Lys | Asp | Val |  |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |  |
| Leu | Xaa | Cys | Lys | Trp |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Ser | Ala | Ile | Phe | Glu | Pro | Glu | His | Leu | Glu | Ala | Leu | Leu | Ala | Gln |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Val | Ser | Ile | Lys | Pro | Val | Ile | Asn | Gln | Val | Glu | Tyr | His | Pro | Tyr | Leu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Thr | Gln | His | Lys | Leu | Lys | Leu | Tyr | Leu | Ala | Ala | Gln | His | Ile | Val | Met |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Glu | Ser | Trp | Ser | Pro | Leu | Met | Asn | Ala | Gln | Ile | Leu | Asn | Asp | Glu | Thr |  |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ile | Lys | Asp | Ile | Ala | Gln | Glu | Leu | Gly | Lys | Ser | Pro | Ala | Gln | Val | Val |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Leu | Arg | Trp | Asn | Val | Gln | His | Gly | Val | Val | Ile | Ile | Pro | Lys | Ser | Val |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Thr | Pro | Asn | Arg | Ile | Ser | Glu | Asn | Phe | Gln | Ile | Phe | Asp | Phe | Glu | Leu |  |
|     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |  |
| Ser | Asp | Glu | Gln | Met | Thr | Leu | Val | Pro | Gly | Leu | Asn | Leu | Asp | Lys | Arg |  |
|     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |  |
| Ile | Gly | Pro | Asp | Xaa | Xaa | Thr | Phe | Glu | Gly |     |     |     |     |     |     |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

```
Val Phe Lys Gly Ser Glu Tyr Gln Leu Ser Glu Ile Asn Ser Gly Ser
 1 5 10 15
Val Lys Tyr Glu Gln Thr Tyr Asp Asn Phe Pro Ile Leu Asn Asn Ser
 20 25 30
Lys Ala Met Leu Asn Phe Asn Ile Glu Asp Asn Lys Ala Ala Ser Tyr
 35 40 45
Lys Gln Ser Met Met Asp Asp Ile Lys Pro Thr Asp Gly Ala Asp Lys
 50 55 60
Lys His Gln Val Ile Gly Val Arg Lys Ala Ile Glu Ala Leu
65 70 75
```

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

```
Val Asn Glu Thr Asn Val Gln Leu Leu Gln Pro Asn Trp Glu Ile Lys
 1 5 10 15
Val Lys His Asp Gly Lys Asp Lys Thr Asn Thr Tyr Tyr Val Glu Ala
 20 25 30
Thr Asn Asn Asn Pro Lys Ile Ile Asn His
 35 40
```

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

```
Val Leu Ile Tyr Phe Ile Glu Gly Leu Met Ser Xaa Asn Gln Pro Ala
 1 5 10 15
Glu Ala Leu Glu Xaa Leu Ser Tyr Val Asp Pro Ser Pro Xaa Xaa Leu
 20 25 30
Met Xaa Lys Lys
 35
```

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

```
Val Gly Ile Asn Ser Lys Gln Gly Lys Asn Leu Ile Gly Ala Phe Tyr
 1 5 10 15
Arg Pro Thr Ala Val Ile Tyr Asp Leu Asp Phe Leu Lys Thr Leu Pro
 20 25 30
Phe Glu Gln Ile Leu Ser Gly Tyr Ala Glu Val Tyr Lys His Ala Leu
 35 40 45
Leu Asn Gly Glu Ser Thr Thr Gln Glu Ile Glu Gln His Phe Lys Asp
 50 55 60
Arg Glu Ile Leu Gln Pro Leu Asn Gly Ile Gly
65 70 75
```

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

```
Val Val Thr Leu Phe Leu Cys Pro Xaa Asn Ser Phe Leu Met Ile His
 1 5 10 15
Asn Ser Trp Val Met Thr Val Gly Asn Ala Glu Glu Leu Arg Lys Thr
 20 25 30
Ala Asp Leu Leu Glu Lys Thr Asp Ala Val Ser Asn Ser Ala Tyr Leu
 35 40 45
Asp Lys Xaa Xaa Asp Leu Asp Gln Glu His Leu Lys Gln Met Leu Asp
 50 55 60
Ala Glu Thr Trp Leu Thr Ala Glu Glu Ala Leu Ser Phe Gly Leu Ile
65 70 75 80
Asp Glu Ile Leu Gly Ala Asn Glu Ile Ala Ala Ser Ile Ser Lys Glu
 85 90 95
Gln Cys Arg Arg Xaa Glu Xaa Val Pro Glu Asp Leu Lys Lys Asp Val
 100 105 110
Xaa Lys Ile Thr Lys Ile Asp Asp Xaa Arg Tyr Asp Leu Asp Trp Leu
 115 120 125
Lys Pro Pro Lys Glu Ser Met Ser Leu Glu Glu Xaa Xaa Xaa Arg Xaa
 130 135 140
Xaa Ile Val Arg Ser Asn Ala Lys Phe
145 150
```

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

```
Val Lys Glu Ile Pro Asp Ala Ser Ile Ser Phe Glu Val Phe Ala Asp
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Asp | Leu | Glu | Thr | Met | Glu | Lys | Glu | Ala | Ala | Ile | Leu | Lys | Gln | Tyr | Gly |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Glu | Asn | Val | Phe | Val | Lys | Ile | Pro | Ile | Val | Asn | Thr | Lys | Gly | Glu | Ser |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Thr | Ile | Pro | Leu | Ile | Lys | Lys | Leu | Ser | Ala | Asp | Asn | Val | Arg | Leu | Asn |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Val | Xaa | Ala | Val | Tyr | Thr | Ile | Glu | Gln | Gly | Lys | Glu | Ile | Thr | Glu | Ala |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Val | Thr | Glu | Gly | Val | Pro | Asn | Ile | Cys | Phe | Ser | Ile | Cys | Arg | Thr | Tyr |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Cys | Arg | Tyr | Arg | Arg | Arg | Ser | Ile | Thr | Ile | Asn | Glu | Arg | Gly | Cys | Lys |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ser | Tyr | Ala |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     | 115 |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Tyr | Xaa | Arg | Val | Asn | Glu | Met | Asn | Ala | Lys | Glu | Xaa | Leu | Val | Asp |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Xaa | Leu | Met | Lys | Thr | Ser | Ser | Gln | Leu | Phe | Lys | Xaa | His | Gly | Glu | Val |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
| Xaa | Met | Gln | Leu | Xaa | Leu | Asn | Asp | Glu | Leu | Lys | Leu | Pro | Ser | Ile | Xaa |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
| Glu | Ile | Cys | Val | Glu | Arg | Lys | Arg | Leu | Ser | Asp | Ile | Val | Lys | Val | Ile |  |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |  |
| Pro | Gln | Ser | Tyr | Ala | Leu | Leu | Tyr | Ile | Asp | Lys | Gln | Asp | Gln | Ala | Arg |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Ala | Lys | Xaa | Xaa | Leu | Ser | Leu | Xaa | Lys | Ile | Ala | Lys | Val | Tyr | Val | Gln |  |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |  |
| Tyr | Asp | Asp | Thr | Thr | Ile | Met | Ser | Ile | Phe | Val | Tyr | Asp | Val | Val | Asn |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Asp | Glu | Trp | Ile | Leu | Arg | Leu | Asp | Pro | Asn | Ile | Arg | Ile | Pro | Lys | Ser |  |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |  |
| Asn | Ile | Tyr | Phe | His | Ser | Leu | Asn | Trp | Asp | Val | Asp | Tyr | Ile | Lys | Pro |  |
|     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |     |  |
| Glu | Ile | Val | Leu | Met | Tyr | Asp | Leu | Met | Gln | His | His | Gln | Tyr | His | His |  |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |  |
| Tyr | Ser | Asn | Tyr | Lys | Arg | Val | Ile | Asp | Xaa | Leu | Ser | Tyr | Tyr | Gln | Phe |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |  |
| Phe | Ile | Leu | Lys | Phe | Val | Val | Gly | Glu | Xaa | Arg | Ile | Lys | Asp | Ala | Ile |  |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |  |
| Gln | Lys | Asn | Asn | Lys |     |     |     |     |     |     |     |     |     |     |     |  |
|     |     | 195 |     |     |     |     |     |     |     |     |     |     |     |     |     |  |

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Pro | Gln | Gln | Gln | Ala | Pro | Thr | Lys | Gln | Arg | Pro | Ala | Lys | Xaa |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Asn | Asp | Asp | Lys | Ala | Ser | Xaa | Asp | Glu | Ser | Lys | Asp | Lys | Asp | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Ala | Ser | Gln | Asp | Xaa | Ser | Asp | Asp | Thr | Gln | Lys | Lys | Thr | Asp | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Thr | His | Pro | Ala | Ala | Arg | Xaa |     |     |     |     |     |     |     |     |
|     | 50  |     |     |     |     |     | 55  |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Met | Leu | Lys | Met | Xaa | Leu | Ile | Lys | Lys | Leu | Thr | Gln | Met | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Leu | Val | Asn | Gln | Asn | Asp | Xaa | Leu | Thr | Asp | Glu | Glu | Lys | Gln | Xaa |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ile | Gln | Val | Ile | Glu | Glu | His | Lys | Asn | Glu | Ile | Ile | Gly | Asn | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Asp | Gln | Thr | Thr | Asp | Asp | Gly | Val | Thr | Arg | Ile | Thr | Arg | Ser | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Thr | Asp | Leu | Lys | Trp | Gly | Tyr | Cys | Asn | Thr | Gly | Cys |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Lys | Trp | Ile | Lys | Arg | Leu | Leu | Lys | Asp | Leu | Lys | Lys | Leu | Ser | Met |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Phe | Lys | Asp | Ile | Leu | Gln | Leu | Val | Pro | Lys | Gln | Leu | Phe | Gly | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Asp | Ala | Glu | Leu | Gln | Leu | Thr | Glu | Ala | Asp | Tyr | Leu | Thr | Ala | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Asp | Ile | Val | Val | Gln | Pro | Gly | Lys | Lys | Leu | Gln | His | Leu | Ser |     |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Leu | Leu | Ser | Gly | Gly | Glu | Arg | Ala | Leu | Thr | Ala | Ile | Ala | Leu | Leu | Phe |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Ile | Leu | Lys | Val | Arg | Ser | Ala | Pro | Phe | Val | Ile | Leu | Asp | Glu | Val |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |
| Glu | Ala | Ala | Leu | Asp | Glu | Ala | Asn | Val | Ile | Arg | Tyr | Ala | Lys | Tyr | Leu |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |
| Asn | Glu | Leu | Ser | Asp | Glu | Thr | Gln | Phe | Ile | Val | Ile | Thr | His | Arg | Lys |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |
| Gly | Thr | Met | Glu | Phe | Ala | Asp | Arg | Leu | Tyr | Gly | Val | Thr | Met | Gln | Glu |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |
| Ser | Gly | Val | Thr | Lys | Leu | Val | Ser | Val | Asn | Leu | Asn | Thr | Ile | Asp | Asp |  |  |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |  |  |
| Val | Leu | Lys | Glu | Glu | Gln |     |     |     |     |     |     |     |     |     |     |  |  |
|     |     |     |     | 165 |     |     |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Val | Arg | Asp | Gln | Phe | Lys | Phe | Tyr | His | Val | Arg | His | Glu | Glu | Val | Ala |  |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |  |  |
| Ser | Leu | Ala | Ala | Ala | Gly | Tyr | Thr | Lys | Leu | Thr | Gly | Xaa | Ile | Gly | Val |  |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |  |
| Ala | Leu | Ser | Ile | Gly | Xaa | Pro | Gly | Leu | Ile | His | Leu | Leu | Asn | Gly | Met |  |  |
|     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |     |  |  |
| Tyr | Asp | Ala | Lys | Met | Asp | Asn | Val | Leu | Val | Pro | Ile | Asn | Ile | Ile | Trp |  |  |
| 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |     |  |  |
| Thr | Asn | Xaa | Ile | Val | Gln | His | Leu | Glu | Arg | Lys | His | Phe | Lys | Lys | Gln |  |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |  |  |
| Ile | Tyr | Lys | Asn | Tyr | Val | Lys | Met |     |     |     |     |     |     |     |     |  |  |
|     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |     |     |  |  |

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Val | Lys | Leu | Ser | Xaa | Tyr | Tyr | Pro | Gln | Gly | Leu | Arg | Ser | Leu | Asn | Gly |  |  |
| 1   |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |  |
| Gly | Arg | Met | Ala | Arg | Phe | Gly | Arg | Thr | Pro | Leu | Leu | Asp | Ala | Met | Glu |  |  |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |  |
| Met | Ala | Asn | Glu | His | Ile | Met | Val | Ile | Ala | Met | Ile | Glu | Asp | Val | Xaa |  |  |
|     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |     |  |  |
| Gly | Val | Met | Ala | Ile | Asp | Asp | Ile | Ala | Gln | Val | Glu | Gly | Leu | Asp | Met |  |  |
| 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |     |     |  |  |
| Ile | Val | Glu | Gly | Ala | Ala | Gly | Phe | Ile | Ala | Val | Thr | Trp | His | Thr | Xaa |  |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |  |  |
| Ala | Asn | Glu | Arg | Asp | Asp | Gln | Val | Thr | Ser | His | Xaa | Gln | His | Ile | Xaa |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |  |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Val | Val | Asn | Ala | His | Gly | Lys | His | Xaa | Cys | Ala | Leu | Pro | Arg | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Glu | Asp | Ile | Ala | Lys | Trp | Gln | Ala | Gln | Gly | Val | Gln | Thr | Phe | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Gly | Thr | Ser | Gly | Lys | Ile | Tyr | Arg | His | Leu | Ser | Ala | Ser | Leu | Ala |
|     | 130 |     |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| Thr | Ser | Lys | Gln | Lys | Gly | Asp | Asp | Gly |     |     |     |     |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Thr | Ser | Leu | Asp | Ala | Asp | Glu | Ala | Lys | Arg | Asn | Ala | Tyr | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Ala | Val | Thr | Gln | Ala | Xaa | Gln | Ile | Leu | Asn | Lys | Ala | Gln | Gly | Pro |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Asn | Thr | Ala | Lys | Asp | Gly | Val | Glu | Thr | Ala | Leu | Gln | Asn | Val | Gln | Arg |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ala | Lys | Asn | Glu | Leu | Ser | Gly | Asn | Gln | Asn | Val | Ala | Asn | Ala | Lys | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Thr | Ala | Lys | Asn | Ala | Leu | Asn | Asn | Leu | Thr | Ser | Ile | Asn | Asn | Ala | His |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Lys | Ala | Ala | Leu | Lys | Ser | Gln | Ile | Glu | Gly | Ala | Thr | Thr | Val | Ala | Gly |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Val | Asn | Gln | Val | Ser | Thr | Met | Ala | Ser |     |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Thr | Ala | Lys | Thr | Ala | Leu | Asn | Gly | Asp | Ala | Arg | Leu | Asn | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Lys | Asn | Thr | Ala | Lys | Gln | Gln | Leu | Ala | Thr | Met | Ser | His | Leu | Thr |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| Asn | Ala | Gln | Lys | Ala | Asn | Leu | Thr | Glu | Gln | Ile | Glu | Arg | Gly | Thr | Thr |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Val | Ala | Gly | Val | Gln | Gly | Ile | Gln | Ala | Asn | Ala | Gly | Thr | Leu | Asn | Gln |
|     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| Ala | Met | Asn | Gln | Leu | Arg | Gln | Ser | Ile | Ala | Ser | Lys | Asp | Ala | Thr | Lys |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ser | Ser | Glu | Asp | Tyr | Gln | Asp | Ala | Asn | Ala | Asp | Leu | Gln | Asn | Ala | Tyr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asn | Asp | Ala | Val | Thr | Asn | Ala | Gly | Gly | Ile | Ile | Ser | Ala | Xaa | Asn | Asn |



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Glu | Met | Asn | Pro | Asp | Thr | Ile | Xaa | Gln | Lys | Ala | Ser | Gln | Val | Asn |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Ala | Lys | Ser | Ala | Leu | Xaa | Gly | Asp | Glu | Lys | Leu | Ala | Ala | Ala | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gln | Thr | Ala | Lys | Ser | Asp | Ile | Gly | Arg | Val | Thr | Asp | Leu | Asn | Asn | Ala |
| 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |     |
| Gln | Arg | Thr | Ala | Xaa | Asn | Ala | Glu | Val | Asp | Gln | Ala | Pro | Xaa | Leu | Ala |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Ala | Val | Thr | Ala | Ala | Lys | Asn | Lys | Ala | Thr | Ser | Leu | Asn | Thr | Ala | Met |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Gly | Asn | Val | Lys | His | Ala | Leu | Ala | Glu | Lys | Asp | Asn | Thr | Xaa | Arg | Ser |
|     | 195 |     |     |     |     |     | 200 |     |     |     | 205 |     |     |     |     |
| Val | Asn | Tyr | Thr | Asp | Ala | Asp | Gln | Pro | Xaa | Gln | Gln | Ala | Xaa | Asp | Thr |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Gly | Thr | Gln | Ala | Glu | Ala | Ile | Thr | Asn | Ala | Asn | Gly | Ser | Xaa | Ala |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Asn | Glu | Thr | Gln | Val | Gln | Ala | Ala | Leu | Asn | Gln | Leu | Asn | Gln | Ala | Lys |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| Asn | Asp | Leu | Glu | Trp | Val | Ile | Ile | Lys | Leu | Leu | Lys | Arg | Lys | Lys | Gln |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Gln | Asn | Val | His |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     | 275 |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Thr | Thr | Lys | Ala | Ala | Leu | His | Gly | Asp | Val | Lys | Leu | Gln | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Lys | Asp | His | Ala | Lys | Gln | Thr | Val | Ser | Gln | Leu | Ala | His | Leu | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Ala | Gln | Lys | His | Met | Glu | Asp | Thr | Leu | Ile | Asp | Ser | Glu | Thr | Thr |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Arg | Thr | Ala | Val | Lys | Gln | Asp | Leu | Thr | Glu | Val | Gln | Ala | Leu | Asp | Gln |
|     | 50  |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |     |
| Leu | Met | Asp | Ala | Leu | Gln | Gln | Ser | Ile | Ala | Asp | Lys | Asp | Ala | Thr | Arg |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Ser | Ser | Ala | Tyr | Val | Asn | Ala | Glu | Pro | Asn | Lys | Lys | Gln | Ala | Tyr |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| Asp | Glu | Ala | Val | Gln | Asn | Ala | Glu | Ser | Ile | Ile | Ala | Gly | Leu | Asn | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Thr | Ile | Asn | Lys | Gly | Asn | Val | Ser | Ser | Ala | Thr | Gln | Ala | Val | Ile |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Ser | Ser | Lys | Asn | Ala | Leu | Asp | Gly | Val | Glu | Arg | Leu | Ala | Gln | Asp | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Gln | Thr | Ala | Gly | Asn | Ser | Leu | Asn | His | Leu | Asp | Gln | Leu | Thr | Pro | Ala |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| Gln | Gln | Gln | Ala | Leu | Glu | Asn | Gln | Ile | Asn | Asn | Ala | Thr | Thr | Arg | Asp |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| Lys | Val | Ala | Glu | Ile | Ile | Ala | Gln | Ala | Gln | Ala | Leu | Asn | Glu | Ala | Met |
|     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |     |
| Lys | Ala | Leu | Lys | Xaa | Ser | Ile | Lys | Asp | Gln | Pro | Gln | Thr | Glu | Ala | Ser |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 195 |     | 200 |     | 205 |     |     |     |     |     |     |     |     |     |     |
| Ser | Lys | Phe | Ile | Asn | Glu | Asp | Gln | Ala | Gln | Lys | Asp | Ala | Tyr | Thr | Gln |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Ala | Val | Gln | His | Ala | Arg | Arg | Cys | Leu | Xaa |     |     |     |     |     |     |
| 225 |     |     |     |     | 230 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ala | Glu | Ile | Ile | Ala | Gln | Ala | Gln | Ala | Leu | Asn | Glu | Ala | Met | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Leu | Lys | Glu | Ser | Ile | Lys | Asp | Gln | Pro | Gln | Thr | Glu | Ala | Ser | Ser |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Phe | Ile | Asn | Glu | Asp | Gln | Ala | Gln | Lys | Asp | Ala | Tyr | Thr | Gln | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Gln | His | Glu | Arg | Lys | Ile |     |     |     |     |     |     |     |     |     |
| 50  |     |     |     |     |     | 55  |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Val | Leu | Arg | Met | Ala | Ser | Asn | Met | Pro | Ser | Leu | Xaa | Lys | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Asn | Val | Glu | Met | Ile | Ala | Phe | Cys | Asp | Val | Asp | Ile | Ser | Lys | Ala |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ser | Ala | Ala | Glu | Ala | Tyr | Gly | Thr | Asp | Asn | Ala | Lys | Val | Tyr | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Tyr | Lys | Ala | Leu | Leu | Lys | Asp | Asp | Thr | Ile | Asp | Val | Ile | His | Val |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Cys | Thr | Pro | Asn | Asp | Ser | His | Cys | Glu | Ile | Thr | Val | Ala | Gly | Leu | His |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ala | Gly | Lys | His | Val | Met | Cys | Glu | Lys | Pro | Met | Ala | Lys | Thr | Thr | Ala |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Ala | Gln | Lys | Met | Ile | Asp | Thr | Ala | Lys | Ser | Thr | Gly | Lys | Lys | Leu |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Ile | Gly | Tyr | Gln | Asn | Arg | Phe | Arg | Pro | Asp | Ser | Gln | Phe | Leu | His |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Ala | Ala | Gln | Arg | Gly | Asp | Leu | Gly | Asp | Ile | Tyr | Phe | Gly | Lys | Ala |
|     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |     |     |
| His | Ala | Ile | Arg | Arg | Arg | Ala | Val | Pro | Thr | Trp | Gly | Val | Phe | Leu | Asn |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     | 160 |     |
| Glu | Glu | Ala | Gln | Gly | Gly | Gly | Pro | Leu | Ile | Asp | Ile | Gly | Thr | His | Ala |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |

Leu Asp Leu Thr Leu Trp Met Met Asp Asn Tyr Glu Pro Glu Ser Val  
                   180                  185                  190  
 Met Gly Ser Thr Phe His Lys Leu Asn Lys Gln His Asp Ala Pro Asn  
                   195                  200                  205  
 Ala Trp Gly Ser Trp Asn Pro Asp Glu Leu Thr Val Glu Asp Ser Ala  
                   210                  215                  220  
 Phe Gly Phe Ile Lys  
 225

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

Val Asp Glu Ala Lys Cys Ser Leu Leu Gly Thr Lys Ala Gly Ala Asp  
 1                  5                  10                  15  
 Met Lys Asp Val Leu Arg Ile His Gly Glu Asp Met Gly Thr Leu Tyr  
                   20                  25                  30  
 Thr Lys His Val Glu Xaa Glu Asn Lys Gly Val Asp Phe Tyr Glu Gly  
                   35                  40                  45  
 Asn Glu Val Asp Glu Ala Glu Glu Glu Xaa Lys Ala Trp Ile Asp Ala  
                   50                  55                  60  
 Val Val Asn Asp Thr Glu Pro Val Val Lys Pro Glu Gln Ala Met Val  
 65                  70                  75                  80  
 Val Thr Lys Ile Leu Glu Ala Ile Tyr Gln Ser Ala Lys Ser Gly Lys  
                   85                  90                  95  
 Ala Ile Tyr Phe Glu  
                   100

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

Val Asp Pro Pro Gly Cys Arg Asn Ser Thr Arg Thr Arg Ala Ala Phe  
 1                  5                  10                  15  
 Thr Val Ala Ser Ile Asp Leu Gly Ala His Pro Glu Phe Leu Gly Lys  
                   20                  25                  30  
 Asn Asp Ile Gln Leu Xaa Lys Lys Glu Ser Val Glu Asp Thr Xaa Lys  
                   35                  40                  45  
 Val Leu Gly Arg Met Phe Asp Gly Ile Glu Phe Lys Leu  
                   50                  55                  60

(2) INFORMATION FOR SEQ ID NO:522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

```

Val Ile Pro Asn Glu Phe Leu Lys His Ser Gly Lys Val His Ala Gln
 1 5 10 15
Ala Phe Phe Thr Gln Asn Gly Ser Asn Asn Val Val Val Glu Arg Gln
 20 25 30
Phe Ser Phe Asn Ile Glu Asn Asp Leu Val Ser Gly Xaa Asp Gly Ile
 35 40 45
Thr Lys Leu Val Tyr Ile Lys Ser Ile Gln Asp Thr Ile Glu Ala Val
 50 55 60
Gly Lys Asp Phe Asn Gln Leu Lys Gln Asn Met Ala Asp Thr Gln Thr
65 70 75 80
Leu Ile Ala Lys Val Asn Asp Ser Ala Thr Lys Gly Ile Gln Gln Ile
 85 90 95
Glu Ile Lys Gln Asn Glu Ala Ile Gln Ala Ile Thr Ala Thr Gln Thr
 100 105 110
Ser Ala Thr Gln Ala Val Thr Ala Glu Val Gly
 115 120

```

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

```

Val Met Asn Ile Ile Asn Leu Glu Lys Pro Lys Gly Val Val Val Gln
 1 5 10 15
Phe Gly Gly Gln Thr Ala Ile Asn Leu Ala Asp Lys Leu Ala Lys His
 20 25 30
Gly Val Lys Ile Leu Gly Thr Ser Leu Glu Asn Leu Asn Arg Ala Glu
 35 40 45
Asp Arg Lys Glu Phe Glu Ala Leu Leu Arg Lys Ile Asn Val Pro Gln
 50 55 60
Pro Gln Gly Lys Ser Ala Thr Ser Pro Glu Glu Ala Leu Ala Asn Ala
65 70 75 80
Ala Glu Ile Gly Tyr Pro Val Val Val Arg Pro Ser Tyr Val Leu Gly
 85 90 95
Gly Arg Ala Met Glu Ile Val Asp Asn Asp Lys Glu Leu Glu Asn Tyr
 100 105 110
Met Thr Gln Ala Val Lys Ala Ser Pro Glu His Pro Val Leu Val Asp
 115 120 125
Arg Tyr Leu Thr Gly Lys Glu Ile Glu Val Asp Ala Ile Cys Asp Gly
 130 135 140
Glu Thr Val Ile Ile Pro Gly Ile Met Glu His Ile Glu Arg Ala Gly
145 150 155 160
Val His Ser Gly Asp Ser Ile Ala Val Tyr Pro Pro Gln Thr Leu Thr
 165 170 175
Glu Asp Glu Leu Ala Thr Leu Glu Asp Tyr Thr Ile Lys Leu Ala Lys
 180 185 190

```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Leu | Asn | Ile | Ile | Gly | Leu | Ile | Asn | Ile | Gln | Phe | Val | Ile | Ala | His |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Asp | Gly | Val | Tyr | Cys | Phe | Arg | Ser | Lys | Pro | Thr | Val | Leu | Val | Glu | Arg |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Xaa | His | Ser | Arg | Ala |     |     |     |     |     |     |     |     |     |     |     |
| 225 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Phe | Met | Thr | Asn | Asn | Lys | Val | Ala | Leu | Val | Thr | Gly | Gly | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Gly | Ile | Gly | Phe | Lys | Ile | Ala | Glu | Arg | Leu | Val | Glu | Asp | Gly | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Val | Ala | Val | Val | Asp | Phe | Asn | Glu | Glu | Gly | Ala | Lys | Ala | Ala | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Lys | Leu | Ser | Ser | Asp | Gly | Thr | Lys | Ala | Ile | Ala | Ile | Lys | Ala | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Ser | Asn | Arg | Asp | Asp | Val | Phe | Asn | Ala | Val | Arg | Gln | Ala | Thr | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Ala | Ile | Trp | Arg | Phe | Pro | Cys | His | Gly |     |     |     |     |     |     |
|     |     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Arg | Ile | His | Tyr | Val | Asp | Ile | Ile | Met | Phe | Lys | Asp | Val | Val | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Trp | Glu | Val | Cys | Leu | Ile | Arg | Leu | Leu | Val | Ile | Lys | Val | Leu | Lys | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Ile | Phe | Ala | Arg | Ala | Lys | Phe | Glu | Lys | Glu | Tyr | Gly | Val | Lys | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Pro | Lys | Ala | Gly | Lys | Asp | Asn | His | Glu | Met | Val | Glu | Gly | Ile | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Gly | Glu | Val | His | Ser | Leu | Tyr | Leu | Tyr | Gly | Glu | Asp | Thr | Gly | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Asp | Ser | Asn | Ile | Asn | Phe | Val | Gln | Ala | Ala | Phe | Glu | Lys | Leu | Asp |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Phe | Met | Val | Val | Gln | Asp | Glu | Phe | Leu | Thr | Phe | Thr | Ala | Thr | Tyr | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| Asp | Val | Val | Leu | Pro | Ala | Ser | Pro | Ser | Leu | Glu | Lys | Asp | Gly | Thr | Phe |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Asn | Thr | Glu | Arg | Arg | Ile | Gln | Arg | Leu | Tyr | Gln | Ala | Leu | Glu | Pro |

|                     |                 |                 |             |     |  |
|---------------------|-----------------|-----------------|-------------|-----|--|
| 130                 |                 | 135             |             | 140 |  |
| Leu Gly Asp Ser Lys | Pro Asp Trp Lys | Ile Phe Gln Ala | Ile Ala Asn |     |  |
| 145                 | 150             | 155             | 160         |     |  |
| Arg Leu Gly Ile Trp | Ile Gly Ile Thr | Ser Ile Leu Val | Lys Leu Trp |     |  |
|                     | 165             | 170             | 175         |     |  |
| Ile Glu Gly Arg Thr | Leu Asn Thr Ser | Ile Cys Trp Gly | Lys Leu     |     |  |
|                     | 180             | 185             | 190         |     |  |

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Val Pro Ile Arg His Glu Arg Xaa Asp Lys Cys Glu Xaa Ile Met Tyr |  |
| 1 5 10 15                                                       |  |
| Ala Asp Asn Met Thr Asp Xaa Met Lys Tyr Ala Ile Asp Glu Thr Gln |  |
| 20 25 30                                                        |  |
| Arg Arg Arg Glu Ile Gln Met Lys His Asn Glu Lys His Gly Ile Thr |  |
| 35 40 45                                                        |  |
| Pro Lys Thr Ile Asn Lys Xaa Val His Asp Leu Ile Ser Ala Thr Val |  |
| 50 55 60                                                        |  |
| Glu Asn Asp Glu Asn Xaa Asp Xaa Ala Gln Thr Val Ile Pro Lys Lys |  |
| 65 70 75 80                                                     |  |
| Met Pro Lys Arg Ala Arg Xaa Lys Thr Ile Asp Asn Ile Glu Lys Glu |  |
| 85 90 95                                                        |  |
| Met Lys Gln Ala Ala Lys Asp Leu Asp Phe Glu Lys Ala Xaa Glu Leu |  |
| 100 105 110                                                     |  |
| Arg Asp Met Leu Phe Glu Leu Lys Ala Xaa Gly                     |  |
| 115 120                                                         |  |

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Val Xaa Ala Asn Glu Ile Xaa Lys Xaa Lys Ile Asp Ala Asn Lys Asp |  |
| 1 5 10 15                                                       |  |
| Val Asp Lys Gln Val Gln Ala Leu Ile Asp Glu Ile Asp Arg Asn Pro |  |
| 20 25 30                                                        |  |
| Asn Leu Thr Asp Lys Glu Lys Gln Ala Leu Lys Arg Ser Tyr         |  |
| 35 40 45                                                        |  |

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Glu | Phe | Asn | Glu | Ile | Ile | Ile | Ala | Thr | Pro | Ala | Gln | Trp | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | His | Thr | Gln | Asp | Ile | Leu | Lys | Lys | Tyr | Asn | Ile | Thr | Asp | Gln | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Lys | Val | Val | Ala | Gly | Gly | Xaa | Asp | Arg | Asn | Glu | Thr | Ile | Met | Asn |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Ile | Asp | His | Ile | Arg | Asn | Val | Asn | Gly | Ile | Asn | Asn | Asp | Asp | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ile | Val | Thr | His | Asp | Ala | Val | Arg | Pro | Phe | Leu | Thr | Gln | Arg | Ile | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Lys | Glu | Asn | Ile | Glu | Val | Ala | Xaa | Xaa | Tyr | Gly | Ala | Val | Asp | Thr | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Glu | Ala | Ile | Asp | Thr | Ile | Val | Met | Ser | Lys | Asp | Lys | Gln | Asn | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| His | Ser | Ile | Pro | Val | Arg | Asn | Glu | Met | Tyr | Gln | Gly | Gln | Thr | Pro | Gln |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Phe | Asn | Ile | Lys | Leu | Leu | Gln | Asp | Ser | Tyr | Arg | Ala | Leu | Ser | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Pro | Xaa | Arg | Asn | Leu | Ile | Arg | Cys | Met |     |     |     |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Phe | Thr | Ser | Asp | Ser | Arg | Pro | Thr | Met | Ser | Gly | Asn | Phe | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Ile | Tyr | Asn | Glu | Met | Leu | Arg | Gln | Asn | Leu | Asp | Lys | Lys | Tyr | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | His | Thr | Val | Phe | Lys | Ala | Asn | Ile | Thr | Asp | Arg | Arg | Gly | Ile | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asp | Lys | Phe | Arg | Leu | Pro | Tyr | Leu | Leu | Gly | Lys | Ala | Asp | Tyr | Ile | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Asp | Asp | Phe | His | Pro | Leu | Ile | Tyr | Thr | Val | Arg | Phe | Arg | Arg | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Gln | Glu | Val | Ile | Gln | Val | Trp | His | Ala | Val | Gly | Ala | Phe | Lys | Thr | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Phe | Ser | Arg | Thr | Gly | Lys | Lys | Gly | Gly | Pro | Phe | Ile | Asp | Ser | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | His | Arg | Ser | Ser | Cys | Gln | Ser | Leu | Cys | Ile | Ile |     |     |     |     |
|     |     | 115 |     |     |     |     |     | 120 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Xaa | His | Ala | Val | Gly | Ala | Phe | Lys | Thr | Val | Gly | Phe | Ser | Arg | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Xaa | Lys | Gly | Gly | Pro | Phe | Ile | Asp | Ser | Leu | Lys | Pro | Ile | Val | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Pro | Lys | Ala | Tyr | Val | Ser | Ser | Glu | Thr | Arg | Tyr | Ser | Ile | Leu | Cys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Tyr | Phe | Asp | Leu | Gly | Lys | Thr | Ser | Gly | Ser | Gly | Thr | Asn | Ala | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Val | Thr | Ile | Thr | Lys | Ile | Met | Gly | Trp | Lys |     |     |     |     |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Glu | Ile | Met | Lys | Ile | Thr | Val | Asn | Asp | Lys | Asn | Glu | Val | Ile | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Val | Asn | Thr | Gly | Gly | Leu | Arg | Asn | Ser | Leu | Asp | Val | Asp | Asp | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Val | Pro | Ile | Lys | Phe | Lys | Glu | Glu | Phe | Glu | Pro | Arg | Lys | Phe | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Thr | Asn | Gly | Glu | Ile | Lys | Tyr | Asn | Ser | Asn | Phe | Glu | Lys | Glu | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Val | Pro | Asn | Ala | Ser | Ser | Gln | Gln | Ser | Glu | Ser | Asp | Leu | Ser | Asp | Glu |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Glu | Leu | Arg | Gly | Met | Val | Ala | Ser | Met | Gln | Met | Gln | Val | Ala | Gln | Val |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asn | Val | Leu | Thr | Met | Glu | Leu | Ala | Gln | Gln | Asn | Ala | Met | Leu | Thr | Gln |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Leu | Thr | Glu | Leu | Lys | Thr | Asn | Lys | Thr | Ser | Thr | Glu | Gly | Asp | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |



(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Arg | Gln | Leu | Ala | Gln | Ala | Lys | Lys | Lys | Ser | Thr | Ala | Lys | Lys | Lys | 1   | 5   | 10  | 15  |
| Thr | Ala | Ser | Lys | Lys | Arg | Thr | Asn | Ser | Arg | Lys | Lys | Lys | Asn | Asp | Asn | 20  | 25  | 30  |     |
| Pro | Ile | Arg | Tyr | Val | Ile | Ala | Ile | Leu | Val | Val | Val | Leu | Met | Val | Leu | 35  | 40  | 45  |     |
| Gly | Val | Phe | Gln | Leu | Gly | Ile | Ile | Gly | Arg | Leu | Ile | Asp | Ser | Phe | Phe | 50  | 55  | 60  |     |
| Asn | Tyr | Leu | Phe | Gly | Tyr | Ser | Arg | Tyr | Leu | Thr | Tyr | Ile | Leu | Val | Leu | 65  | 70  | 75  | 80  |
| Leu | Ala | Thr | Gly | Phe | Ile | Thr | Tyr | Ser | Lys | Arg | Ile | Pro | Lys | Thr | Arg | 85  | 90  | 95  |     |
| Arg | Thr | Ala | Gly | Ser | Ile | Val | Leu | Gln | Ile | Ala | Leu | Leu | Phe | Val | Ser | 100 | 105 | 110 |     |
| Gln | Leu | Val | Phe | His | Phe | Asn | Ser | Gly | Ile | Lys | Ala | Glu | Arg | Glu | Pro | 115 | 120 | 125 |     |
| Val | Leu | Ser | Tyr | Val | Tyr | Gln | Ser | Tyr | Gln | His | Ser | His | Phe | Pro | Asn | 130 | 135 | 140 |     |
| Phe | Gly | Gly | Gly | Val | Leu | Gly | Phe | Tyr | Leu | Leu | Glu | Leu | Ser | Val | Pro | 145 | 150 | 155 | 160 |
| Leu | Ile | Ser | Leu | Phe | Gly | Val | Cys | Ile | Ile | Thr | Ile | Leu | Leu | Leu | Cys | 165 | 170 | 175 |     |
| Ser | Ser | Val | Ile | Leu | Leu | Thr | Asn | His | Gln | His | Arg | Asp | Val | Ala | Lys | 180 | 185 | 190 |     |
| Val | Ala | Leu | Glu | Asn | Ile | Lys | Ala | Trp | Phe | Gly | Ser | Phe | Asn | Glu | Lys | 195 | 200 | 205 |     |
| Met | Ser | Glu | Arg | Asn | Gln | Glu | Lys | Gln | Leu | Lys | Arg | Glu | Glu | Lys | Ala | 210 | 215 | 220 |     |
| Arg | Leu | Lys | Glu | Glu | Gln | Lys | Ala | Arg | Gln | Asn | Glu | Gln | Pro | Gln | Ile | 225 | 230 | 235 | 240 |
| Lys | Asp | Val | Ser | Asp | Phe | Thr | Glu | Val | Pro | Gln | Glu | Arg | Asp | Ile | Pro | 245 | 250 | 255 |     |
| Ile | Tyr | Gly | His | Thr | Glu | Asn | Glu | Ser | Lys | Ser | Gln | Cys | Gln | Pro | Ser | 260 | 265 | 270 |     |
| Arg | Lys | Lys | Arg | Val | Phe | Asp | Ala | Glu | Asn | Ser | Ser | Asn | Asn | Ile | Val | 275 | 280 | 285 |     |
| Asn | His | Gln | Ala | Asp | Gln | Gln | Gln | Leu | Thr | Glu | Gln | Thr | His | Asn |     | 290 | 295 | 300 |     |
| Ser | Val | Glu | Ser | Glu | Asn | Thr | Ile | Glu | Glu | Ala | Gly | Glu | Val | Thr | Asn | 305 | 310 | 315 | 320 |
| Val | Ser | Tyr | Val | Val | Pro | Pro | Leu | Thr | Leu | Leu | Asn | Gln | Pro | Ala | Lys | 325 | 330 | 335 |     |
| Gln | Lys | Ala | Thr | Ser | Lys | Ala | Glu | Val | Gln | Arg | Lys | Gly | Gln | Val | Pro | 340 | 345 | 350 |     |
| Lys | Arg | Tyr | Xaa | Lys | Arg | Phe | Trp | Gly | Xaa | Ile | Xaa | Lys | Xaa | Thr | Gln | 355 | 360 | 365 |     |
| Xaa | Lys | Leu | Ser | Xaa | Ser | Asn | Ser | Ile |     |     |     |     |     |     |     | 370 | 375 |     |     |

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Met | Thr | Glu | Glu | Xaa | Cys | Leu | Leu | Lys | Arg | Val | Phe | Met | Arg | Met |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Lys | Arg | Phe | Leu | Thr | Ile | Val | Gln | Ile | Leu | Leu | Val | Val | Ile | Ile | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Phe | Gly | Tyr | Lys | Ile | Val | Gln | Thr | Tyr | Ile | Glu | Asp | Lys | Gln | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Ala | Xaa | Tyr | Glu | Lys | Leu | Gln | Xaa | Lys | Phe | Xaa | Met | Leu | Met | Xaa |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | His | Gln | Glu | His | Val | Arg | Pro | Gln | Phe | Glu | Ser | Leu | Glu | Lys | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Asn | Lys | Asp | Ile | Val | Gly | Trp | Ile | Lys | Leu | Ser | Gly | Thr | Ser | Leu | Xaa |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Tyr | Pro | Val | Leu | Gln | Gly | Lys | Thr | Asn | His | Asp | Tyr | Leu | Asn | Leu | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Glu | Arg | Glu | His | Arg | Arg | Lys | Gly | Ser | Ile | Phe | Met | Asp | Phe | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Glu | Leu | Xaa | Asn | Leu | Asn | His | Asn | Thr | Ile | Leu | Tyr | Gly | His | His |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Gly | Asp | Asn | Thr | Met | Phe | Asp | Val | Leu | Glu | Asp | Tyr | Leu | Lys | Gln |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |     |
| Ser | Phe | Tyr | Glu | Lys | His | Lys | Ile | Ile | Gly | Phe | Asp | Asn | Lys | Tyr | Gly |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Lys | Tyr | Gln | Leu | Gln | Val | Phe | Ser | Ala | Tyr |     |     |     |     |     |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     |     |     |